

ASSIGNMENT

QUESTION 1

-Define bioinformatics and explain its importance in biological research

Answer: Bioinformatics is defined as the use of computational tools and techniques to generate, store, access, analyze interpret biological data such as DNA, RNA and Protein.

- Provide two examples of how genomics and bioinformatics can be applied in your field, such as in healthcare, agriculture, or disease research.

Answer:

a) I am a Microbiologist and in my field, genomics and bioinformatics can be applied in microbial bioremediation.

With the use of genomics, I can identify and characterize microorganisms with capabilities to detoxify pollutants.

With bioinformatics, I can help analyze genomic data to discover metabolic pathways involved in biodegradation.

b) Secondly, in my field, genomics and bioinformatics can be applied in agricultural biotechnology

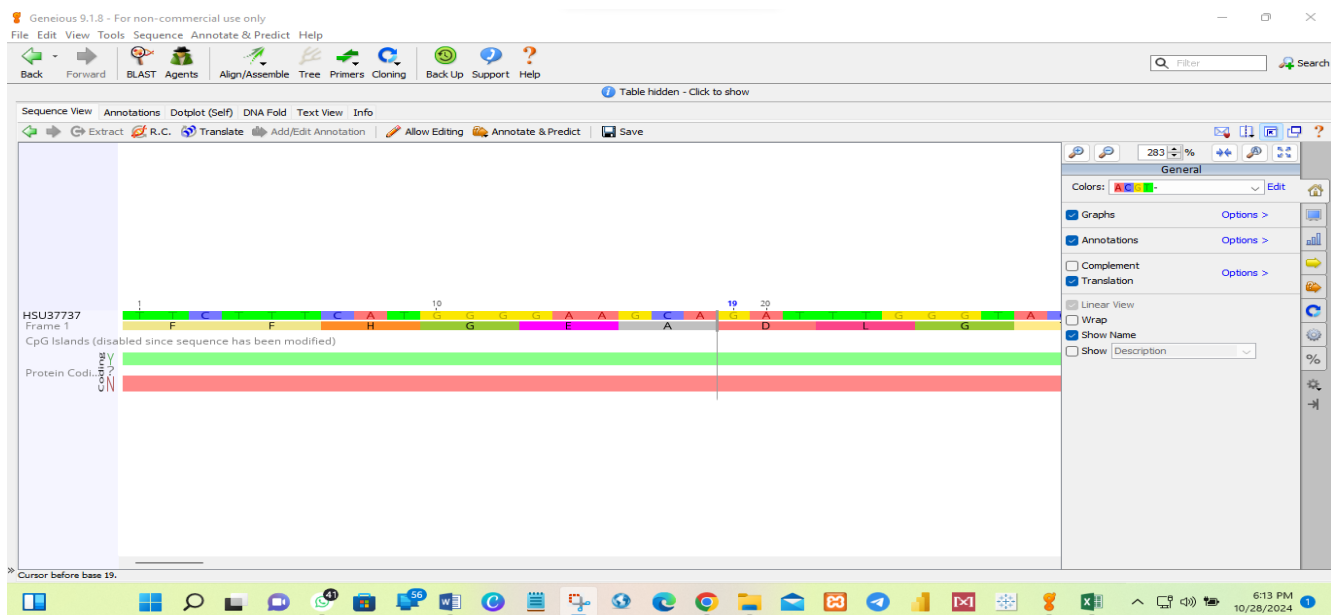
Through genome sequencing, microbiologists can identify and manipulate genes responsible for desirable traits in crops.

Bioinformatics can also be useful in identifying genes with special characteristics which will assist in the development of genetically modified organisms (GMOs) to create resilient and high-yielding varieties.

