Bioinformatics

This paper discusses bioinformatics and computational techniques, such as DNA and RNA sequencing and analyzing patterns of triplet code to predict the biological function and three-dimensional structure of proteins inside the human genome. My research project examines methods to store and analyze the information of the transcription process, which is the synthesis of RNA from a DNA template, and translation, which is the synthesis of protein into amino acid sequence. It covers the method to analyze polypeptides to find its function and its structure on living organisms. Bioinformatics are useful in medicine to analyze the genetic code of virus such as coronavirus to develop a vaccine or treat patient with a disease or cancer. This paper also discusses about the nitrogenous bases and the RNA codon table, which identify the amino acids inside a codon.

Integrating computational techniques and algorithms allow to target specific patterns in a genetic code to match them with other genetic code quicker and more efficiently with a higher accuracy on the data obtained. My research incorporates *The Human Genome Project,* which is an international effort to use bioinformatics to decipher the organization of genes within animals and humans and look for similarities in their patterns.

Keywords: Database, DNA sequencing, amino acids, strands, genes, mutations, mRNA, codon, algorithm, genome, codon, nitrogenous bases, translation, transcription, TATA box, triplet codon, nucleotides, cells, diseases