2 Bioinformatics (PL)

(a) Explain the steps and the complexity of the Hirschberg algorithm and illustrate them with an example. [7 marks]

(b) Give one example why the multiple alignment, as implemented in the software Clustal, needs a guide tree. [5 marks]

(c) Explain what an amino acid exchange propensity matrix is and how you would construct it. [3 marks]

(d) Explain with an example why a compression algorithm is often needed in genome assembly. [5 marks]