QUESTION 2

- Identify Codons

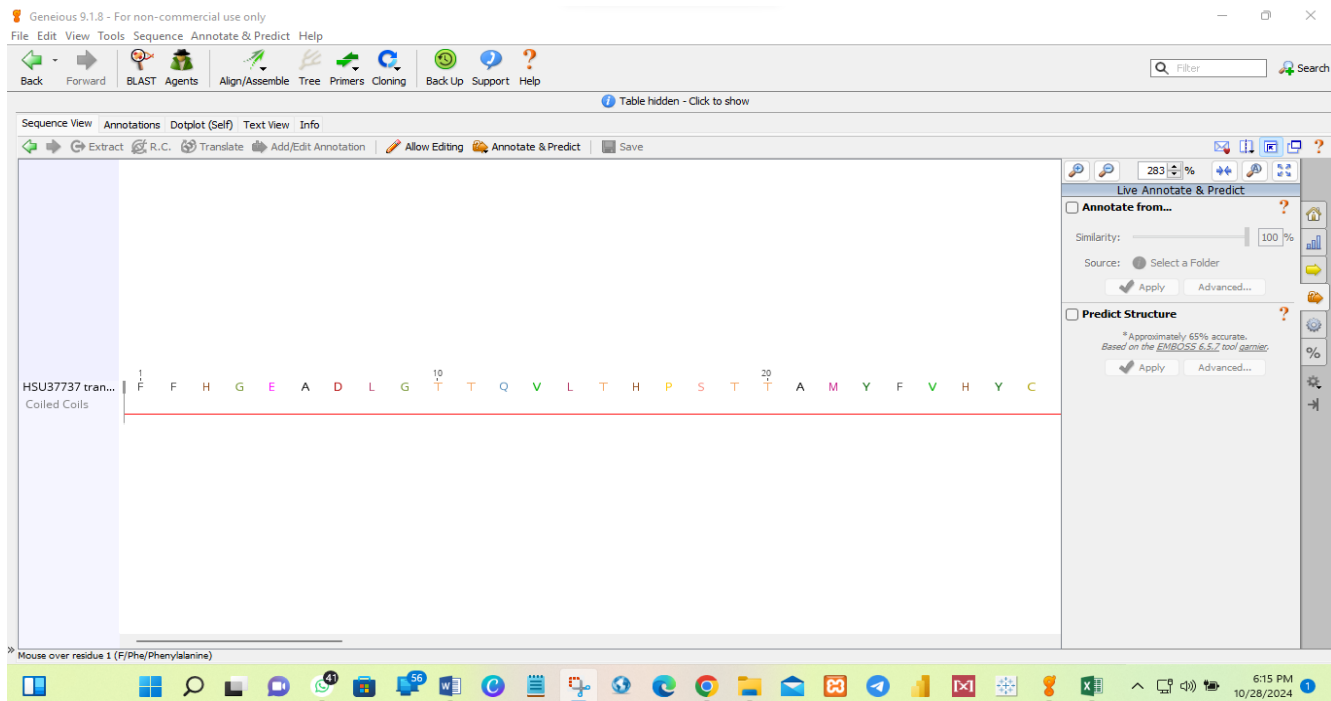
Codons are three nucleotide bases that code for an amino acid. To identify codons, I navigate the DNA sequence and change the colour. To identify these codons, translation must take place so I selected the translation icon to have a clearer vision of the codons.



- Translate sequence into proteins

Translation is the process by which RNA is converted to Protein.

To achieve this on Geneious software, I navigate the DNA sequence, and then select the sequence on the taskbar and then save in FASTA sequence/alignment format.

