W1-2-60-1-6

JOMO KENYATTA UNIVERSITY OF AGRICULTURE AND TECHNOLOGY

UNIVERSITY EXAMINATIONS 2025/2026

TIM 3112

GENOMICS AND BIOINFORMATICS

SEMESTER II *(2025/2026):*

SUPPLEMENTARY

Instructions

(1) Answer any four (4) questions.

(2) All questions carry equal marks.

(3) Time allowed is 3 hours.

DATE: JUNE 2026

Question One (25 Marks)

a) Outline the major steps in analyzing raw sequencing data (FASTQ files) to detect virulence or resistance genes. Your explanation should include the roles of quality control, read trimming, genome assembly or mapping, and database searching. (20 marks)

b) List and briefly describe the role of any two software tools or environments commonly used in such workflows (e.g., Python, Bioconda, Shovill, Flye). (5 marks)

Question Two (25 Marks)

a) Outline the goals and key achievements of the Human Genome Project. (8 marks)

b) Discuss how projects such as 1000 Genomes, ENCODE, and H3Africa have advanced our understanding of global and African genomics. (10 marks)

c) Explain how African genetic diversity provides insights into human evolution and disease. (7 marks)

Question Three (25 Marks)

a) Explain the mechanism of CRISPR-Cas9 genome editing and compare it briefly with older tools such as ZFNs and TALENs. (10 marks)

b) Discuss two applications of genome editing in medicine and two in agriculture, using African examples where possible. (10 marks)

c) Identify one environmental application of metagenomics and explain its importance. (5 marks)

Question Four (25 Marks)

a) Compare Nanopore sequencing and Illumina sequencing in terms of their principles, speed, throughput, and accuracy. (15 marks)

b) Discuss the major applications, advantages, and limitations of each technology in research and diagnostics. (10 marks)

Question Five (25 Marks)

You are working with a large FASTA file generated from a sequencing project.

a) Explain how you would quickly estimate the total number of sequences present, highlighting what feature of the FASTA format makes this possible. (5 marks)

b) Outline the approach you would use to determine the shortest sequence in the file and why this information might be useful in downstream analysis. (10 marks)

c) Some sequences may contain a restriction enzyme recognition site such as "GAATTC" (EcoRI site). Describe how you would identify and extract only the sequences containing this motif. Give an appropriate example to illustrate your explanation. (10 marks)

Question Six (25 Marks)

a) Explain with examples how specific genomic variations (e.g., sickle cell, lactase persistence, skin pigmentation) illustrate human adaptation. (10 marks)

b) Discuss the role of genomics in outbreak surveillance and vaccine development, citing African examples. (10 marks)

c) Should African genomic data be shared internationally or retained locally? Provide two arguments for your position. (5 marks)