

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT  
TEST-2 EXAMINATION APRIL 2016  
B.TECH.-VI SEMESTER

COURSE NAME: COMPARATIVE AND FUNCTIONAL GENOMICS  
COURSE CODE: 10B11BT611  
CREDIT: 04

MAX. MARKS: 25  
MAX TIME: 1.5 HRS

**Note: All questions are compulsory. Carrying mobiles during examination will be treated as a unfair means.**

1. Write down the important characteristics of DNA microarray that accounted the successfully method for whole genome expression profile? 2 marks
2. What is SNP? What is the frequency of SNP in human genome? How SNPs are introduced in the individual's genome? 2 marks
3. What is probe? Signify the use of probe in DNS microarray vs Southern blotting? 2 marks
4. What are the elements you look for to predict a gene from the given sequence? 2marks
5. Compare the number of genes/genome size in *E. coli* vs *S. cerevisiae*? 2marks
6. If you have given sets of gene expression data, how you are going to approach to represent the large scale gene expression data? 2 marks
7. How do we carry out normalization in DNA microarray data and why we need in the context of gene expression? Describe the equation to understand the pre-normalization data and post-normalization of DNA microarray data? 4 marks
8. What is SAGE? Give a descriptive approach of gene expression analysis method by sequencing? 4 marks
9. If you are given oligoarray of mouse genome, how do you proceed to identify genes that are responsible for lung Cancer in an induced mice model in comparison to normal mice? Use a diagram/flow chart if required? 5 marks