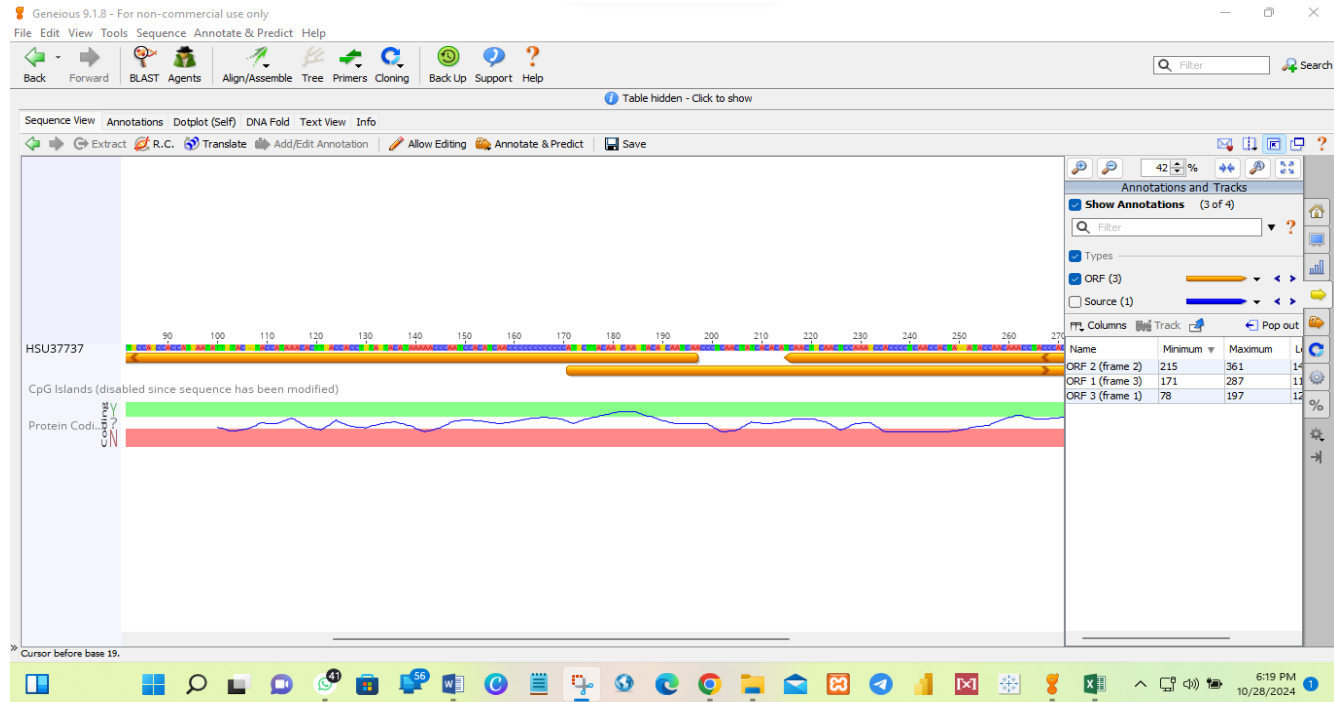


- **Predict Open Reading Frames (PRFs)**

Open Reading Frames allows you to identify regions that code for proteins in a sequence.

To achieve this, after the protein-coding icon is selected, the ORF is then selected and applied.

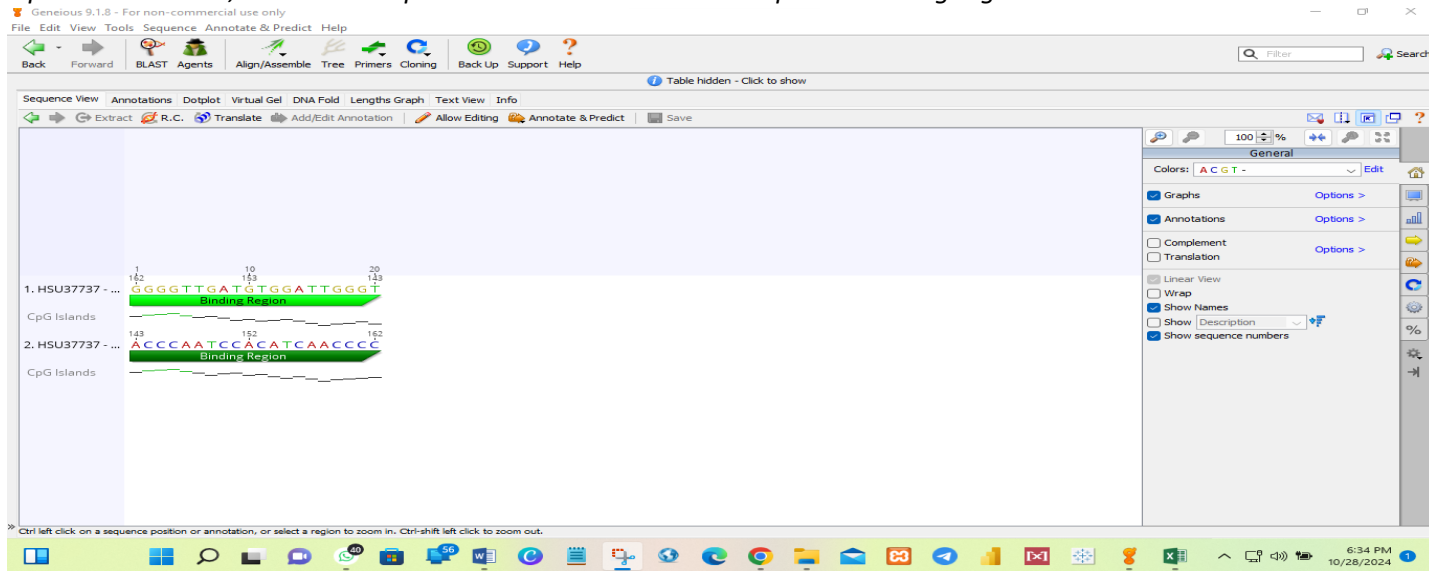
This then shows a clearer vision of the protein-coding regions.



