JARAMOGI OGINGA ODINGA UNIVERSITY OF SCIENCE & TECHNOLOGY

SCHOOL OF BIOLOGICAL AND PHYSICAL SCIENCES

UNIVERSITY EXAMINATION FOR THE DEGREE OF BACHELOR OF SCIENCE IN BIOLOGICAL SCIENCES

4th YEAR 1st SEMESTER 2018/2019 ACADEMIC YEAR

MAIN CAMPUS - REGULAR

COURSE CODE: SBI 3431

COURSE TITLE: **BIOINFORMATICS AND COMPUTATIONAL BIOLOGY**

EXAM VENUE: **STREAM:**

DATE: **EXAM SESSION:**

TIME: 2 HOURS

Instructions:

1. **Answer ALL questions in Section A and Any two questions in Section B**

2. **Candidates are advised not to write on question paper**

3. **Candidates must hand in their answer booklets to the invigilator while in the examination room**

SECTION A: SHORT ANSWER QUESTIONS (30 MARKS)

1. Define the term gene ontology. Identify two organizing principles of gene ontology? (3 Marks)
2. Biology is flooded with data that cannot be understood without bioinformatics computational tools. Identify three main sources of biological data. (3 Marks)
3. Describe three data retrieval systems that are of great relevance to a molecular biologist. (3 Marks)
4. Outline three major functions of National Center for Biotechnology information (3 Marks)
5. Consider the multiple alignment below of four nucleotide sequences. Use a method of maximum parsimony to deduce the most likely phylogenetic tree. (3 Marks)
   Human   GAACGGACTTCA
   Mouse   GAACGGACTTGA
   Frog   AACCGGGCTAGA
   Zebrafish   AATCGGCCTACA
6. Outline three advantages of evolutionary computation (3 Marks)
7. Identify three strengths of genetic algorithms (3Marks).
8. Distinguish among the terms protein domain, motif and family (3 Marks)
9. Below is the multiple sequence alignment of three sequences:
   seq1 IVFLGE
   seq2 LVLLGEAV
   seq3 LVLLGDSVG

	seq1	seq2	seq3
seq1			
seq2			
seq3			

   Suppose that a gap scores 1, a mismatch 1, and a match +2. Fill in the matrix with the pairwise scores. (3 marks)
10. Differentiate between Needleman-Wunsch and Smith-Waterman pairwise alignment methods (3 marks)

SECTION B: ESSAY QUESTIONS (40 MARKS)

11. Discuss the various molecular biology tasks that can be analyzed comprehensively using bioinformatics and computational biology (20 marks)
12. Discuss the two rapid alignment methods (FASTA and BLAST) and identify both advantages and disadvantages for each. (20 Marks)
13. Discuss dot matrix analysis plot method of pairwise sequence alignment. (20 Marks)
14. Discuss the process involved in shotgun sequencing and sequence assembly. (20 Marks)