Role of Bioinformatics and Islamic Perspective in Fighting Against COVID-19

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Abstract- The aim of this study is to take a brief review on Islamic perspective and role of bioinformatics in fighting against deadly microbe that is corona virus cause of COVID-19 disease. Coronaviruses are a group of non-segmented, single-stranded, positive-sense RNA viruses. Extreme acute coronavirus syndrome (SARS-CoV) and Middle East (MERS-CoV) are zoonotic and very pathogenic coronaviruses that contribute to global and regional epidemics. Islam, in particular, presents a perspective that largely emphasizes compassion, solidarity, and responsibility to fellow human beings during pandemic. Bioinformatics, an interdisciplinary emerging science and possess great influential impact in findings from genome sequencing, drug development trials, tackle contagious corona virus and developing preventive measures. This review provides information about introduction, Islamic perspective towards pandemic, role, applications of bioinformatics, work, phylogenetic relationships of corona virus, researchers' struggles have performed in the field of bioinformatics in order to overcome COVID-19 pandemic.

Index Terms BIOINFORMATICS; COVID-19; ; ISLAM; APPLICATIONS; ROLE; PHYLOGENETIC RELATIONSHIP; PUBLISHED WORK; TECHNIQUES

I. INTRODUCTION

Bioinformatics" is an emerging interdisciplinary science which combines mathematics, statistical measurements, computational science, and molecular biology for biological information collection, interrelation and evaluation of the data. Across most disciplines of the biological science and research, the utilization of biological data has expanded rapidly, particularly in the areas of medication, molecular genetics, farming, pharmaceuticals, preservation of natural resources and biodiversity, evolutionary relationships and so forth (Xiong, 2006). It has significantly made a significant contribution to our knowledge of all these disorders, the origin, mechanism and proliferation of antimicrobial tolerance, recipient immune responses, possible detection indicators, and immunization goals by emphasizing on the implementation of Bioinformatics on contagious diseases. Infectious agents and animal models that merge genomics knowledge to offer treatment alternatives just as expected medication and the production of vaccines and potential pharmaceutical products (Xiong, 2006).
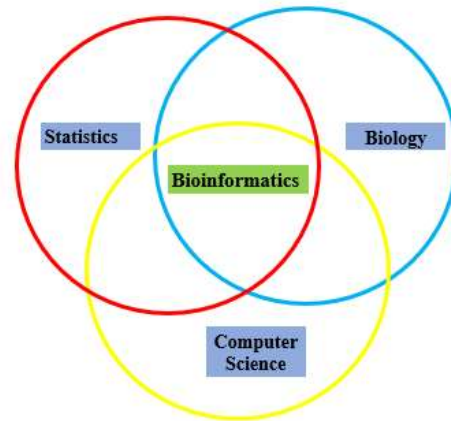

Figure 1: Represent relationship of different discipline leads to Bioinformatics

In addition to being vital for fundamental biological and genomics research, bioinformatics has a major influence on a variety of fields of biotechnology and medical science. It has implications such as forensic DNA analysis and agronomic biotechnology in the area of knowledge-based product design. Protein ligand interactions computer simulations offer a reasonable framework for the fast detection of novel guidance for alternative medicine. Insight including its 3-D structures of molecules enables development of substances which can attach with raised affinity and similarity to the specific receptor of the desired protein (Xiong, 2006). Bioinformatics has wide range of applications which are as following: Academic institutions, businesses, national and foreign scientific organizations are interested in bioinformatics around the world. Bioinformatics presently focuses on assessing the roles of genetic materials, controlling features, identifying similar patterns, evaluating the restrictions, determine the structure of nucleotide by removal of proteins, modeling a primer, identifying the reactive groups of metabolites, calculating the progressive gap for phylogenetic reconstruction, mutation detection, determine protein associations, molecular assay technologies, two dimensional researches, SNP's analysis etc as in Fig. 2 (Rashid, 2006).
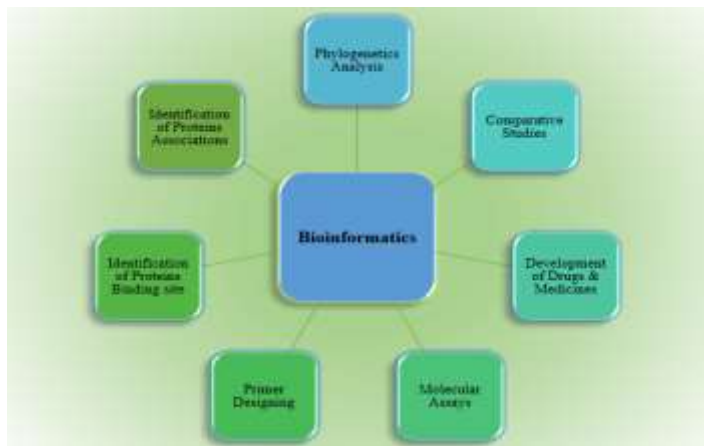
Figure 2: Applications of Bioinformatics

