**COMPUTER SCIENCE TRIPOS  Part II – 2014 – Paper 7**

## 3   Bioinformatics (PL)

(*a*)  Describe the differences in complexity and usage between parsimony and distance phylogenetic methods. Give an example of the usage of both methods.

[6 marks]

(*b*)  Describe the differences in complexity and usage between hierarchical clustering and the Markov clustering (MCL) algorithm.                      [5 marks]

(*c*)  Explain how to identify different gene features using Hidden Markov Model methods such as Genescan.                      [5 marks]

(*d*)  Explain how you could identify a regulatory network involving a set of genes.

[4 marks]