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JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

END SEMESTER EXAMINATION-2015

B.Tech VI Semester

COURSE CODE: 10B11BT611 MAX. MARKS: 45

COURSE NAME: COMPARATIVE AND 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. Draw a well of any fluorescently labeled nucleotide used in Sanger sequencing
2. What do you understand by haplotyping? Write the application?
3. What do mean by biomarker? Explain with example the application protein biomarker?
4. Draw the structure of Alanine?
5. Define Parallelism and where do you find its application?
6. Name two protease inhibitors? Why it is needed in proteomic studies?
7. Name the fluorescence dyes used in gene array, provide its excitation and emission spectra?
8. What are the important steps involved in prediction of protein function?
9. Define ESTs? Why its study is important in gene discovery?

Section B (13.5)

1. What is the size of *S. cerevisiae* genome and the approximate number of genes if contains? Calculate the gene density? What do you understand by gene density number you get?
2. How SNP of different from point mutation in a population? Describe methods to screen SNP? What do you mean by p-value <0.01?
3. What are post-translational modification proteins? Explain with example why there is a need of modification of proteins?

Section C (22.5)

1. What is micro-RNA and silencing-RNA? Explain the mechanism through which the expression of gene is regulated with the interference of small RNA? Give example of few micro-RNA that has been discovered in development process of organism?

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 given proteomic facilities, how do you proceed to identify the important proteins from the samples obtained from lung cancer patients? Explain how do come up with a protein biomarker?