COMPUTER SCIENCE TRIPOS Part II – 2012 – Paper 9

1 Bioinformatics (PL)

(*a*) Considerable recent research has focused on *alignment of sequences.*

  (*i*) Why do we use dynamic programming algorithms for sequence alignment problems? [3 marks]

  (*ii*) Describe what needs to be taken into account for gaps in DNA sequence alignment. [3 marks]

(*b*) Considerable recent research has focused on sequence database search methods.

  (*i*) What are the most important differences between PatternHunter, BLAST, Smith-Waterman and Needleman-Wunsch algorithms? [9 marks]

  (*ii*) Compare the heuristic used by Clustal with a dynamic programming algorithm for multiple alignment. [5 marks]