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Advanced Empirical Studies on Group Governance of the Novel Corona Virus, MERS, SARS and EBOLA: A Systematic Study

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ABSTRACT

Coronavirus condition (COVID-19) is a contagious illness brought on by a freshly discovered Coronavirus. Most individuals contaminated with the COVID-19 infection will certainly experience moderate to modest respiratory system health problems and recoup without needing unique therapy. Older people and those with underlying clinical problems like cardiovascular disease, diabetic issues, persistent respiratory conditions, and cancer are more likely to create a significant health problem.

Aim and Objective: This paper gives the best way to prevent and reduce transmission is to be well educated about the COVID-19 infection, its causes, and its spread. Protect your own and others from infection by cleaning your hands or using an alcohol-based rub frequently and not touching your face. The COVID-19 infection spreads out primarily via beads of saliva or discharge from the nose when an infected person coughs or sneezes, so it is vital that you additionally exercise breathing rules (for instance, by coughing right into a flexed elbow joint). Right now, there are no detailed vaccinations or therapies for COVID-19. Nevertheless, there are several ongoing professional trials assessing capacity treatments.

Method: The study aimed to develop a statistical model to predict how the cases are growing exponentially in various parts of the world. Even after starting from a low base, there is no proper statistical analysis of cases we can expect. It is an ambiguous thing that numbers of cases are exponentially increasing. We have analyzed the mortality rate, the number of deaths per country, and the number of recovery cases.

Conclusion: By comparing the statistical analysis of confirmed cases vs. deaths within a short period, nCov-19 affected the most compared with Zoonotic viruses. The coronavirus disease remains to spread out throughout the globe, adhering to a trajectory that is challenging to predict. The health, altruistic, and socio-economic policies have taken on by nations will certainly figure out the rate and stamina of the healing. There has to be a global human-centred reaction that is based on solidarity.

Key Words: nCoV-19, SARS, MERS, EBOLA, Mortality, Zoonotic, Exponential Growth.

INTRODUCTION

Coronaviruses are a large, diverse team of viruses and need a useful microscopic lens to see them. There are several types of coronaviruses, and also they infect a broad range of creatures and birds. Moreover, some even create moderate respiratory system illnesses in people each year. The infection that causes COVID-19, we call SARS Coronavirus 2. This virus originated in bats, indicating that bats lug this infection and are infected with this virus at all times. However, this virus developed a unique technique. It developed

the ability to leap between varieties and also infect people. All of these coronaviruses likewise originated in bats currently infect individuals and can be spread from one person to another. So the initial of these viruses was called acute severe breathing disorder, or SARS Coronavirus, the initial SARS Coronavirus. More just recently, at the end of 2019, SARS Coronavirus 2 emerged in Wuhan, China. Viruses need to live in other cells, and afterwards, they duplicate in those cells and go on to infect various other cells in the body. The natural history of SARS-coronavirus-2. Indicators of the disease are objective dimensions to define an

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ailment or condition observed during a physical examination. So, as an example, the temperature is a sign of illness, because it can be determined by taking temperature level. Breathing faster than typical is another sign because a person can count the variety of times that we are taking a breath per min and identify whether it is faster than usual. Signs are not something that can be reasonably measured, however how the person claims they are feeling. The essential points regarding the Corona Virus Condition 2019.

Instigated by a SARS-COV-2 Coronavirus and first case identified in Wuhan, Hubei, China.

Primary reported symptoms occurred on 1 December 2019.

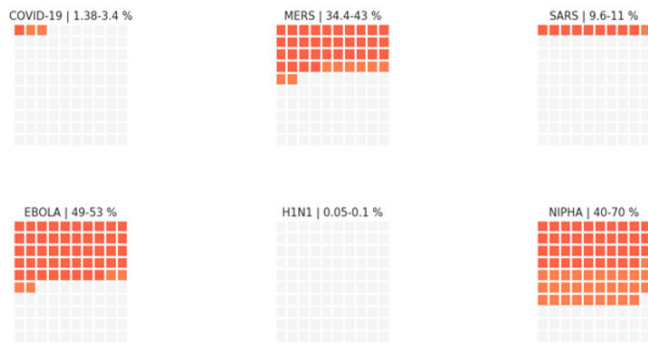


Figure 1: Statistics of Zoonotic Diseases Case Fatality Rate.¹⁷

The proportion of individuals who pass away from a defined disease amongst all individuals identified with the condition over a specific time as shown in Fig.1¹⁷. In this paper, we are working towards the statistical analysis of the Zoonotic diseases and their impact on people's timeline of existence. Diseases like Ebola, SARS, and MERS created a significant loss to humankind over some time.

