

2 Bioinformatics (pl219)

- (a) Calculate the dynamic programming matrix and one or more optimal alignment(s) for the sequences GAATTC and GATTA, scoring +2 for a match, −1 for a mismatch and with a linear gap penalty of $d = 2$. [5 marks]
- (b) Determine whether the RNA string GGACCACCAGG should be folded into two substructures. [7 marks]
- (c) Discuss how to carry out the multiple sequence alignment of the following three sequences: TTTTAAAA, AAAACCCC, CCCCTTTT. [4 marks]
- (d) Discuss which steps of the 1994 Adleman’s DNA computation approach would particularly affect the scalability of the number of the visited cities. [4 marks]