JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

END SEMESTER EXAMINATION-2015

M. Tech II Semester/ Ph.D.

COURSE CODE: 14M11BT213   MAX. MARKS: 45

COURSE NAME: FUNCTIONAL GENOMICS

COURSE CREDITS: 3   MAX. TIME: 3 HRS

Note: *All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means.*

Section A (9 MARKS)

1. What is normalization that is commonly used microarray studies?
2. What do you mean by MA plot?
3. What is SNP? Write the importance of SNP analysis?
4. Define Multiplexing and where do you find its application
5. Name two protease inhibitors and the enzyme it acts on ? Why it is needed in proteomic studies?
6. Why different fluorescence dyes are used in DNA microarray, provide its excitation and emission spectra?
7. What are the important sequencing methods available to sequence whole genome of the organism? Write its principle?
8. Define pharmacogenomics? Why its study is important?
9. Draw the structure ATP?

Section B (13.5)

1. What are post-translational modification proteins? Explain with example why there is a need of modification of protein?
2. Why expression of genes is regulated? Explain a mechanism of gene expression regulation?
3. What are the characteristics of gene array? Explain the importance of cDNA-based and oligo-based array? What is your thought that why gene array studies have been very successful in recent years?

Section C (22.5)

1. Why protein-protein interaction studies are important? Give the example of protein-protein interaction studies that are being carried out in in-vivo model? Why in-vitro translation of protein is an important tool in proteomics studies?

2. If you are ask to generate the gene expression data from leaf, shoot and root from a medically important plant, describe the steps to gather the data? How do get the overall pattern of gene expression data that are specific to shoot? Can you compare the expression pattern of root, shoot and leaf together? How do present such data?

3. If you are provided with proteomic facility, how do you proceed to identify the differentially expressed proteins? Write the mechanism MALDI TOF to identity the peptide sequence? How do you assign the function of the amino acid sequence?

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