RAJARATA UNIVERSITY OF SRI LANKA
FACULTY OF APPLIED SCIENCES, MIHINTALE.

B.Sc. (4 year) Degree in ICT
Fourth Year – Semester I Examination – April/May 2015

ICT 4207 BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

Time: Two (2) hours

Answer all questions

1. Write short notes on
   a. Amino acid substitution matrices
   b. Use of primer designing tools instead of manual method for specific primer PCR
   c. Importance of query coverage and e value in homology search
   d. Bootstrapping

(25 X 4 marks)

2. a. Describe challenges for sequence analysis.

(25 Marks)

b. Explain what a paralog is and indicate why it may not be useful in homology search.

(25 Marks)

c. Explain how BLAST algorithm avoids time complexity.

(30 Marks)

d. Compare global alignment with local alignment.

(20 Marks)

3. a. Describe what is meant by multiple sequence alignment and discuss its applications

(50 Marks)

b The recent influenza outbreak in Sri Lanka was identified as due to infection caused by H1N1 virus. A group of scientists hypothesized that this is a new variant of the virus which originated in Sri Lanka. Using your knowledge in bioinformatics design a method to investigate the claim.

(50 Marks)

4. a. List major steps in comparative modeling and explain how they are carried out.

(25 Marks)

b. Explain the problems associated with using root mean square deviation (RMSD) when scoring an alignment.

(25 Marks)

c. Enzyme Z (only DNA sequence is available) is involved in a vital function of the human body. A group of scientists claims that a mutation in A makes it non functional and unable to bind with substrate X. Design a bioinformatics based solution to investigate this claim.

(50 Marks)

1