- Design Primers

Primers are short strands of SNA sequence required to begin DNA synthesis.

To design a primer, the sequence is navigated and then the primer is selected on the taskbar. In selecting a primer to extract, I ensured the primer I extracted was under a protein-coding region

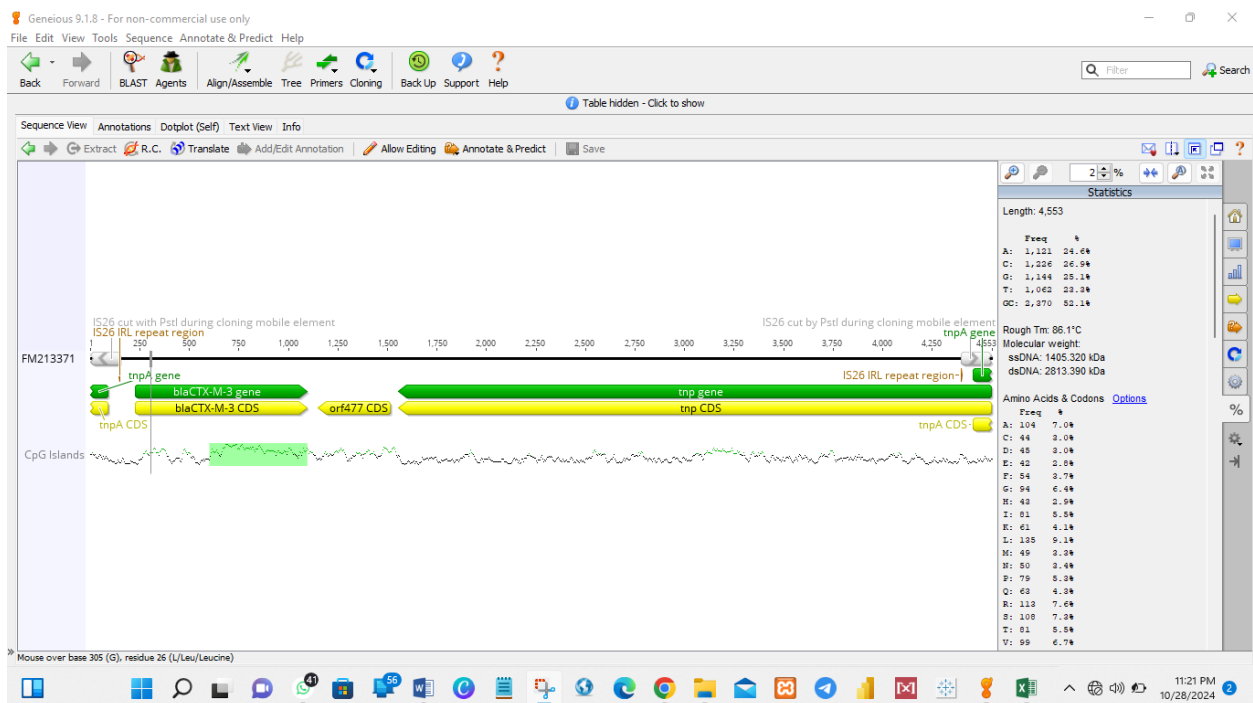
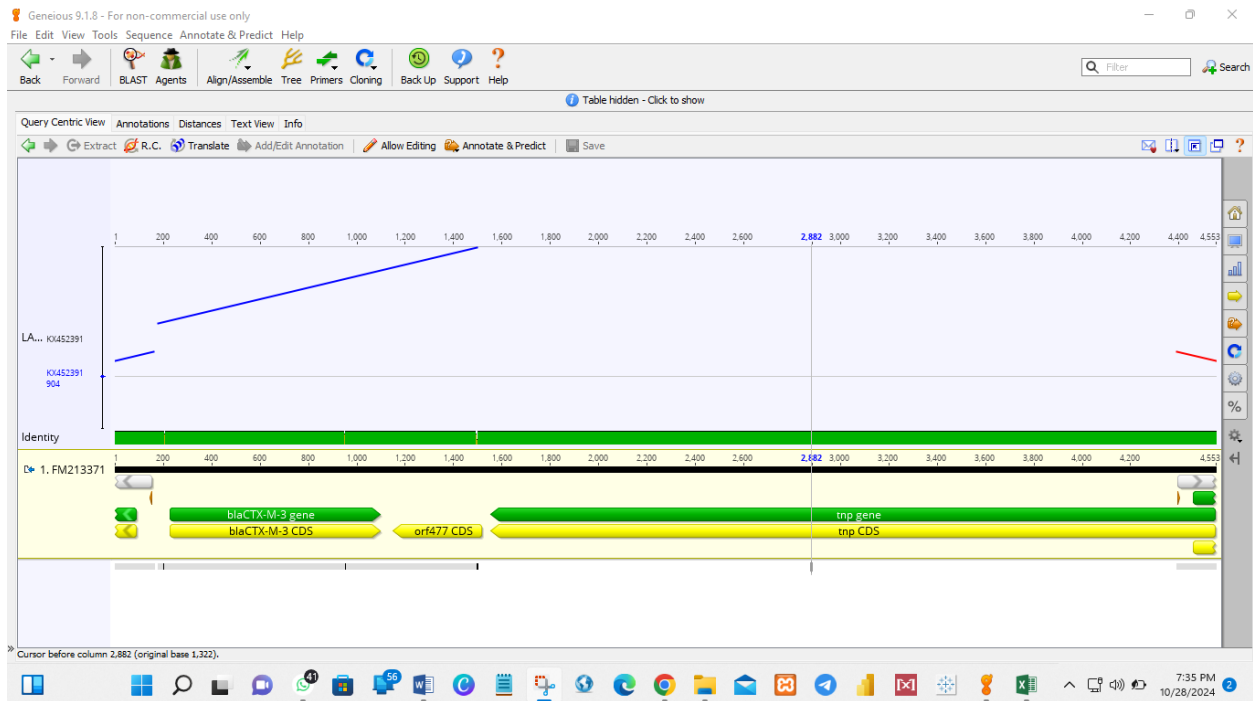


