

COMPUTER SCIENCE TRIPOS Part II – 2019 – Paper 8

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]