

COMPUTER SCIENCE TRIPOS Part II – 2016 – Paper 9

2 Bioinformatics (PL)

- (a) Explain the steps and the complexity of the Hirschberg algorithm and illustrate them with an example. [7 marks]
- (b) Give one example why the multiple alignment, as implemented in the software Clustal, needs a guide tree. [5 marks]
- (c) Explain what an amino acid exchange propensity matrix is and how you would construct it. [3 marks]
- (d) Explain with an example why a compression algorithm is often needed in genome assembly. [5 marks]