2 Biinformatics (PL)

(a) For problems involving hidden Markov models (HMM), when would you use the Baum-Welsh algorithm and when the Viterbi algorithm and why? [6 marks]

(b) Discuss how a sequence alignment might be evaluated statistically, illustrating your answer with an example. [6 marks]

(c) What is the condition for fitting a phylogenetic tree to a matrix? [2 marks]

(d) Discuss how to find matches in a genome sequence efficiently. [6 marks]