



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

**B.Sc. (Four-year) Degree in Information and Communication Technology  
Fourth Year - Semester I Examination – September/October 2019**

**ICT 4307 – Bioinformatics and Computational Biology**

**Time: THREE (03) hours**

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• **Answer FOUR (04) questions.**

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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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