Throughout the disciplines of microbial genetics, agricultural and clinical, bioinformatics is commonly utilized. Within these sectors, the following is the adaptation of the bioinformatics industry. This collection of evidence provides practitioners with a broad framework for this research of biological modification, the environment, the growth of cyanobacteria, and other various organisms' genomes. It also promotes the usage of multiplex strategies, including expression of high-performance technology such as RNA sequencing microarrays, and proteomics (Abberton et al., 2016). Through the study of the genetic makeup of microbes, researchers can immediately start the basic understanding of these pathogens and extract the genetic traits that enable them to stay alive in harsh environments (Field, 2014). Algorithms in bioinformatics are also being used to develop new techniques and experimental studies for enhanced crop manufacturing. For particular, genomics approach allows the explanation of genes and their roles and the biological features of every organism (Mochida & Shinozaki, 2010).

Genetic modification of the toxin to different food crops has also been used to boost cultivated output with the help of advanced field of bioinformatics (Abberton et al., 2016). Gene therapy is a modern medicine approach of area of bioinformatics that lists the patient's cell's synthetics to produce a medicinal agent. Gene therapy involves the successful incorporation of the functioning gene into patient's viable cells to produce adequate protein expressed by the gene to fix this correctly and reliably (Hack & Kendall, 2005). Bioinformatics is fundamentally collaborative, since both are based on machine learning and data mining. The scientific and mathematical developments in the micro arraying sector, thinking computers, TFT bio sensors, Bayesian networks, and others have influenced the area. It is being encouraged and offers the powerful way to arrange and deduce facts (Bianchi & Liò, 2007).

Introduction of COVID-19:

Coronaviruses did not suddenly appear because it exists for a long period of time. Certain diseases including severe acute respiratory issue coronavirus (SARS-CoV), human coronavirus, PEDV (porcine epidemic diarrhea virus), Middle East Respiratory Syndrome (MERS) etc. caused by vast family of viruses named as coronaviruses. Seven coronaviruses may contribute to infection in humans across the worldwide, although certain human coronaviruses also infect individuals usually that

are: HKU1, NL63, 229E, and OC43 strains. In December 2019, first case of human coronavirus was reported in Wuhan, China and related to seafood market and outbreak has spread rapidly to a large number of countries worldwide (Hafeez et al., 2019). Although COVID-19 is diagnosed on the basis of the viral genome magnification in real time PCR but the current treatment of the people involved is confined to a combination of PCRs with relevant large variety of antiviral medicines (Xu et al., 2020).
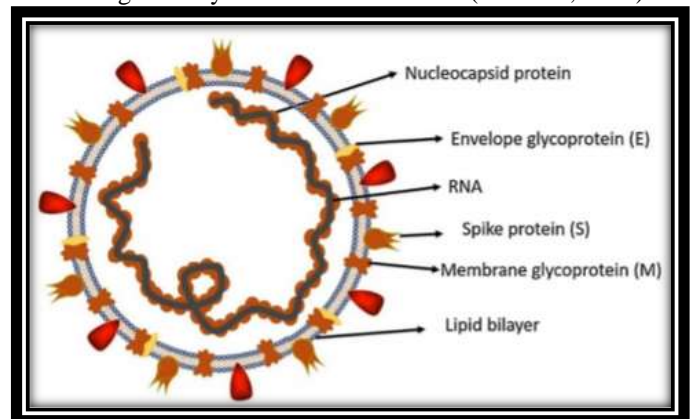

Figure 3: Structural representation of corona virus (Hafeez et al., 2019).

Human corona virus is single stranded RNA virus from Coronaviridae family possess specific structural proteins that are spike proteins vital for inflammation and arrangement. These are also helpful in introduction process into host cells through attachment with host cell receptor ACE2. Figure represent structure of deadly corona virus (Chen et al., 2020).

