2 Bioinformatics (pl219)

(a) Describe Ruth Nussinov's algorithm on RNA folding and its complexity. Illustrate with one example.   [4 marks]

(b) Describe the neighbour joining algorithm for phylogenetic analysis and its complexity.   [5 marks]

(c) Hidden Markov models (HMM) are widely used in Bioinformatics.

  (i) Describe how to build an HMM to identify exons and introns in genome sequences.   [5 marks]

  (ii) Discuss how to assess the performance of an HMM to identify exons and introns in genome sequences.   [2 marks]

(d) Discuss the advantages and disadvantages of Leonard Adleman's approach to the travelling salesman problem with respect to the computational approach.
                                                                           [4 marks]