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 (3 Marks)

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  

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)