

## 2007 Paper 12 Question 10

### Bioinformatics

- (a) Describe with *one* example the difference between Hamming and Edit distances. [2 marks]
- (b) Discuss the Smith–Waterman algorithm. What is the complexity and the relationship with the problem of finding the longest common subsequences? [5 marks]
- (c) Describe the Banded algorithm for local alignment and its complexity. [5 marks]
- (d) Describe the four Russian speedup algorithm. [8 marks]