2010 Paper 9 Question 3

Bioinformatics

(a) Discuss why the use of spaced seeds in sequence database search is better than the use of consecutive seeds.   [5 marks]

(b) Discuss the complexity of Sankoff's parsimony method.   [5 marks]

(c) Describe the four points conditions in phylogeny.   [5 marks]

(d) Discuss the assumptions of the Gillespie algorithms.   [5 marks]