This infection isn't new to the world; however, a new virus to human beings. At the point experts declared it novel coronavirus in 2019, when they discovered that humans were rapidly infected and hospitalized from this novel coronavirus. The epidemic of COVID-19 induced by a severe acute Coronavirus 2 disease (SARS-CoV-2) has a massive global distribution. Since about 15 April 2020, more than 1,998,111 confirmed and 126,604 COVID-19 deaths were recorded to six continents and 210 countries around the world by WHO (Hafeez et al., 2019). According to current statistics of COVID-19 of 3 July 2020, WHO reported nearly 10,719, 946 confirmed cases and 517,337 fatalities across the world. While in Pakistan, 221, 896 confirmed case and 4,551 fatalities of COVID-19 has reported by WHO (World Health Organization [WHO], 2020).

Islamic perspective and COVID-19:

The COVID-19 pandemic has presented challenges and changes to people's lives worldwide. However, the Islamic perspective and Muslim ethics have provided a unique way of dealing with such a crisis. According to Islamic tenets, humanity's primary purpose is to worship Allah and live a virtuous life based on tolerance, justice, equality, and compassion (Rashid, 2014). To fight COVID-19, the core of these values, which form the bedrock of Islamic ethics, was seriously brought into question and implementation (Meraj, 2016).

First and foremost, among these ethics is the sanctity of life. Islamic teachings stress the paramount importance of protecting life. The Quran significantly notes: "Whosoever saves the life of one, it shall be as if he had saved the life of all mankind" (Quran:

5:32). During such a crisis as COVID-19 pandemic, the implementation of this ethic has encouraged Muslims to take all possible precautions to prevent the virus's spread and protect human lives (Xiong, 2020).

Next, solidarity and responsibility stand as core values in the Muslim ethics code. The Quran mentions, "And cooperate in righteousness and piety, but do not cooperate in sin and aggression" (Quran: 5:2). This verse compels every Muslim to uphold their social responsibilities, including following health guidelines and practicing social distancing, to prevent the COVID-19 spread.

Furthermore, the principle of social solidarity in Islam establishes obligations toward other society members, particularly those in need (Quran 2:177). This becomes very significant during crises like COVID-19, where Muslims are encouraged to support one another by sharing resources, providing emotional support, helping those in isolation, and spreading authentic information.

Moreover, Muslim ethics harbour a strong focus on community welfare and protection from harm. Prophet Muhammad, in one of his sayings (Hadith), stated, "There should be neither harming nor reciprocating harm." These words drive the Islamic perspective into playing a proactive role in this pandemic. Wearing face masks, washing hands frequently, and avoiding public gatherings become acts of piety, serving the wider community's wellbeing and safety.

Almost every Muslim country has taken admirably proactive steps to shield their population from the worst of the pandemic, guided in part by Islamic teachings related to public health and welfare. Countries like the United Arab Emirates and Qatar are among the top nations with the highest rates of COVID-19 testing, demonstrating the Islamic principle of 'prevention is better than cure (Jazeera, 2020).

In conclusion, from the Islamic perspective, dealing with the COVID-19 pandemic involves adhering to public health guidelines, seeking authentic knowledge about the virus, exercising patience, promoting social solidarity, and having faith in Allah's protective care.

Role of Bioinformatics and COVID-19:

Bioinformaticians are attempting to make every effort to succeed the scientific war against that kind of devastating infection throughout this world emergency. While they operate much of the time behind confined doorway, they offer valuable data to scientists and researchers around the world. Information of the modern coronavirus sequence and the COVID 19 genetic makeup and the particular surface morphology of the proteolytic enzymes were the most significant bioinformatic achievement in this outbreak and were used to create antibiotics, a vaccine, and testing devices for this lethal viral strain. This research also helped to identify the genes involved for viral multiplication and the protein required for the host cell association through sequencing technology (Rudra, 2020).

➢ **RT-PCR Techniques and Data bases of Bioinformatics:**

In the view of this data, experts have discovered testing instruments with a WHO-approved reverse transcription polymerase chain (RT-PCR) reaction. A fundamental aspect of PCR's primer designing was developed using technologies

focusing on the sequence alignment approach to bioinformatics. It just indicates that bioinformatics has been influential in improving the laboratory technique for COVID-19 diagnostic testing quite rapidly. In addition, use of such information from various databases such as NCBI, PDB (Protein Data Bank), GenBank, FAST, Blast, PubChem, drug bank etc. to produce products and in particular antibiotics, vaccine and utilizing computation chemistry techniques will have a significant role for Bioinformatics. The next move will be tremendous molecular algorithms with quantum computers to get the best alternative additives to be expanded in the wet research lab as chemotherapeutic drugs production against deadly corona virus (Rudra, 2020).

