O.C.

B 411

B.E./B.Tech. DEGREE EXAMINATION, NOVEMBER/DECEMBER 2005.

Sixth Semester

Industrial Biotechnology

IB 341 — BIO–INFORMATICS

Time : Three hours Maximum : 100 marks

Answer ALL questions.

PART A — (10 × 2 = 20 marks)

1. What protocol would you use to transfer data from one computer to the other?

2. Give two network protocols developed by IEEE and their descriptions.

3. Mention the criteria used in amino acid scoring matrices for sequence alignment.

4. What is meant by Gumbel extreme value distribution?

5. What is ASNI? Where it is used?

6. Write two database types, explain and give examples.

7. What is a phylogenetic tree? Mention three method of tree building.

8. Describe two methods of computational gene prediction.

9. Give two methods adopted by HGP for physical mapping and two salient findings of HGP.

10. What is the EM Algorithm.

PART B — (5 × 16 = 80 marks)

11. (i) What is Shotgun sequencing. (4)

(ii) Describe the steps used in SAGA for MSA. (10)

(iii) Give two iterative methods of Multiple Sequence Alignment. (2)

12. (a) (i) Explain Different Versions of BLAST Program. (6)

(ii) Explain the FASTA search method and what are the recommended steps for a FASTA search. (10)

Or

(b) Abbreviate and give the salient points of the following BLAST related programs : (4 × 4 = 16)

(i) BEAUTY

(ii) PHI–BLAST

(iii) PROBE

(iv) PSI–BLAST

13. (a) (i) Explain the concept of maximum parsimony method of tree building with example. (10)

(ii) Write three programs that perform parsimony analysis for DNA and protein. (6)

Or

(b) Construct a phylogenetic tree using the UPGMA method. (16)

	OTU			
OTU	A	B	C	D
B	3			
C	8	7		
D	7	6	3	
E	11	16	13	12

14. (a) Explain how DP is exploited in the Gene Parser program to predict exons and introns. (16)

Or

(b) (i) How will you evaluate a gene prediction methods. (8)

(ii) Explain HMM method of gene prediction in bacterial genomes. (8)

15. (a) Explain the following : (4 × 4 = 16)

(i) Gap penalties

(ii) Dayhoffs PAM matrix

(iii) BLOSUM

(iv) Log odd score.

Or

(b) (i) Write two sequence databases and explain the database formats. (6)

(ii) Explain the three steps in Dynamic programming and how will you align a pair of sequence using DP. (10)