Statistics of countries facing these Pandemics

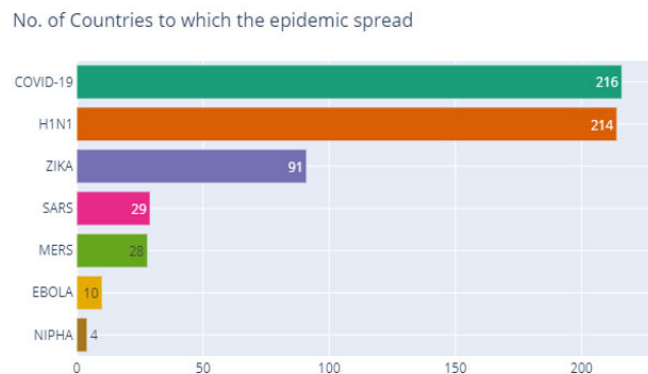


Figure 2: Number of countries Estimated to which the epidemic spread.¹⁷

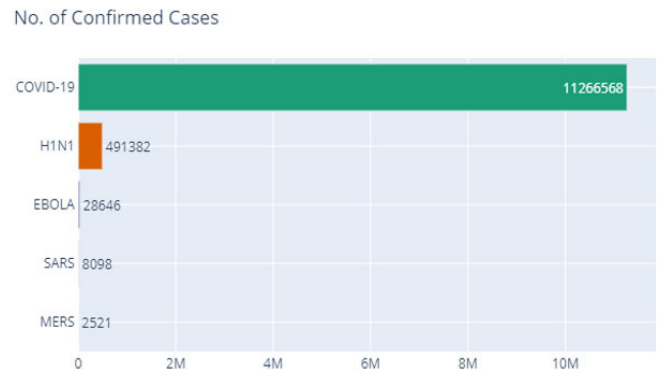


Figure 3: Number of Confirmed Cases Till July from the Outbreak of this pandemic.¹⁷

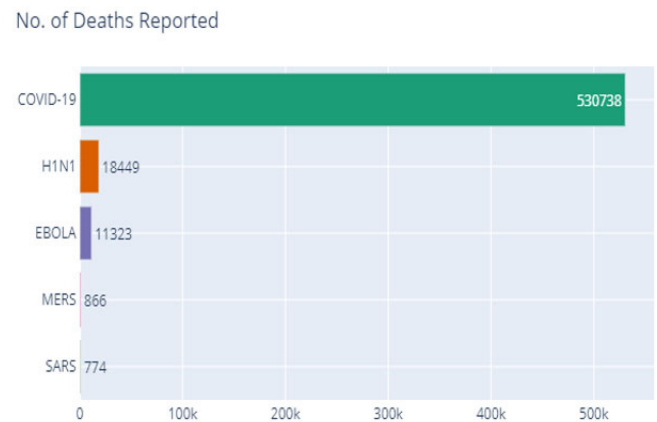


Figure 4: Number of Reported Deaths Till July from the Outbreak of this pandemic (Only estimated statistics in case of COVID-19).¹⁷

Symptoms

Coming to the clinical symptoms of this life-threatening viral disease, they range from having no symptoms at all (asymptomatic) to very severe respiratory problems, which may eventually lead to people losing their lives. MERS-CoV's most common symptoms reportedly are fever, cough, cold, and a shortage of breath. Pneumonia is also found in most people suffering from this disease but not certainly in every individual affected by it. Gastrointestinal problems like diarrhoea are also some of the symptoms. If the illness becomes too severe, it may lead to various respiratory severe problems. Patients need to be kept on the ventilators and have to be treated in intensive care units to bring the situation back to normal. Although figures say that around 35% of the patients have died fighting this dangerous disease, it should be considered that many of the mild cases of MERS have been excluded in the scrutiny. These rates are counted based on only the information provided by the well-recognized laboratories as shown in Fig 2¹⁷, Fig3¹⁷ and Fig4¹⁷.

