JAYPEE UNIVERSITY OF INFORMATRION TECHNOLOGY, WAKNAGHAT
MID SEMESTER EXAMINATION-2015
B. Tech. VIth Sem.

COURSE CODE: 10B11BT611

COURSE NAME: COMPARATIVE AND FUNCTIONAL GENOMICS

COURSE CREDITS: 04

MAX. MARKS: 30

MAX. TIME: 2 HRS

Note:- All questions are compulsory

Section A (Marks 6)

1. Gene Density of *S. cerevisiae* is greater than *Homo sapiens* (T/F)

2. The genome of *Homo sapiens* contains …. bases and …………of genes

3. What do you understand by VNTR

4. What are difference between RFLP and RAPD technique

5. SNP can be detected by …..and ……

6. ESTs are from coding region of the genome (T/F) and GSS are from non-coding region of the genome (T/F)

Section B (Marks 9)

1. The genome size of *S. cerevisiae* is 12 Mb and the approximately number of genes are 5990, calculate the gene density? What do you understand by the gene density number you get?

2. What are the characteristics of DNA Microarray? Explain with example where microarray can be best used?

3. Define functional genomics, describe one of the techniques in detail (e.g., SSR, RFLP, RAPD) used in functional genomics studies to compare the different organism?

Section C (Marks 15)

1. What do mean by solid phase sequencing by illumina? Describe the steps with proper well labeled diagram?

2. Explain, how Human genome is organized? Describe the methods/ approaches are being used to predict or annotate the genes from sequenced genome?

3. Describe the Pyrosequencing with reaction steps? Discuss the enzymes, their source and their role in it? What are the different applications of pyrosequencing?