Assignment 1 :Abstract and Introduction Summary (An Efficient and rapid method for detection of mutation in deoxyribonucleic acid\_sequences)

The structural and functional relationships between genes are largely determined by comparing genomic sequences. This distinction is made by determining the

genomic similarities, variations, and mutation

sequences of events This allows researchers to investigate and interpret the genetic code.

and the evolution of species' relationships.

Alignment algo Since it is a field that encompasses life sciences disciplines such as genomics, proteomics, and biology through informatics, bioinformatics is the convergence of biology and informatics.

Methods involving computers This research area's main goal is to

deoxyribonucleic acid analysis and interpretation (DNA)

sequences in central databases that are available from anywhere in the world

make it possible for scientists to present and scan biological datarithms have been around for a long time. 2) Semi-global alignment: used when one series is shorter than the other or when looking for overlaps at the ends without taking into account the gaps' penalties.

3) Local Alignment: this method looks for the two most important factors.

only the conserved sub-regions between two sequences

There will be two regions that will be aligned. Algorithms by Smith and Waterman