A computational perception of locating multiple longest common subsequence in DNA sequences

Abstract:

-Bioinformatics is a growing field that combines biological and computer science research.

-The longest common subsequence (LCS) is a problem in computational science that must be resolved. Finding LCS is a fundamental task in deoxyribonucleic acid (DNA) structure research and other molecular biology. for determining the LCS of two DNA sequences and their region. To do this, DNA sequences are stored in an array, and the matching algorithm is used to compare DNA sequences. After the matching process is completed, the longest common subsequence(s) is found. The maximum length of LCS obtained is 8. The calculation time depends on the length of the DNA.

Introduction:

-(LCS) method is used to find the longest common subsequence between two subsequences. It is important to detect the presence of disease-causing sequences in human DNA at an early stage in order to avoid disease's consequences. One of the goals of bioinformatics is to provide a way for the analysis of data.

- Every living thing is made up of one to trillions of cells, which are the basic unit of all living things. Cell performs various operations such as molecule transportation, energy conversion and reproduction. DNA is a macromolecule composed of a series of nucleotides, each of which contains a nitrogen base, as well as a deoxyribose sugar and phosphate. There are four nucleotide bases in a DNA molecule. Cytosine (C), thymine (T), adenine (A), and guanine (G). The instructions for making proteins are encoded in DNA. A gene is a DNA sequence that plays a role in the functional part of protein or RNA molecule development, and inherited characteristics from generation to other.

- Human genome contains three billion nucleotide bases and about 20,000 genes. There are 46 chromosomes in the human genome. DNA is a chemical substance that is used for a variety of purposes in industry.

Cell ⟶ Nucleus ⟶ chromosome ⟶ DNA