Transmission

SARS-CoV-2 is transmitted very efficiently. It is due to two main reasons that it transmits between the persons. When the virus stays in the person their respiratory tract, mouth nose and throat contains the virus and in some when the droplets come out will also have the possibility of holding the virus. When it falls on some others there is a high chance of transmitting the virus that makes very difficult to detect and stop. There may be a chance of not transmitting the virus in a few cases also. so they could also infect other people without knowing that they are infected. So, we need to test symptomatic people and identify whom they have had contact with quickly to limit the spread. This is done through contact tracing. Due to this, the transmission of the virus is likely to occur when the affected person comes closer to another. Prisons and jails are examples of congregate housing, as are group homes and dormitories like schools or shelters. These places are all high risk for the rapid spread of the infection because people live close together and share spaces. When we think about the risk of transmission, nursing homes represent a worst-case scenario for COVID-19.

One is a diagnostic test, and that test identifies a virus that's in the body. It is called a PCR test, which stands for a polymerase chain reaction. That is the chemical reaction that's done in the lab to look for the virus. The other one is the antibody test³. Antibodies³ are made by your immune system to fight off viruses or bacteria. We can identify antibodies that are specific to this virus in your blood.

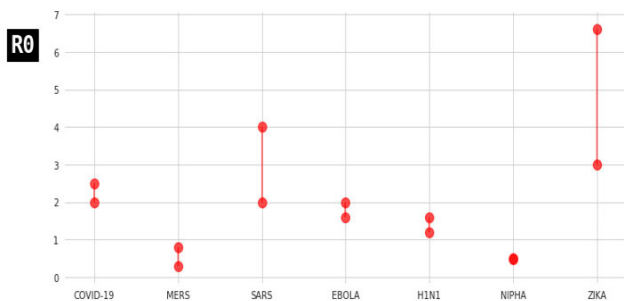


Figure 5: Estimated R0 scores of zoonotic diseases mean the¹⁷.

The typical variety of people who will undoubtedly get a transmittable illness from someone keeping that illness as shown in Fig 5.¹⁷ It especially applies to a population of people who were previously without infection and have not been vaccinated.

Health-care facilities

The virus is transmitted easily in healthcare environments in several countries, especially from patient to patient and patient to the health care worker and visitors before the MERS-CoV Virus was diagnosed as shown in Table 1¹⁷. It is highly

challenging to diagnose the MERS-CoV Virus without testing, owing to the non-specific nature of clinical features and symptoms that do not show in the disease's early onset. It is critical to prevent the infection and implement control measures to prevent the possible spread of MERS-CoV Virus in health care environments. The facilities that cater to the patients of MERS-CoV Virus need to take adequate measures to avert the risk of transmission of the virus from infected patients to others, including doctors, visitors, and health care workers. Health care workers should be extensively educated and continuously updated about the measures and protocols to prevent and control the virus as shown in Fig 6¹⁷ and Fig 7.¹⁷

Table 1: Symptoms over disease mapping.¹⁷

Symptoms of the Disease	nCoV-19	SARS	EBOLA	MERS
Fever	87.90%	87.90%	78.90%	87.90%
Dry Cough	67.90%	66.90%	61.90%	66.90%
Fatigue	38.10%	38.10%	29.10%	38.10%
Sputum Production	33.40%	33.40%	32.40%	33.40%
Shortness of Breath	18.60%	18.60%	19.60%	18.60%
Muscle Pain or Joint Pain	14.80%	13.80%	13.80%	13.80%
Sore Throat	13.90%	12.90%	14.90%	12.90%
Headache	13.60%	13.60%	11.60%	13.60%
Chills	11.40%	10.40%	9.40%	10.40%
Nausea or Vomiting	5%	6%	28.14%	6%
Nasal Congestion	4.80%	5.80%	5.80%	5.80%
Diarrhea	3.70%	3.70%	3.70%	3.70%
watery or red eyes	0.00%	0.00%	0.00%	0.00%
Abdominal pain	0.00%	0.00%	58%	0.00%
Bleeding	0.00%	0.00%	69.89%	0.00%

