

Assignment 1: Abstract and Introduction summary.

Abstract:

- Nowadays bioinformatics is considered as an active research field that acts as an interface between the computer science and biology.
- We have two sequences, A subsequence is a sequence that appears in the same relative order, but not necessarily contiguous.
- The longest common subsequence (LCS) is one of the essential issue to be solved viably in computational science.
- In this paper, we will discuss new calculation for LCS of two DNA sequences, will find all common subsequences in the Dna Sequences and determine their location and length then will determine the length and location of longest subsequence present between all sequences and the time complexity will be computed too.
- To achieve this, we store DNA sequences in an array then start to compare them using matching algorithm.
- nowadays DNA sequence comparison is an important and upcoming area in computational molecular biology

Intro:

- Bioinformatics helps us to understand and organize the information associated with biological molecules and to build up a guide in the examination of organic information .
- Cell is the basic unit of all living tissue, each Cell performs several operations like molecule transportation, energy conversion and reproduction.
- Each cell contains the genetic information as a form of (DNA) sequence. DNA contains the instructions for making proteins(genes).
- Human genome contains approximately 3 billion base pairs and about 20,000 genes.
- DNA sequence analysis and gene analysis are used for finding forensics related problems and discovering changes in human DNA sequence or genes and biotechnology related problems .
- To discover changes in DNA sequence we compare the affected DNA sequence with the normal one, and these kind of comparisons would take long time for processing because human genome contains three million nucleotide bases.
- biological data are big and very complex, and we need efficient ways to analyze it
- Computational methods can be useful to reduce the time and space complexity.
- Subsequences are used to determine how similar the two strands of DNA are, so it will help in discovering diseases.
- Effective subsequence match still remains challenging.