Bioinformatics

(a) Discuss, with one example, the complexity of the Nussinov algorithm for RNA folding. [5 marks]

(b) In the context of algorithms on strings, what is the advantage of using spaced seeds in database search? [3 marks]

(c) Hidden Markov models (HMM) are used to identify genes in genome sequencing projects.

(i) Describe how you would build a hidden Markov model to identify genes in a genome sequence. [7 marks]

(ii) How would you assess the sensitivity and specificity performance of the HMM? [5 marks]