

## 2006 Paper 9 Question 13

### Bioinformatics

- (a) Hidden Markov models (HMM) are widely used in Bioinformatics.
- (i) In a HMM when would you use the Baum–Welch algorithm, and when the Viterbi algorithm, and why? Give biologically motivated examples. [8 marks]
  - (ii) Any machine learning model (such as a HMM) for protein secondary structure determination or gene finding relies on discovering characteristic statistical properties of protein sequences. Name a property (and justify your answer) that helps to localise (and distinguish) transmembrane segments and coils in a protein sequence, or exon/intron boundaries in a genomic region. [2 marks]
- (b) Discuss the complexity of an algorithm to reconstruct a genetic network from microarray perturbation data. [7 marks]
- (c) What is the difference in terms of connectivity between a scale-free network and a random network? Give biological examples of scale-free networks. [3 marks]