4 Bioinformatics (PL)

(a) Discuss the time and space complexity of dynamic programming algorithms in the context of sequence alignment problems. [6 marks]

(b) Describe the differences between Soft and Hard Clustering. [6 marks]

(c) Construct the de Bruijn graph of TACCTTCAGGCGCCTTC by splitting it into k-mers for a suitable value of $k$. Comment on how the choice of $k$ affects the construction. Discuss the use of de Bruijn graphs in the context of genome sequencing. [8 marks]