➢ **Artificial Intelligence:**

The uniqueness of physiological reactions that occur can be implemented by software (MEGA, Blast etc.) and advanced powerful computers so that they are very similar to the wet laboratory setting. Faster solutions to previously published research documents are another benefit of bioinformatics in the current emergency scenario. By use of artificial intelligence (AI) and natural language processing for interpreting data on the dispersal of the global epidemic and the adverse effect of outbreak to empower the battle against the deadly coronavirus may also be an important requirement. The goal could be to examine national and worldwide socio-economic effects of the infection. The objective may be to identify markers, structures and facts and figures for faster and more efficient assessments by state governments (Rudra, 2020).

➢ **Nanotechnology and Biotechnology:**

The biotechnology definition encompasses a broad variety of treatments for human movement modification of live species, plant breeding, animal care and reproductive improvements utilizing engineered techniques for choice. Advance implementation also involves research methods for hereditary, cell and tissue analysis. Organisms and microorganisms known as being very useful in the milk products processing and food industries in the domain of computational biology and biotechnology. For example, *Lactococcus Lactis* is really essential microbes that engaged with the food industry. The results on a molecular, nuclear, and super-molecular scopes are due to the nanotechnology (Aken et al., 2016).

➢ **Drug Development, Discovery and Bioinformatics:**

Across almost all areas of drug exploration, risk testing and product creation, bioinformatics play an increasingly prestigious place. This increasing significance is attributable not only to the usage of vast quantities of bioinformatic data but also the use of costs and benefits associated methods in medical and clinical trials studies to deter, evaluate and assist analysis. Drug development measures predominantly face a range of ambiguity in exploring new medicines for medicine and science. There was an extraordinary development in bioinformatics owing to the growing demand to manufacture so many more medications in limited periods of duration at affordable prices. Currently, a modern area called computer aided drug development (CADD) is now being adapted. To order to solve costs and cycles to different areas, bioinformatics offers tremendous assistance. It offers a broad variety of drug-related information repositories,

something that could indeed be employed to build and create drug-related implementations (Katara, 2013; Wishart, 2005).

The world's leading murderers of kids and young people have traditionally become contagious disorders like COVID-19 and such other diseases. "These are ultimately responsible for over 13 million fatalities annually, in industrialized nations, one in two deaths," as WHO reported. Within developed nations, the number of deaths from infectious diseases arise. The reason was the shortage of appropriate medications and the high expense involved with such medications if at all accessible. Some of the big challenges confronting humanity is the production of effective and inexpensive medicines for an illness. The logical drug development employing bioinformatics is an appropriate response to this challenge. The pharmaceutical sector has adapted from the testing and malfunctioning in drug development method to sound product design, structurally dependent. The production of effective chemotherapeutic drugs will minimize time and expenses through a productive and efficient drug discovery approach. Computer technologies are employed to forecast future 'medications' and only recognize and exclude therapeutic targets that are impossible to sustain subsequent phases of exploration and advancement. Optimization algorithms and computer program strategies can confirm the similarity of the medication (Iskar et al., 2012; Dahiya & Lata, 1938).

Forecasting drug is a scientific discipline containing predictions of the risk of illness and precautionary procedures in attempt to avoid or substantially minimize the effects on the individual. Predictive medicine of infant includes testing, early pregnancy checking, therapeutic monitoring, preconceived notion testing, clinical computational biology, carrier evaluation etc. The techniques include newly born laboratory tests. Confirmatory testing is a health care initiative intended to test babies for a number of preventable measures, but not diagnostically readily apparent disorders promptly after childbirth (Hack & Kendall, 2005).

Preventive Medications: Both physicians are implementing preventative treatment in order to ensure good patients. The American Bureau of Medical Specialties (ABMS) also has a special medical central idea. The wellbeing of people, populations and identified public considerable attention in preventative care. In the age of modern medicine, widespread interest in vaccination is a gateway to the effectiveness of world-wide vaccine training programs. Preventative care or preventative medicine includes precautions to minimize and handle signs of disorder. Various approaches such as recovery and critical care and the strategies utilized in health care. The diagnosis of overweight and visual impairments is also effective. The Department of endocrinology has utilized testing techniques, markers and factors of the public's wellbeing and illness and turn the awareness into disease-resistant systems (Tiwari, 2015).

