

## JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

## MID SEMESTER EXAMINATION-2015

M. Tech. 2<sup>nd</sup> Sem./ Ph.D.

COURSE CODE: 14M11BT213

MAX. MARKS: 30

COURSE NAME: FUNCTIONAL GENOMICS

COURSE CREDITS: 03

MAX. TIME: 2 HRS

Note:- All questions are compulsory

## Section A (Marks 6)

1. The genome of *S. cerevisiae* contains .... bases and .....of genes
2. What do you understand by SCAR
3. In eukaryotic gene the common splicing signal is.....
4. Draw well labeled structure of eukaryotic gene
5. Draw the structure of any fluorescently labeled nucleotide used in Sanger sequencing
6. In DNA microarray, Excitation and emission spectra of Cy3 dye is at ..... and at ..... respectively?

## Section B (Marks 9)

1. What is the size of human genome and approximate number of genes, calculate the gene density? What do you understand by the gene density number you get?
2. What are the characteristics of DNA Microarray? Explain cDNA-based and oligoarray-based Microarray? Explain why microarray has been a successful technique to study gene expression?
3. Define functional genomics is different from structural genomics? Discuss a technique in detail used to study the functional genomics of the given organism?

## Section C (Marks 15)

1. What do understand by solid phase sequencing by Illumina and pyrosequencing? Describe the steps with proper well labeled diagram? What are the different applications of next generation sequencing in functional genomics?
2. If you have been provided with oligoarray of mouse genome, how do you proceed to identify genes that are associated to lung cancer mice model in comparison to normal mice? Use diagram to explain if needed?
3. What is SAGE? Describe the methods and its application? Use diagram to explain if needed?