

COMPUTER SCIENCE TRIPOS Part II – 2017 – Paper 9

2 Bioinformatics (PL)

- (a) For problems involving hidden Markov models (HMM), when would you use the Baum-Welsh algorithm and when the Viterbi algorithm and why? [6 marks]
- (b) Discuss how a sequence alignment might be evaluated statistically, illustrating your answer with an example. [6 marks]
- (c) What is the condition for fitting a phylogenetic tree to a matrix? [2 marks]
- (d) Discuss how to find matches in a genome sequence efficiently. [6 marks]