

COMPUTER SCIENCE TRIPOS Part II – 2019 – Paper 9

2 Bioinformatics (pl219)

- (a) Describe, with one example, the complexity of using dynamic programming in multiple alignment. [3 marks]
- (b) Describe the differences between genome assembly (i.e. using a reference genome) and genome de novo sequencing from a bioinformatics perspective. [5 marks]
- (c) The de Bruijn Graph is widely used in Bioinformatics.
- (i) Describe with one example how to construct the paired de Bruijn Graph. [5 marks]
- (ii) Describe the advantages of the paired de Bruijn Graph versus the non paired version of the de Bruijn Graph. [3 marks]
- (d) Discuss the advantages of using soft k-means versus hard clustering. [4 marks]