

LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034

B.Sc. DEGREE EXAMINATION – COMP.SCIENCE.,COMP.APP.&PYSICS

FOURTH SEMESTER – APRIL 2010

PB 4208 - BIOINFORMATICS - II (GENOMICS & PROTEOMICS)

Date & Time: 19/04/2010 / 9:00 - 12:00 Dept. No.

Max. : 100 Marks

PART A

(20 marks)

I Choose the best answer

(5 x 1 = 5)

1. Current estimate of the mouse transcriptome is _____ bases.
a) 39,000 b) 47,000 c) 30,000 d) 20,366
2. A prediction program, which offer models for introns and exons is_____.
a) FGENESH b) GENEMARK c) GENOMESCAN d) TWINSCAN
3. The total number of protein families identified is _____.
a) 58,000 b) 59,000 c) 60,000 d) 60,050
4. _____ pathway turns on or off the genes.
a) Metabolic b) Signaling c) Biological d) Gene regulation
5. Which of the following is the third step in phylogenetic analysis?
a) tree building b) alignment c) substitution d) evaluation

II State whether the following statements are True or False

(5 x 1 = 5)

6. Comparative based method is used in predicting genes.
7. Whole genome shotgun sequencing was developed by J.Craig and V.Smith.
8. Proteomics involves coordinated functioning of cellular proteins.
9. *H.influenzae* was sequenced in the year 1996.
10. Co-immunoprecipitation is a technique that uses antibody.

III Complete the following

(5 x 1 = 5)

11. Alu elements in the genome organization account for _____.
12. _____ database gives information on the 2D gel electrophoresis of proteins.
13. Discovery of exons and introns occurred in the year _____.
14. _____ method is based on physical and chemical properties of amino acid.
15. An example for phylogenetic analysis database is_____.

IV Answer in one or two sentences, each in about 50 words

(5 x 1 = 5)

16. Define reterotransposons.
17. What is promoter?
18. Define trGENE.
19. What is meant by A level in CATH?
20. Expand PAUP.

PART B

V Answer any FIVE of the following, each in about 350 words

(5 x 8 = 40)

21. Explain any one method to find genes in larger genomes.
22. Explain whole genome shotgun sequencing method.
23. Write notes on splice site and shotgun libraries.
24. Briefly explain glycosylation, phosphorylation and signal peptides.
25. Explain any two types of intermolecular interactions.
26. Define homology? Explain how it is used in phylogenetic studies.
27. List out the completed genome projects in animals.
28. What are biological pathways? Discuss the role of IT in studying the biological pathways.

PART C

VI Answer the following, each in about 1500 words

(2 x 20 = 40)

29. (a) Give a brief account of the genome structure. Add a note on gene prediction program.

OR

- (b). Explain the working principle and applications of DNA microarray.
30. (a) Define exons and introns. Explain the various tools used in their prediction.

OR

- (b) Draw a dynamic programming for the following sequences

ABCNJRQCLCRPM

AJCJNRCKCRBP
