

COMPUTER SCIENCE TRIPOS Part II – 2016 – Paper 7

4 Bioinformatics (PL)

- (a) Explain the uses of Eulerian and Hamiltonian graphs in the context of genome assembly. [4 marks]
- (b) Discuss, giving an example, how to apply de Bruijn graphs to genome assembly. [6 marks]
- (c) Discuss how the choice of different K-mer length affects the accuracy of genome reconstruction. [3 marks]
- (d) Discuss the additive property in phylogeny. [3 marks]
- (e) Show one example of additive and one of non-additive matrices. [4 marks]