

N.B. (1) All questions carry equal marks.

(2) Question No. 1 is compulsory.

(3) Answer any three out of the remaining five questions.

(4) Figures to the right indicate full marks.

(5) Illustrate answers with sketches wherever required.

1. Write Short Notes on

(a) Relational Databases

(b) Object Oriented Databases

(c) Hidden Markov Models

(d) NCBI

(20)

2. (a) Explain different types of protein structures.

(10)

(b) What is Ab-Initio modelling. Explain the steps involved in it.

(10)

3. (a) Explain Needleman and Wunsch algorithm in detail with an example.

(10)

(b) Differentiate between pairwise and multiple sequence alignments.

(05)

(c) What is Dot Matrix Alignment, explain with an example.

(05)

4. (a) Seq 1: ACTGATAT

Seq 2: TAGGACTA

Perform Smith-Waterman algorithm to get best alignment

(12)

(b) Discuss Chao Fasman Algorithm in detail

(08)

5. (a) What is Threading? Explain different steps involved in it

(08)

(b) Explain Homology Modelling and different steps involved in it.

(12)

6. (a) What are three major nucleotide databases. Explain any two in detail.

(12)

(b) What are flat file databases? Explain in detail with an example.

(08)