LAIKIPIA UNIVERSITY

UNIVERSITY EXAMINATIONS

SECOND SEMESTER 2023/2024 ACADEMIC YEAR

FOURTH YEAR EXAMINATION FOR THE DEGREE BACHELOR OF SCIENCE IN BIOCHEMISTRY

BIOC 424: INTRODUCTORY BIOINFORMATICS AND SYSTEMS BIOLOGY

STREAM: ***BIOCHEMISTRY*** ***TIME: 2 HRS***

DAY: TUESDAY [8.30A.M – 10.30A.M] ***DATE: 16/04/2024***

THIS QUESTION PAPER CONSISTS OF THREE (3) PAGES

PLEASE DO NOT OPEN UNTIL THE INVIGILATOR SAYS SO.

INSTRUCTIONS
Answer all questions in section A and only one in section B

SECTION A : Answer ALL questions (50 Marks)

QUESTION ONE

Highlight databases most commonly used for molecular analyses **(10 Marks)**

QUESTION TWO

a) Define the term algorithm **(2 Marks)**

b) Differentiate between local and global alignment **(4 Marks)**

c) Describe basic approaches for choosing an algorithm for analyzing biological datasets for genome assembly **(4 Marks)**

QUESTION THREE

a) Differentiate between Fasta and Fastq file **(3 Marks)**

b) Write an R script reading fasta/fastq sequence and determining the nucleotide base composition **(7 Marks)**

QUESTION FOUR
Discuss the steps that can be used to model a JAK- STAT signaling cascade **(10 Marks)**

QUESTION FIVE

Supposing you have genotyped elephant populations from various parts of Kenya using microsatellites, describe the various bioinformatic tools that you can use to analyze this data **(10 Marks)**

SECTION B: ANSWER ONLY ONE QUESTION (20 MARKS)

QUESTION SIX

Supposing you are doing a functional analysis of a given protein, explain how you can predict:

a) whether it shuttles between the nucleus and cytoplas **(5 Marks)**

b) Whether it is regulated by phosphorylation, the potential regulatory sites and enzymes **(5 Marks)**

c) Supposing you want to design cloning primers, explain how you would do this **(10 Marks)**

QUESTION SEVEN

Supposing you are doing a functional analysis of a given protein, explain how you can predict:

a) Whether it is a secretory protein **(5 Marks)**

b) Whether it is an enzyme **(5 Marks)**

c) Describe the process of sequence deposition and retrivial from any database **(10 Marks)**