Assignment 1

Abstract and Introduction Summary

- Alignment algorithms have been in the spotlight for the last few decades, due to a vast genomic data explosion.

- We need a lot of computational resources and time to process biological data, both of which are expensive for us, so we'd like to process the data in the shortest time possible with the fewest resources available.

- The structural and functional relationships between genes are determined largely through the comparison of genomic sequences. This distinction is made by comparing genomic sequences for similarities, variations, and mutations. This enables researchers to investigate and examine species' genetic and evolutionary relationships.

- Comparison of DNA sequences is done through software based on alignment algorithms that give results in the form of scores and percentages of similarities and identities.

- The main mission of this research area is to analyze and interpret deoxyribonucleic acid (DNA) sequences in central databases, accessible worldwide, to enable scientists to present and search biological information.

- Concerning sequence alignment, three types of alignment of the DNA sequences can be distinguished: Global alignment, Semi-Global alignment, and Local alignment.

- This study will present a new DNA sequence alignment algorithm called Discrete-To-Continuous (DTC) that ensures three forms of alignment. The proposed methodology was compared against other existing methods, which are largely based on the concept of string matching.

- The DTC algorithm delivers supremely efficient alignment with a reduced response time.

- Unlike string matching algorithms, which try to find a point-to-point correspondence of the chains, the DTC approach solves this problem in its entirety by superimposing the discrete representation of the test points on the continuous representation of the reference points.

- DTC is based on polynomial interpolation of data and uses dynamic programming.