Bioinformatics

(a) Compute the global alignment between the two strings \( s_1 = \text{ACCGTT} \) and \( s_2 = \text{AGTTCA} \), considering the following scoring parameters: +1 for match, −1 for mismatch, and −1 for a gap.

(i) What is the maximum similarity score between the two sequences \( s_1 \) and \( s_2 \)? [2 marks]

(ii) Find an alignment with this similarity score. [2 marks]

(iii) Is the alignment you found unique, or are there multiple alignments achieving the maximum similarity score? [1 mark]

(b) Discuss the complexity of the Sankoff parsimony algorithm. [4 marks]

(c) Discuss the main differences between K-means, Superparamagnetic and Markov clustering algorithms. [7 marks]

(d) Discuss the utility of the Gillespie algorithm in system biology. [4 marks]