2 Bioinformatics (pl219)

(*a*) Describe the time and space complexity for finding the global alignment between two DNA sequences when they are very similar. [4 marks]

(*b*) Describe how match, mismatch and gap penalty (initiation and elongation) affect the score in global sequence alignment. [4 marks]

(*c*) Describe, with one example, how the number of mutations affects the phylogenetic analysis using the distance algorithm. [4 marks]

(*d*) Describe the differences in algorithmic complexity between the distance and parsimony phylogenetic methods. [4 marks]

(*e*) Describe why the Viterbi algorithm can help identify protein structural parts (alpha helix, beta sheet, coil) in a sequence of amino acids and describe how it works. [4 marks]