

2006 Paper 8 Question 13

Bioinformatics

- (a) Why do we use dynamic programming algorithms for pairwise sequence alignment problems but not for multiple pairwise alignment? [5 marks]
- (b) Compare the use of the affine gap penalty with the constant gap penalty. [3 marks]
- (c) Discuss the properties and assumptions of the Jukes–Cantor and the Kimura 2-parameter models of DNA evolution. [5 marks]
- (d) Describe the UPGMA algorithm. [4 marks]
- (e) What does the ultrametric property of a tree tell us about the evolutionary process? [3 marks]