QUESTION 3

-Define Comparative Genomics and explain how it can solve real-world problems with example(s) of practical applications.

Answer: Comparative Genomics is a field of biological research in which the genome sequence of different organisms or same of different species are compared

It can be used to solve antibiotic resistance and crop improvement



Title: Comparative Analysis of the beta Lactamase Gene in *Escherichia coli* Strains

Methods:

1. Data Acquisition: The beta lactamase gene sequence were obtained from the NCBI database and included 3 *E.coli* strains.

2. Sequence Alignment & Assembly: The sequences were imported into Geneious software where multiple sequence alignment was performed to identify conserved regions and differences among the strains.
3. Statistical Analysis; The percentage difference between the reference sequence and other sequence is 0.3%.
4. Variation and Identification of Unique genes: the unique genes to the reference sequence are tnP gene and tnPCDS.

Result & Discussion

-Sequence Alignment: the alignment revealed several conserved regions in the beta lactamase gene across *E.coli* strains, including functional importance.

-Implications: Understanding the genetic variation in beta lactamase genes is crucial for addressing antimicrobial resistance

Conclusion

The comparative genomics analysis of the beta lactamase gene in various *E.coli* strains demonstrated significant genetic variation, which is crucial for understanding antimicrobial resistance mechanisms. The finding underscores the importance of continuous genomic surveillance in addressing public health challenges related to multi drug resistant bacteria.

Reference

NCBI Database. *Escherichia coli* blaCTX-M-3 gene for beta-lactamase and flanking regions, isolate 16ST(NMI421/06)

<https://www.ncbi.nlm.nih.gov/nuccore/FM213371.1>