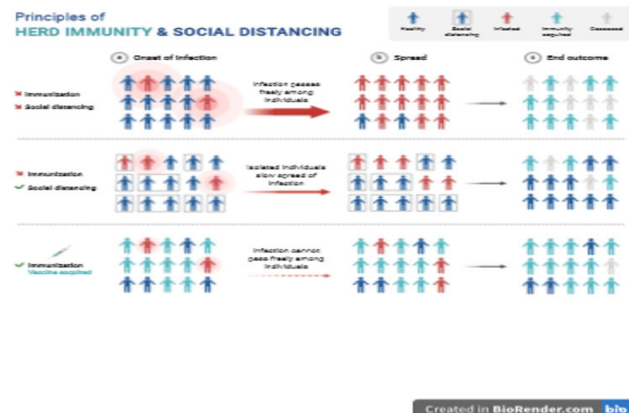


Figure 6: Showing the trend of persons effecting with Covid-19.¹⁷

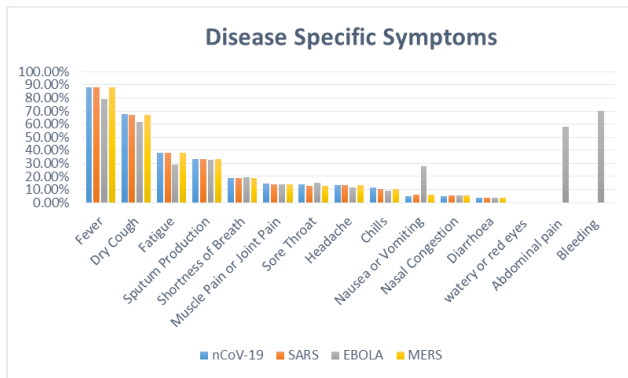


Figure 7: Disease-Specific Symptoms.¹⁷

Exploring the nCoV-2019 dataset

The data set, 'covid_19_data.csv', contains the following columns:

- Sno Identification Number
- Observation Day Date of the monitoring in MM/DD/YYYY
- Province/State Province or state of the monitoring
- Country/Region Country of observation
- Last Update Time in UTC at which the row updated for the offered district or area
- Confirmed Cumulative variety of confirmed cases up until that day
- Deaths Advancing variety of deaths till that day
- Recouped Cumulative number of recovered instances up until that date

NCov-19 was epidemiological from 22 January 2020, and the World Health Organization declared a pandemic in March. Presentall the datasets are maintained by the John Hopkins University Center for Systems Science Engineering (JHUCCSE) from the various sources like Ministry of Health Italy, the Republic of China, The Government of Spain, Hong Kong Department of Health Commission, Taiwan ministry of health sciences, Ministry of Health Singapore, European Disease prevention Centre for disease prevention maintain the updated information of every hour and minute. The Republic of China, JSU, and CCSE maintain the entire data process in the GITHUB repository. The Attributes present in the dataset Province/State, Country/Region, Update list, Confirmed, Suspected, Deaths, and Recovered. Hence this data is sufficient for finding out of occurrence or finding out about the severity of the disease. For the Statistical finding, it plays a crucial role.

The proposed framework was shown in Fig 8. for predicting the cases.

Literature Review

In a study,¹have taken around 142 DNA coding sequences of Middle East respiratory syndrome from the Biotechnology information centre, and also South Korean Quarantined

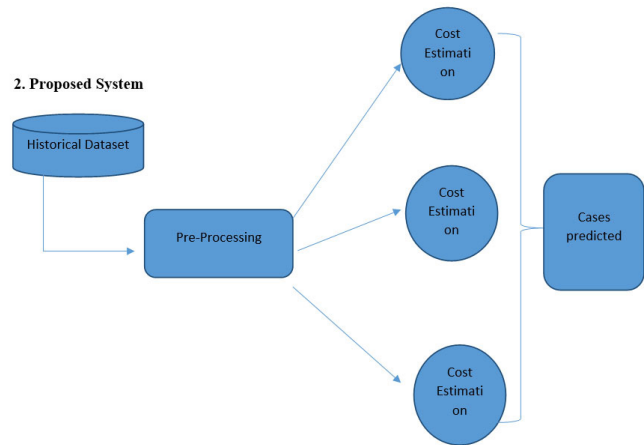


Figure 8: Proposed Framework.

