RAJARATA UNIVERSITY OF SRI LANKA
FACULTY OF APPLIED SCIENCES

B.Sc. (Four-year) Degree in Applied Sciences
Fourth Year - Semester I Examination – September/October 2019

COM 4202 – Bioinformatics and Computational Biology

Time: THREE (03) hours

- **Answer FOUR (04) questions.**

1. Describe the three (03) major databases that are presented in the NCBI ENTREZ suite. What information does each contains? How can we find relevant data within these databases?

    (100 marks)

2. What is dynamic programming? How is it applied to pairwise alignment of sequences? What programs generally use dynamic programming?

    (100 marks)

3. Describe multiple sequence alignment. How is it performed? What information can be obtained from multiple alignments? Give examples.

    (100 marks)

4. Discuss the concept of homology (include various classes of homologues and how they arise). How to search for homologues of a particular nucleotide or amino acid sequence? How do we know we have identified a homologue in our search results?

    (100 marks)

5. Write short notes on the following DNA sequencing technologies. (in your answer, include a description on their operating principle, rapidity, operating cost, advantages and pitfalls)
    a. Sanger sequencing
    b. Ion-Torrent sequencing
    c. Illumina Sequencing
    d. Oxford Nanopore sequencing

    (100 marks)

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