



**RAJARATA UNIVERSITY OF SRI LANKA  
FACULTY OF APPLIED SCIENCES**

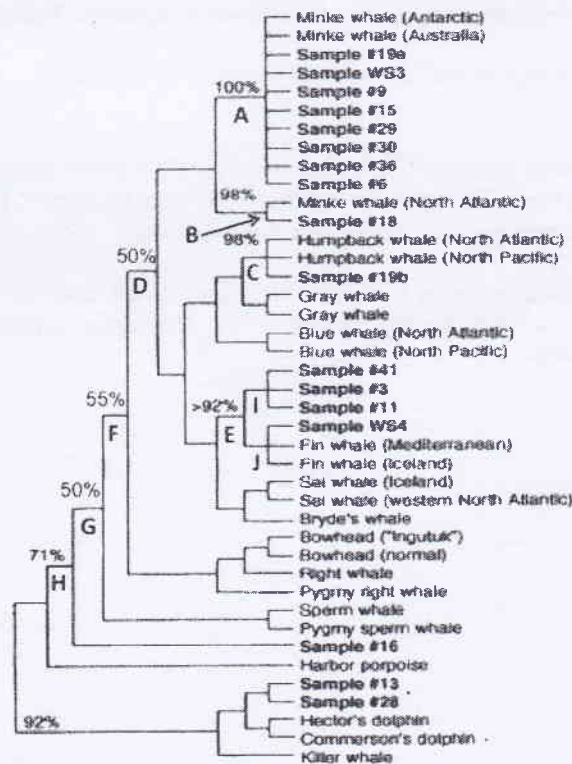
**B.Sc. (Special) Degree in Applied Biology  
Fourth Year – Semester I Examination – June/July 2018**

**MIB 4204 – BIOINFORMATICS**

**Time: Two (02) hours**

**Answer ALL questions.**

1. Hunting whales and the international trade of whale meat have been banned since 1986. However, countries like Japan continue to hunt whales for scientific purposes and sell their meat in the local market. The following is the maximum parsimony tree (from Baker & Palumbi, 1994) constructed to examine the identities and the geographic origin of whale meat in a Japanese market. The phylogeny has been constructed using DNA sequences of the mitochondrial control region with reference sequences of whales and dolphins and sequences generated from the meat samples.



- a) Write the most likely sequence of steps the scientists must have taken to construct this phylogeny. (15 marks)
- b) Based on the phylogeny what can you infer about the identity of samples #9, #15, #18, #19b and WS4. (20 marks)

- c) What would be the most likely geographic origin of sample '#18'? (5 marks)
  - d) What is meant by the numerical value with a percentage at certain nodes? (15 marks)
  - e) Name four nodes that you can have high confidence in. (20 marks)
  - f) What do you call the nodes labelled C, I and J and what is implied by these nodes? (10 marks)
  - g) State what is meant by the term 'maximum parsimony tree' and write two disadvantages of the parsimony method. (15 marks)
2. a) Explain advantages of using molecular data for phylogenetic studies. (30 marks)
- b) Explain why it is necessary to check E-values and query coverage in similarity searches even if there is a high score for a given alignment. (20 marks)
- c) Discuss why proteins could be considered better than DNA for similarity searches. (20 marks)
- d) Compare BLOSUM with PAM (30 marks)
3. a) Indicate the basic steps in comparative modelling of proteins. (20 marks)
- b) Illustrate the most commonly used transformations in structural alignment of proteins. (20 marks)
- c) Explain the drawbacks of using RMSD for evaluation of structural alignments (20 marks)
- d) Discuss how homology modelling could be useful to the industry. (40 marks)
4. a) A research group hypothesizes that human disease "Y" is due to a defect in the protein "A". This makes it difficult for it convert substrate "E" into products " B" and "C". Deduce a computational strategy to prove or disprove this hypothesis. (50 marks)
- b) A scientist claims that a variant of enzyme "X" converts substrate "D" into product "F" more efficiently than the commercially available "X". Design a computational procedure to authenticate the claim. (50 marks)

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