DNA Protein sequences and made a comparative study. They further classified the patterns into several groups. A unique technique for web scraping data from the Twitter handle for the development of a better system for supervision, and they have examined swain flu pandemic and compared the difference between the hypothesis and evidence.^{2,3}In 2016, in an article, Al-Hazmi had made a drastic improvement to find out the symptoms caused by Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS). He implemented this with the help of various machine learning algorithms. In 2016, Chen established a mathematical induction model to analyze and predict the Ebola virus that originated in Middle Africa. With the help of a Bio Python, they analyzed the sequence of an E protein from various MERS-CoV, causing factors that severely affected humanity.^{4,5,6} To predict this E protein, MERS he separated the B cells from the sequence using Lase Gene software. In 2019, Kelly et al., statistically proven the accuracy of the SARS by comparing the number of forecasted samples vs. actual outbreak size, by applying the hypothesis testing and out of sample log the likelihood of the person affecting diseases can also be predicted. Machine learning algorithms work fine because of the increase in computational speed.^{7,8,9} In this paper, he implemented CNN, where he analyzed the result on the epoch's values using Wiener series to predict things and decision making through computational methodologies.^{10,11,12,13,15}

RESULTS

The first thing we can do is generate some statistics on the 'Confirmed' column as shown in Fig.9⁷.

Let us take a look at the mean and standard deviation in confirmed cases:

Mean: 611.8238586156112

Standard Deviation: 5121.319656069395

We can also generate a histogram of confirmed cumulative cases:

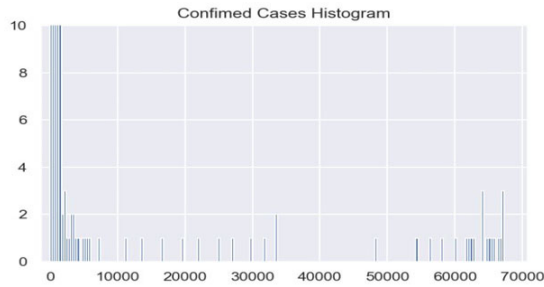


Figure 9: Showing a Generated Histogram of Confirmed cumulative cases.⁷

We can generate similar statistics for recovered cases as shown in Fig 10.¹⁷

Mean: 167.7042709867452

Standard Deviation: 1650.055340859415

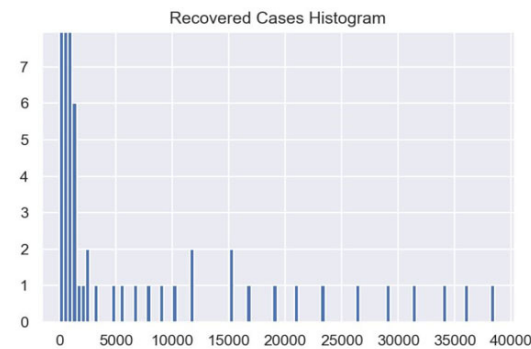


Figure 10: Showing a Generated Histogram of Recovered cases.¹⁷

Moreover, finally, we can look at the statistics for deaths as shown in Fig 11.¹⁷

Mean: 17.756111929307806

Standard Deviation: 187.19536561001198

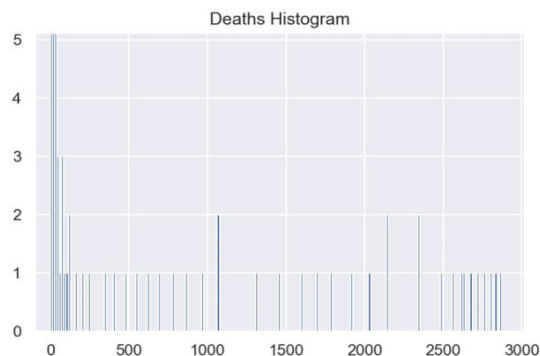


Figure 11: Showing a Generated Histogram of Death cases.¹⁷

We can also use box plots to visualize the distribution in numeric values based on the minimum, maximum, median, first quartile, and third quartile as shown in Fig 12.¹⁴

