4 Bioinformatics (PL)

(a) Explain the uses of Eulerian and Hamiltonian graphs in the context of genome assembly. [4 marks]

(b) Discuss, giving an example, how to apply de Bruijn graphs to genome assembly. [6 marks]

(c) Discuss how the choice of different K-mer length affects the accuracy of genome reconstruction. [3 marks]

(d) Discuss the additive property in phylogeny. [3 marks]

(e) Show one example of additive and one of non-additive matrices. [4 marks]