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**JARAMOGI OGINGA ODINGA UNIVERSITY OF SCIENCE & TECHNOLOGY**

**SCHOOL OF BIOLOGICAL AND PHYSICAL SCIENCES**

**DEPARTMENT OF BIOLOGICAL SCIENCES**

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

**4th YEAR FIRST SEMESTER 2016/2017 ACADEMIC YEAR**

**MAIN CAMPUS - REGULAR**

**COURSE CODE: SBH 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. Describe three different kinds of DNA sequences (3 Marks)
2. Briefly distinguish the terms homologs, orthologs and paralogs. (3 Marks)
3. Outline three advantages of evolutionary computation (3 Marks)
4. Describe three hierarchical levels of protein structure (3Marks)
5. Explain what is meant by gene ontology. Identify two organizing principles

of gene ontology (3 Marks)

1. Define sequence alignment. Describe the difference between local and global alignment (3 Marks)
2. Consider the (pairwise) global alignments below resulting from the application of the algorithm Needleman-Wunsch to the sequences S1, S2 and S3 using the following scoring scheme: match=+2; mismatch=-1 and gap=-1. (3 Marks) 
3. Distinguish among protein domain, motif and family. (3 Marks)
4. Identify three databases available through Entrez (3 Marks)
5. Based on the data in the table shown below, **draw** a phylogenetic tree that reflects the evolutionary relationships of the organisms based on the differences in their cytochrome *c* amino-acid sequences and **explain** the relationships of the organisms. Based on the data, **identify** which organism is most closely related to the chicken and **explain** your choice. (3 Marks)



**SECTION B: ESSAY QUESTIONS (40 MARKS).**

1. Discuss the basic principle of shotgun genome sequencing, assembly and annotation.

 (20 Marks)

1. Describe the dot matrix analysis plot method of pairwise sequence alignment. (20Marks)
2. Discuss the use of computational biology and bioinformatics in functional genomics and proteomics. (20 Marks)
3. Describe the features and importance of NCBI (National Center for Biotechnology Information). (20 Marks)