Most evidence collected on drugs administered throughout the MERS-CoV or SARS-CoV disease outbreak or in vitro studies originate from therapeutic approaches (Ashour et al., 2020). Numerous studies for new COVID-19 treatments are being performed on the basis of immunomodulatory medicines, antioxidants, antiviral, anti-inflammatory, cell therapies and certain other medicines (Zhang et al., 2020). In in-vitro animal studies and experimental data was found to demonstrate the effectiveness of various antivirals medication to tackle COVID-

19. This study findings are quite entirely focused on MERS-CoV and SARS-CoV knowledge (Han et al., 2020). It is advised that patient with a confirm diagnosis for COVID-19 and moderate symptoms should be given antiviral agent by the Italian Society of Infective and Tropical Diseases (Lim et al., 2020).

In multiple COVID-19 patient in China, remdesivir has been effectively utilized (Al-Tawfiq et al., 2020). Remdesivir serves as a nucleotide counterpart by inserting in the nascending viral RNA chain and then triggering its untimely termination. In ongoing clinical trials of MERS-CoV and SARS-CoV illnesses, remdesivir was confirmed to have been involved in viral polymerase of coronavirus (Gordon et al., 2020). The efficacy of remdesivir to decrease infection rate and boost pulmonary function metrics has been seen in a North American MERS-CoV study in mice. There are currently clinical feasibility findings in both the United States and China on the use of remdesivir in COVID-19 patients (Sheahan et al., 2020).

➢ **Phylogenetic Analysis:**

Different studies have been performed to check phylogenetic analysis of corona virus using various bioinformatics softwares. Here are some examples of studies performed for phylogenetic analysis. The delegate sequences from top outcomes, all being Covids either in people or different species, were chosen to construct a phylogenetic tree utilizing the neighbor-joining technique after Blastn analysis by means of SARS CoV-2 genome sequence via NCBI GenBank database. Findings reveals that SARS CoV has approximately 80 percent sequence similarity and is evolutionary nearest arrangement to SARS CoV-2. MERS-CoV is evolutionarily nearest to SARS-CoV-2, with a 50% sequence identification, for all of the human coronaviruses. When the virus is much less commonly identified and researched, this study conducted especially. From that point forward, different extra sequencing investigations have been performed for SARS-CoV-2, including a milestone preprint, which proposed that 2019-nCoV modified into SARS-CoV-2 (Gorbalenya et al., 2020).

Guruprasad (2020) has performed study to examine the basic structure of SARS spike proteins needed for human infection, they have developed several similarity measure and phylogenetic trees for representative spike proteins of SARS CoV and SARS CoV-2 from different host sites. Their findings indicate that two sequence regions in the MESEFR and SYLTPG N terminal domains are unique to human SARS CoV-2 from the examined dataset. The bat genome has been described as the nearest to the latest human SARS coV-2 genetic in the full genome review of representative SARS CoVs from the human, civet and bat host sources and human SARS.

I also have been performed study to find out evolutionary relationship of corona virus between different countries using bioinformatics tool. I took genome sequences of corona virus from NCBI data base of six countries that are Pakistan, China, Japan, North Carolina-USA, South Africa, Italy. Then do alignment and construct phylogenetic tree with help of Blastn tool. Phylogenetic relationship between corona virus of different countries are shown in figure 3:
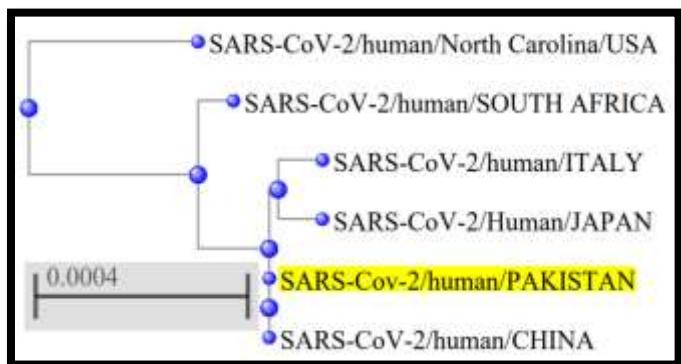
Figure 4: Representation of phylogenetic relationships of SARS-CoV-2 of various countries

Above figure shows that phylogeny of SARS-CoV-2 of Pakistan and China is same, while other countries origin is different.

