

Reg. No

Name

18P420

M Sc DEGREE END SEMESTER EXAMINATION - MARCH 2018
SEMESTER 4 : BOTANY
COURSE : 16P4BOTT14; GENOMICS, PROTEOMICS AND BIOINFORMATICS
(For Regular - 2016 admission)

Time : Three Hours

Max. Marks: 75

Section A
Answer any 8 (2 marks each)

1. What is NGS? Give one example.
2. Discuss about the basic steps in genome sequencing.
3. How is the first generation sequencing differ from next generation sequencing?
4. Explain the significance of sequence alignment.
5. Differentiate Contigs and reads.
6. Write a short note on Chromatin immunoprecipitation (ChIP).
7. What is the significance of gene annotation in functional genomics?
8. Define gene order conservation.
9. Define synteny.
10. Describe a tool for multiple sequence alignment.
11. What is FASTA?
12. Write a short note on ORF search.

(2 x 8 = 16)

Section B
Answer any 7 (5 marks each)

13. Briefly discuss the techniques used for physical mapping of genome.
14. Discuss about dominant and co-dominant markers with suitable example.
15. How is a knock out is differ from knock down mutants?
16. Differentiate CHIP-seq over RNA-seq.
17. Distinguish between orthologs and paralog genes with examples.
18. Explain 2D gel electrophoresis.
19. Briefly describe the major types of databases which store molecular biology information.
20. Compare Local and global alignment
21. Briefly explain the salient features of RASMOL.
22. Descibe the construction of phylogenetic tree in MEGA.

(5 x 7 = 35)

Section C
Answer any 2 (12 marks each)

23. Discuss the various techniques employed for sequencing of DNA.

24. Discuss the methods used for studying the function of a gene.
25. Explain the structure of a gene and mention the tools used for gene prediction. How does it differ from RNA secondary structure prediction?

OR

26. Write an essay on various CADD methods and explain its practical implications.

(12 x 2 = 24)