



WI-2-60-1-6

**JOMO KENYATTA UNIVERSITY OF AGRICULTURE AND TECHNOLOGY**  
**University Examinations 2024/2025**

**EXAMINATION FOR THE DEGREE OF MASTER OF SCIENCE IN MOLECULAR  
MEDICINE**

**TIM 3112: GENOMICS AND BIOINFORMATICS**

**DATE: DECEMBER, 2024**

**TIME: 3 HOURS**

**INSTRUCTIONS: Attempt any FOUR questions (25 Marks Each)**

**Question One**

- a) You have generated whole genome sequence data for a pathogen. Describe how you can identify single nucleotide polymorphisms and structural variants given the reference genome of this pathogen. [15 marks]
- b) Describe maximum likelihood method of phylogenetic tree construction. [10 marks]

**Question Two**

- a) Compare and contrast Kimura-2-parameter and Jukes Cantor (JC) models of nucleotide substitution. [10 marks]
- b) Discuss multiple sequence alignment and its application in identification of genetic variants. [15 marks]

**Question Three**

- a) Describe the process of primer design and evaluation for use in polymerase chain reaction (PCR). [10 marks]
- b) Explain how you can perform gene prediction in prokaryotes or eukaryotes using two different bioinformatics tools. [15 marks]

#### **Question Four**

- a) You have micro array data from 10 infected individuals and 4 uninfected individuals. The data constitutes gene expression values for 4 biomarkers for the disease: A,B,C and D. Explain how you can perform gene expression-analysis. [10 marks]
- b) Discuss BLAST homology search algorithm. [15 marks]

#### **Question Five**

- a) Discuss Structure Based Drug Design (SBDD) and its application in drug discovery. [15 marks]
- b) Describe the following DNA data formats. [10 marks]

- i) BAM
- ii) FASTQ
- iii) FASTA
- iv) Variant call file (VCF)

#### **Question Six**

Describe the following databases:

[25 marks]

- a) VEupathDB
- b) ENA
- c) UripotKB
- d) Ecocyc
- e) COSMIC