Works Done by Researchers in Fighting Against COVID-19:
A lot of work, trials and advancements have been performed with the help of bioinformatics in fighting against the global pandemic COVID-19 by researchers worldwide. They are trying to tackle the adverse impacts of deadly corona virus. Some of published and performed work is described listed below:

1. **Utilization of Q-UEL Language of Bioinformatics:**
   Robson (2020) performed a study for the analysis of the genome isolation thought to be the causing vector of the COVID-19 disorder of the Wuhan Seafood Industry. The goal is to identify and analyze several design opportunities a small segment or portion of the microbial query protein for the slightly earlier developed system of peptide artificial vaccine and peptide therapy. Q-UEL language of bioinformatics utilized to the application of the Q-UEL language in the information acquisition and automatic medicine prediction framework named the BioIngine. Use Q-UEL tools, therefore, to view upcoming publications and communicate with regular currently accessible bioinformatics programs on the Web, managed to help rapidly classify amino acid sequences that are well maintained in several coronaviruses like 2019-nCoV. In this analysis, KRSFIEDLLFNKV has been identified to be well preserved and is compatible with an area across a recognized SARS cutting site considered to be needed to enable the virus for the insertion into a cell (Robson, 2020).

2. **Utilization of AutoSeed Pipeline techniques of Bioinformatics:**
   In this report, they introduced a new network of medicinal items for the repurpose of COVID-2019 to classify possible medicines. At first, they study of the SARS-CoV-2 genome sequence and SARS was focused on the nearest genome sequence, preceded by MERS and other human diseases dependent on genetic similarities. Three four COVID-2019 genes were collected from our AutoSeed pipeline bioinformatics repository (data analysis and repository scan). They immediately developed a molecular framework utilizing these genes to repurpose 24 human routes, five

components and finally 78 medications in drug identification and medication-prioritization algorithms. They also recommend 30 possible re-pursuable drugs for COVID-2019 (comprising thalidomide, andrographolide, pseudoephedrine, abacavir and chloroquine) after systematic screening dependent on clinical experience. According to their results will offer important information into SARS-CoV-2 biology and encourage the advancement of fast-track medical studies for COVID-2019 therapies (Li et al., 2020).

3. **Utilizing GISAID database Sequences and K-mer method and also did Phylogenetic Analysis:**
   The existing methods are focused instead on an in-depth study of the attributes of a disease virus isolated (e.g. very first accessible virus extract) which may contribute to template animals that are not indicative of prevailing or evolving clusters. They recommend a mix of bioinformatics, epidemiological criteria, and studies when selecting virus strain for the production of experimental animals. In the sense of phylogenetic analysis, and in an innovative alignment-free evolutionary computation method, they have addressed the currently identified SARS-CoV-2 strains for Global pandemic COVID-19. This new method investigates genome-wide collaborative mechanisms and therefore also provides a rather dynamic view of the 'a lot of variations' that RNA viruses that acquire as compared to phylogenetic trees, which rely on common mutations of organisms (Bauer et al, 2020).

   This combined analysis suggests that even though the existing animal experiments sufficiently conform to the latest virus types, major developmental behavior is definitely not taken into account in the established models. They recommend isolates for potential laboratory animals focused on findings from a non - overlapping non-alignment-free method and laboratory inferences. For this they utilized sequences of corona virus from GISAID data bases, then allowed alignment using bioinformatics tools, and then do phylogenetic analysis for evolutionary relationship (Bauer et al, 2020).

4. **Providing Web Based Plat Form Fighting Against COVID-19:**
   Lo., et al (2020) thought about researchers to deliver a clear genomic base for epidemiological research and for excellently-informed decision management, a systematic analytical method for producing the genome sequence, especially during outbreaks such as the ongoing COVID-19 global epidemic is essential. In order to address this task, the Illumina or Oxford Nanopore Technologies data for SARS-CoV-2, genomic sequences initiative, Lo., et al (2020) built a web interface (EDGE COVID-19), which implements structured frameworks for genome-based reference assembly. This web platform automates the generation of an SAS-CoV-2 genome prepared to be submitted to GISAID or the GenBank, given the raw Illumina file or

Oxford Nanopore FASTQ read file. EDGE COVID-19 is open-source program accessible in the https Domain for general usage and in the https Domain for local download as a Docker server.

CONCLUSION

Bioinformatics is an emerging discipline which is helpful in development of vaccine against COVID-19 through advanced techniques in algorithms. In order to address complicated biological questions, bioinformatics blends engineering, analysis and computational sciences with information technology. In any area of existence, bioinformatics techniques are effective and a lot of work is done in context of corona virus. Scientist are succeeded in production of vaccine against COVID-19 using bioinformatics modified technologies.

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