

B.TECH DEGREE EXAMINATIONS: NOV/DEC 2010

Fifth Semester

BIOTECHNOLOGY

U07BT506: Bioinformatics

Time: Three Hours

Maximum Marks : 100

Answer ALL Questions:-

PART A (10 x 1= 10 Marks)

1. The name of connection oriented protocol is
 - a) UDP
 - b) TCP
 - c) FTP
 - d) IIP
2. Topology used in LAN is
 - a) Star topology
 - b) Bus topology
 - c) Tree topology
 - d) Ring topology
3. MAML stands for
 - a) Macro array markup language
 - b) Micro array markup language
 - c) Mini array markup language
 - d) Max array markup language
4. The purpose of the database is to facilitate the
 - a) Concept of data
 - b) Analog of data
 - c) Management of data
 - d) Comparison of data
5. Multiple sequence alignment is the
 - a) Easy method
 - b) Comparative method
 - c) Different method
 - d) Unpredictable method
6. Clustal X can be obtained from the following website is
 - a) [www.ebi.ac.uk/ clustal X](http://www.ebi.ac.uk/clustalX)
 - b) [www.ecbi.ac.uk/ clustal X](http://www.ecbi.ac.uk/clustalX)
 - c) [www.ncbi.ac.uk/ clustal X](http://www.ncbi.ac.uk/clustalX)
 - d) [www.ncbi.ac.us/ clustal X](http://www.ncbi.ac.us/clustalX)
7. UPGMA stands for
 - a) Unweighted pair group method using arithmetic mean
 - b) Unweighted pair group method using average
 - c) Unchanged pair group method using arithmetic mean
 - d) Unchanged pair group method using average
8. Neighbour- joining method is very similar to
 - a) Distance matrix method
 - b) Fitch- margoliash method
 - c) Character based method
 - d) Maximum parsimony method
9. Micro array analysis method is used to examine the

- a) mRNA b) tRNA c) rRNA d) Both b & c
10. The result of collaboration between teams at the university of Liverpool and the University of Warwick is
- a) Cellular computing b) Biomolecular computing
- c) System biology computing d) Both a & c

PART B (10 x 2 = 20 Marks)

11. Define Telnet.
12. What is star bus?
13. Define database with suitable examples.
14. Comment on data entry unit.
15. Write a note on Smith- Waterman algorithm.
16. Differentiate between FASTA and BLASTA.
17. What are the different types of mutations?
18. Mention the steps in phylogenetic analysis.
19. What is cellular computing?
20. Define micro array analysis.

PART C (5 x 14 =70 Marks)

21. (a) Explain about the features of TCP / IP in detail.
(OR)
(b) Explain the following topology structure.
(i) Star topology
(ii) Ring topology
(iii) Bus topology
22. (a) Explain in detail about the database management system with suitable examples.
(OR)
(b) Give a detailed account on data lifecycle.
23. (a) (i) Define pattern matching. Write the applications in bioinformatics.
(ii) Explain pair wise sequence alignment.
(OR)
(b) (i) Describe dynamic programming.
(ii) Write a note on hidden Markov models.
24. (a) (i) What is meant by molecular clock hypothesis. Explain the importance of molecular phylogenetics.
(ii) Explain the methods for determining evolutionary trees with suitable examples.
(OR)
(b) (i) Comment on character based method.
(ii) Write down the classification of tree building methods.
25. (a) Give a brief account on biomolecular and cellular computing. **(OR)**
(b) Describe in detail about the scope of Bioinformatics in the present scenario. Mention the application of Bioinformatics in industry and research.
