Reg. No. : | | | | | | | | | | | |

T 3107

B.E./B.Tech. DEGREE EXAMINATION, APRIL/MAY 2008.

Sixth Semester

Biotechnology

BT 1351 — BIO INFORMATICS

(Regulation 2004)

Time : Three hours Maximum : 100 marks

Answer ALL questions.

PART A — ($10 \times 2 = 20$ marks)

1. What are pointers and arrays? Mention their function.

2. What are the design objectives of websites?

3. What is meant by Object-oriented database technology?

4. Name protein structure databases and the tools available in them.

5. Discuss on the utility of PAM substitution matrix for membrane proteins.

6. What is Bayesian rule? Mention two alignment programs using this.

7. The assumption of molecular clock hypothesis. Can we accept it? Why?

8. What is sensitivity and selectivity of a database search? How to assess the results of a search program?

9. What is the role of Microarray in systems biology.

10. What is Kimura model of nucleotide substitution?

PART B — (5 × 16 = 80 marks)

11. (a) (i) Give some basic Unix commands to list and give the location of files and directories. And explain how to create, move, copy, and delete files using Unix commands. (8)

(ii) What is a network? Explain the ISO/OSI Reference Model for networking. (8)

Or

(b) (i) What is the difference between search engine and search directories? Give examples. (8)

(ii) How do search engines rank pages? And how Search Engine Optimization is carried out? (8)

12. (a) What is (i) SRS and (ii) RDBMS Explain their role in Data retrieval and Data management? (16)

Or

(b) (i) What are Interaction databases? Give examples of them at least two and their features and uses. (8)

(ii) What are the various types of protein databases? Which are the most important examples of these types? (8)

13. (a) (i) What are the various method of multiple sequence alignment? Give the programs under each category, what are the drawbacks of progressive alignment. (8)

(ii) Explain msa by genetic algorithm in SAGA. (8)

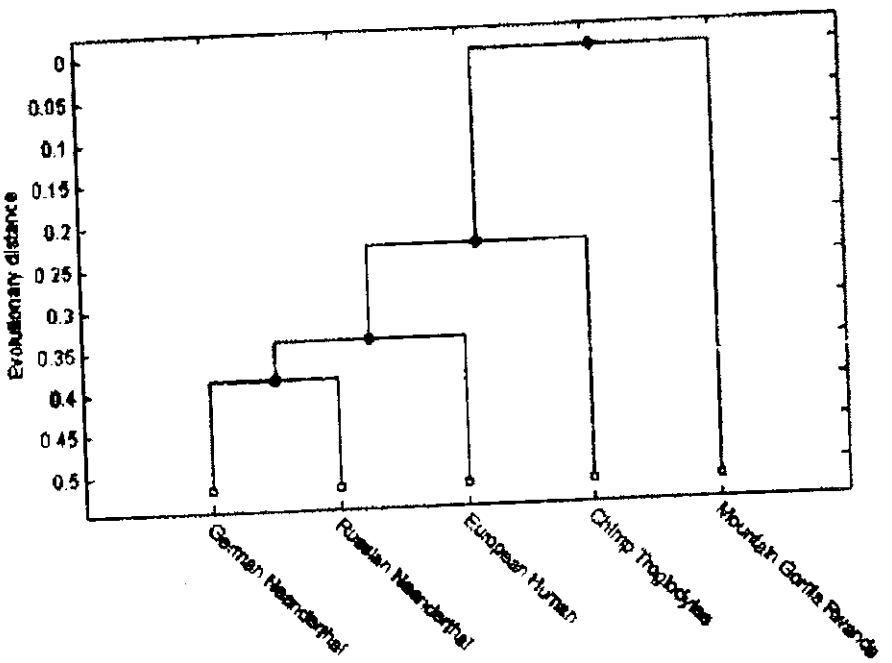
Or

(b) (i) What is sum of pairs how it is calculated? (8)

(ii) Explain the Clustal W algorithm for msa. (8)

14. (a) (i) Why is an outgroup included in a phylogeny? (8)

(ii) Interpret the following phylogenetic tree. (8)



Or

(b) (i) Compare maximum likelihood and Maximum parimony and Distance methods of phylogeny construction principles. (8)

(ii) What is bootstrap analysis? (8)

15. (a) Compare (i) Oligomer array and (ii) cDNA array construction and data analysis with reference to their application. (16)

Or

(b) (i) What is an E-Cell? (8)

(ii) Write its relevance to biomolecular and cellular computing. (8)