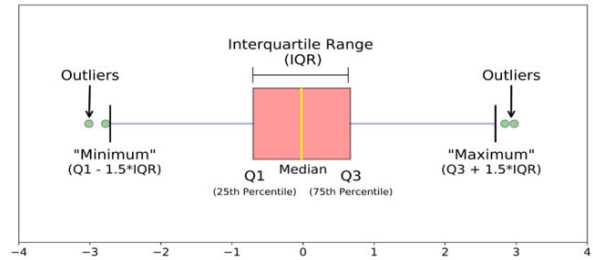


Figure 12: Showing a Generated Boxplot for Numeric Values.¹⁴

Let us plot the distribution in confirmed cases for 'Anhui,' 'Beijing,' and 'Chongqing' as shown in Fig 13.¹⁶

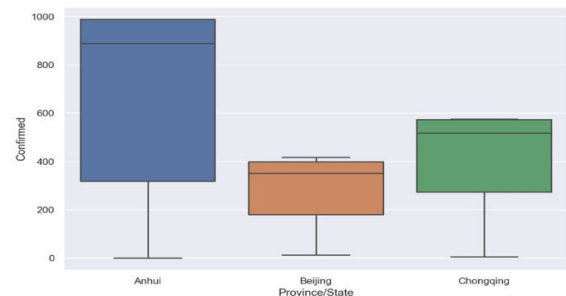


Figure 13: Showing Confirmed Cases in Anhui vs. Beijing vs. Chongqing.¹⁶

We can do the same for recovered cases as shown in Fig 14.¹⁶

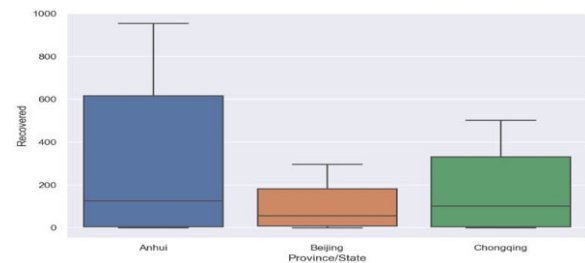


Figure 14: Showing a Recovered Cases.¹⁶

And for deaths as shown in Fig 15.¹⁶

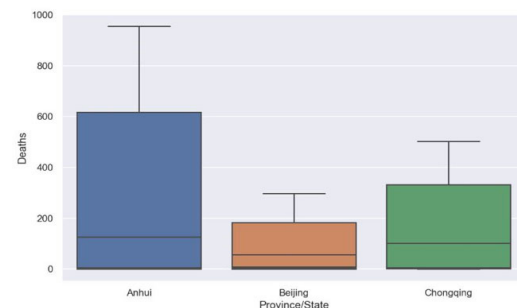


Figure 15: Showing Death Cases.¹⁶

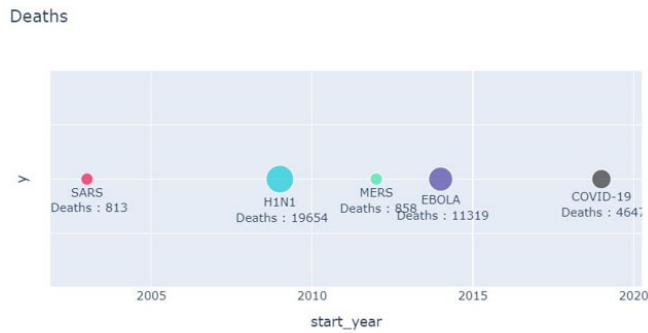


Figure 16: Timeline of Zoonotic Viruses.¹⁶

The above fig 16 shows the timeline of Zoonotic viruses effect from 2003 to 2019 for table 2.¹⁶

Table 2: Comparison of Zoonotic Viruses over the death rates¹⁶

Epidemic	Start-Year	End-Year	Confirmed	Deaths	No of Countries Effected
SARS	2003	2004	8432	813	31
EBOLA	2014	2016	28642	11319	10
MERS	2012	2017	2494	858	27
COVID-19	2019	TILL FEB 2020	126968	4647	114

