

M.TECH.DEGREE EXAMINATIONS: MAY / JUNE 2010

Second Semester

BIOTECHNOLOGY

BTY508: Computational Biology

Time: Three hours

Maximum Marks: 100

Answer All Questions:

PART A (10 x 2 = 20 Marks)

1. Give a short note on the Transmission Control Protocol
2. Define a RAM
3. What is stringency in a dot plot analysis?
4. Assume that you used the NCBI Blast server to look for a match to a fruit-fly gene. Suppose further that the best alignment contained this section of an alignment:

Hit from database: XXXXXXXXXXXXXXXNFSTSQ

User sequence: SLEAEAAPASISPSNFSSSQ

What do the Xs signify?

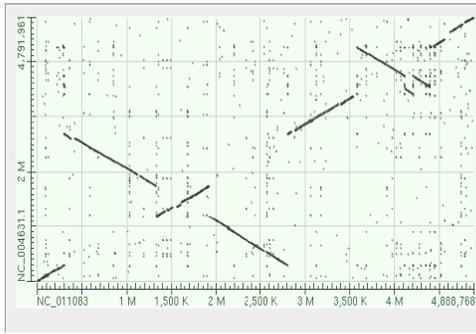
5. Define SAGA
6. What is new molecular clock theory?
7. What is GOR?
8. What is 6th order HMM?
9. Define a microarray
10. List the UNIX commands for printing and for renaming a file?

PART B (5 x 16 = 80 Marks)

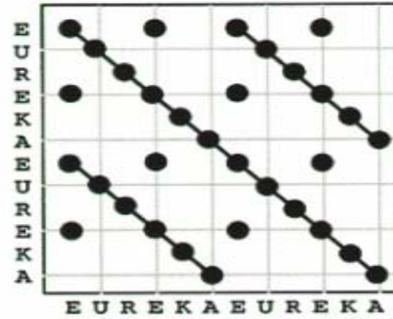
11. (a) (i) Describe in brief the various applications of bioinformatics. (4)
(ii) Describe in detail the various Network protocols and network media with salient features and advantages. (12)

(OR)

- (b) Elaborate in detail the various network topology with its advantages and limitations.
12. (a) (i) Using a gap penalty of -2, match as +2 and mismatch as 0, find the best alignment of two sequences, AWAP and APP using a Needleman-Wunsch dynamic programming approach. Show your working (i.e., draw and fill in the S-W matrix). (10)
(ii) Analyze the given below dot plot analysis and interpret the results. (6)



(A)



(B)

(OR)

(b) Explain in brief the algorithm of NCBI-BLAST and add a note on its families.

13. (a) Write a note on the following multiple alignment techniques:

(i) CLUSTAL-W (8)

(ii) PILEUP and SP method (8)

(OR)

(b) Comment on the following distance based phylogenetic analysis:

(i) UPGMA (8)

(ii) Fitch-Margoliasch method (8)

14. (a) Describe the Protein secondary structure prediction algorithms and software tools?

(OR)

(b) Write short notes on:

(i) Significance of HMM (8)

(ii) Prokaryotic gene finding (4)

(iii) Decision trees (4)

15. (a) Explain five reasons why PERL is a good tool for sequence manipulation. Describe the PERL programming language with emphasis on variables, data types, arrays, and hashes with one example for each type.

(OR)

(b) (i) Explain the concept of system biology? (6)

(ii) Explain in detail the micro array technology and its applications. (10)
