COMPUTER SCIENCE TRIPOS Part II – 2013 – Paper 9

1 Bioinformatics (PL)

(*a*) What are the usage and the limitations of the Bootstrap technique in phylogeny?

[6 marks]

(*b*) We often use Hidden Markov Models (HMM) to predict a pattern (for instance the exons). How can you compute the number of True Positives, True Negatives, False Positives and False Negatives and use them to evaluate your HMM?

[6 marks]

(*c*) How can you evaluate the results obtained (number of clusters and their relative position) using the K means algorithm for clustering? [5 marks]

(*d*) What is the difference between the adjacency list and the accessibility list?

[3 marks]