Roll No. | | | | | | | | | | |

B.E / B.Tech (Full Time) DEGREE END SEMESTER EXAMINATIONS, APRIL / MAY 2014

INFORMATION TECHNOLOGY

Eighth Semester

CS9044 BIOINFORMATICS

(Regulation 2008)

Time: 3 Hours | Answer ALL Questions | Max. Marks 100

PART-A (10 x 2 = 20 Marks)

1. How is protein-protein interaction different from protein?
2. What is the data format used by the Protein Data Bank?
3. Draw the general structure of amino acid?
4. List the different views of biometrics data?
5. What are the three primary roles of Hidden Markov Modeling in biological sequence analysis?
6. List the steps involved in the short sequence identification?
7. What are the Transcription Factors (TF)?
8. All motifs are patterns, but not vice versa. Justify?
9. Specify the strategy of automatic gridding?
10. List three gene regulatory model?

Part – B (5 x 16 = 80 marks)

11. (i) Explain the process involved in the development of biological data integration system?(8)
    (ii) Describe the structural bioinformatics approach in drug discovery?(8)

12. a) (i) What are the major challenge in bioinformatics by predicting the structure and function of biosequences?(6)
    (ii) Explain the comparative modeling of protein structure prediction?(10)

    (OR)

    b) With suitable illustration explain the supervised learning networks and unsupervised learning neural networks. Differentiate the supervised learning networks and unsupervised learning neural networks?

13. a) (i) Explain the Viterbi algorithm for multiple alignment with a HMM example target sequence?(8)
    (ii) Discuss the principles and applications of molecular modeling?(8)

    (OR)

    b) Describe how you would build a Hidden Markov Model (HMM) to predict protein secondary structure?

14. a) (i) What is the central dogma of gene regulations? With suitable illustrations explain the central dogma of gene regulations in detail?(8)

(ii) Give an account on the various motif-finding methods and databases?(8)

(OR)

b) Write short notes on the following:
   (i) Two-dimensional portrait representation of DNA sequences(8)
   (ii) Chaos game representation of biological sequences(8)

15. a) (i) Explain the binary hierarchical clustering algorithm with a data flow diagram?(6)
   (ii) Compare and contrast hierarchical and partitional clustering technique?(10)

(OR)

b) Describe the Self-Splitting and Merging Competitive Learning Clustering framework?