

Assignment 1

Abstract:

As a result of studying the genetic variants and mutations that occurred in 1200 genomes of SARS virus and presenting an analytical study, it was found that some mutations in the SARS genome do not happen randomly. And also found the most important good candidates for drug development and treatment of Covid-19 disease through research, where it was found that the coding region at the nucleotide level of NSP13 protein is relatively conserved compared to other protein regions in the ORF1ab gene.

Introduction:

In December 2019, in the Wuhan region of China, the spread of the COVID-19 virus began as a result of the SARS-CoV-2 virus, as this virus and other pathogens spread rapidly and ferociously as a result of the genetic changes, including the sequence difference, adding unknown variables to the immune system.

Whereas, the variation in the genomic structure of the SARS COVID-19 genome occurs according to environmental conditions (ultraviolet rays ... minerals).

It has been scientifically proven that the highest rate of mutations among all living organisms is in viruses, especially single-stranded viruses .. The biggest difference that affects all mutation rates is DNA and RNA viruses. Despite the dangerousness of SARS-Covid-2, we discovered new chemicals and treatments for Covid-19 disease by studying the differences in the genetic sequence at the level of its nucleotides.

Assignment 2

Related work:

(Li et al., 2020): provide an excellent overview of SARS-evolutionary CoV-2's history and the future intermediate transferring species.

(Yoshimoto,2020): described the full collection of SARS-CoV-2 genes and proteins.

(Saha et al. 2020): The virus will develop into a better version of itself by mutations to suit best in the host environment, according to Saha et al. The virus uses mutation as a method to acclimate with its environment.

(Tai et al. 2020): investigate and present all aspects of the virus and disease in the sense of its transmission to humans through the Spike protein, as well as the sequence of molecular and biological functions involved in the process.

(Petroopoulos and Makridakis,2020): provide realistic predictions for confirmed coronavirus disease, as well as a study and timeline of the disease's possible consequences for preparation and decision-making.

(Andersen et al.2020): present an analysis of the virus's prominent characteristics and origin hypotheses.

(Khailany et al.2020): presented an analysis of genetic differences and mutation comparisons of identified SARS-CoV-2 genetic data across different time frames and places, Analysing 95 SARS-CoV-2 complete genomes submitted to various databases through April 2020.

(Emameh et al .2020): To classify the proteins in the ORF1ab region of the genome, a data mining and computational analysis of SARS-CoV-2 isolates from oronasopharynx of Iranian patients was presented. SARS-CoV-2 polyproteins are cleaved by virus-encoded cysteine proteinases, which encode 16 nonstructural proteins (NSPs), with ORF1a encoding NSP1 to NSP11 and ORF1b encoding NSP12 to NSP16.