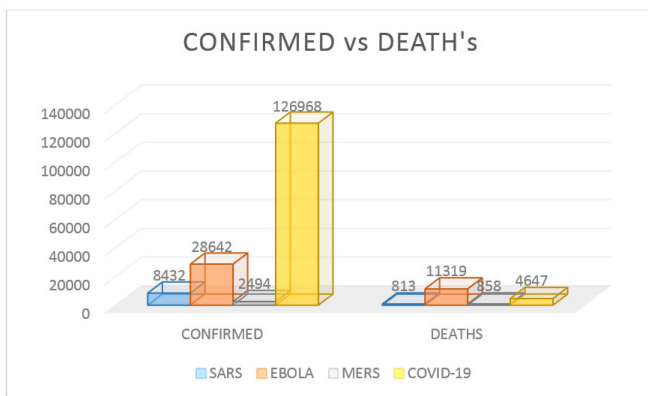


Figure 17: Showing No of cases confirmed vs. Deaths.⁸

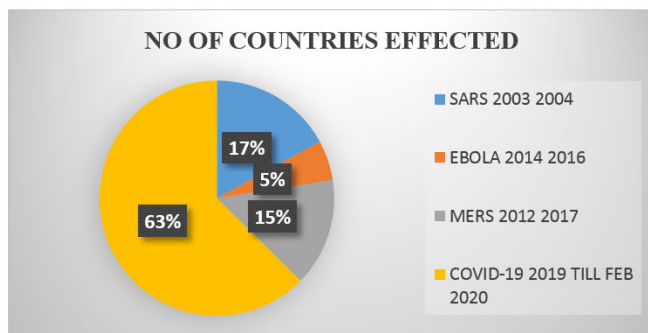
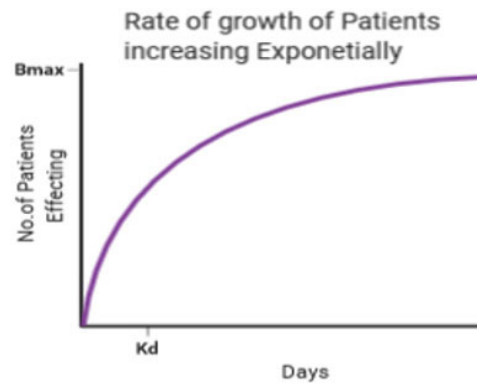


Figure 18: No of Countries Affected over some time.⁸



Created in BioRender.com [bio](https://www.biorender.com)

Figure 19: Rate of Increase of cases Exponentially.⁹

By this, we can estimate the rate of cases confirmed vs. Deaths occurred because of listed viruses in Fig 17.⁸ and the number of countries affected in Fig 18.⁸ and Rate of increase of cases in Fig 19.⁹, which leads to an abnormal increase of effect through the viruses.

CONCLUSION AND FUTURE WORK

Among the family of SARS (Severe Acute Respiratory Syndrome), nCov-19 has dominated all the other Zoonotic Viruses with exponential growth. nCov-19 effected the persons on their protein structure and DNA. By comparing the statistical analysis of confirmed cases vs. deaths within a short period, nCov-19 affected the most compared with Zoonotic viruses. The coronavirus disease remains to spread out throughout the globe, adhering to a trajectory that is challenging to predict. The health, altruistic, and socio-economic policies have taken on by nations will certainly figure out the rate and stamina of the healing. There has to be a global human-centred reaction that is based on solidarity. The unique coronavirus spread out so quickly that it has transformed the rhythm of the globe. Whether from the viewpoint of a single country or multilateral degrees, the solidity of international connections has been put under examination. One of the most noticeable effects includes the economic recession, a situation of global governance, profession protectionism, and also increasing isolationist view. People-to-people, social as well as travel exchanges, have all been restricted. However, this is just the tip of the iceberg. SARS-CoV-2 gets in human cells by binding to ACE2, a cell surface healthy protein that functions as a door to the infected cells. ACE2, an enzyme produced by the ACE2 healthy protein, naturally contributes to the upkeep of high blood pressure but is tricked by the infection into coming to be an entryway. One of the SARS-CoV-2 virus factors

is extremely transmittable because it can bind to the ACE2 cell receptor with greater fondness contrasted to the previous SARS-CoV infection, which created the condition called SARG which was much less transmittable, even though it created an epidemic in 2003. All-natural human ACE2 healthy protein variant inscribed in an individual's DNA can enable the infection to bind to ACE2 either strongly or weakly and, therefore, modify their susceptibility to the illness triggered the present pandemic. Further research can be done on Gene mutations that affect the healthy Z-Form of DNA.

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