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

B.Sc. Degree in Applied Sciences
Fourth Year – Semester II Examination –September/October 2013

COM 4202 BIOINFORMATICS AND COMPUTATIONAL BIOLOGY (THEORY)

Time: Two (2) hours

Answer all (4) questions

1) Write short notes on

    a. Multiple sequence alignment
    b. BLAST
    c. BLOSUM matrix
    d. Bootstrapping   **(4X25 marks)**

2. a. A behavioral scientist working on wild cats observed that feces produced by one type of cats were full of seeds of a particular fruit. Since the fruit eating behavior by these cats was something not observed before, he wanted to identify the exact cat species from the feces he has collected. If this particular area is home for 5 types of wild cats, design a process to identify the fruit eating wild cat. **(60 marks)**

    b. Explain the advantages of molecular data in phylogenetic analysis. **(40 marks)**

3. a. A group of scientists claims that the herpes virus, one of the most devastating threats to elephants living in captivity, has never been recorded among captive elephants in Sri Lanka. Design a procedure to test this hypothesis. **(50 marks)**

    b. A research group has suggested that disease Y happens due to a mutation in gene D and this mutation causes malfunction of the protein so that it cannot convert amino acid phenylalanine to amino acid tyrosine. Develop a procedure to test their claim. **(50 marks)**

4. Explain the following.

    a. In sequence alignment algorithms it is customary to define gap penalties for gap opening and extension.

    b. The amino acid sequence derived from a eukaryotic DNA sequence using a translate algorithm would differ from the actual amino acid sequence.

    c. Filtering of certain sequences is a must in similarity search .

    d. When conducting a similarity search, for the same quarry, the output would differ based on the substitution matrix used. **(4X25 marks)**