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S-I-S Compartmental Modeling and Predictive Analysis of Covid-19 Progression in Selected Countries of the World

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Abstract: *The COVID-19 pandemic has had a significant impact on the global population, with varying impacts in different countries. The objectives of this study were to model and analyse the progression of COVID-19 using the SIS compartmental epidemic model in Nigeria, China, South Africa, and the United States. Using empirical data obtained from credible internet sources like Centers for Disease Control (CDC), Johns Hopkins Center for Systems Sciences and Engineering, Nigeria Centers for Disease Control (NCDC), and World Health Organization (WHO), the study aimed to determine the growth rate and ultimate death toll of the pandemic, predict the ultimate regional peaks, and estimate the number of cases in worst-and best-case scenarios. The results showed that the COVID-19 pandemic has had varying impacts in the analyzed countries, with different cumulative numbers of cases and deaths, reproductive numbers, and fatality rates. The results also show that the R2 were very impressive raging from 0.9903 to 0.9979. This shows that the model was almost perfect. The goodness of fit terms of coefficient of correlation (R2) of the developed model on test data gives excellent validation. For Nigeria, R2 is 0.9962 and 0.9968 for both death and cases test data respectively. For China, R2 is 0.9903 and 0.9912 for both death and cases test data respectively. South Africa R2 death and cases test are 0.9979 and 0.9976 respectively. For United States, R2 is 0.9975 and 0.99649 for both death and cases test data respectively.*

KEYWORDS: COVID-19, COMPARTMENTAL MODELLING, EPIDEMICAL MODELLING

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NOMENCLATURE: CCC: China COVID-19 Cumulative Cases, CCD: China COVID-19 Cumulative Death, FR: Fatality Rate, NCC: Nigerian COVID-19 Cumulative Cases, NCD: Nigerian COVID-19 Cumulative Death, RMSE: Root Mean Square Error, SACC: South Africa COVID-19 Cumulative Cases, SACD: South Africa COVID-19 Cumulative Death, SIS: Susceptible - Infected – Susceptible, SSE: Sum of Square Error, USCC: United State COVID-19 Cumulative Cases, USCD: United State COVID-19 Cumulative Death.

I. INTRODUCTION

The COVID-19 pandemic has had a significant impact on global healthcare, social, and economic structures. The spread of the disease, caused by the novel coronavirus SARS-CoV-2, has resulted in millions of cases and hundreds of thousands of deaths worldwide. To address the spread of the disease, various preventative measures, such as physical distancing and travel restrictions, have been implemented globally. However, the progression of COVID-19 has differed among countries, leading to the need for a better understanding of the dynamics of the disease (World Health Organization, 2020) (Centre for Systems Sciences and Engineering, 2022).

The newly emerged infectious disease known as Coronavirus 2019 (COVID-19) is caused by the novel severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) (Uddin et al., 2020). In December 2019, cases of this new respiratory illness were reported from Wuhan, Hubei Province, China. And was declared a health emergency by the World Health Organization (WHO) on March 11, 2021. This outbreak, which now accounts for the third major outbreak caused by coronaviruses over the last few decades, including SARS-CoV, 2002–2004 and Middle Eastern Respiratory Syndrome, MERS, 2012–present, is the most devastating in terms of the number of infections, mortality and morbidity, and is an exacting global reminder of the challenges posed by

emerging infectious diseases (Uddin et al., 2020; Leontitsis et al., 2021; Centre for Systems Sciences and Engineering, 2022). Indeed, strict measures to contain the exponential spreading of this Coronavirus including physical distancing, closure of businesses, and schools, as well as gathering and travel restrictions were implemented in varying degrees in most countries by government and public health authorities (Uddin et al., 2020).

While preventative measures were globally imposed, the observed progression of COVID-19 amongst selected nations shows noticeable differences. Epidemiologic data according to Johns Hopkins Centre for Systems Sciences and Engineering show that some countries have exponential surges in disease occurrence while others seem to have levelled the curve (Centre for Systems Sciences and Engineering, 2022).

This observation raises an obvious need to understand the dynamics of the COVID-19 disease because the spread of an epidemic depends on the infectivity of the pathogen and the available susceptible population. However, even though the transmission mechanism from infective to susceptible is understood for nearly all infectious diseases and the spread of diseases through a channel of infections is known, the transmission interactions in a population are very complex, making the understanding of large-scale dynamics of disease spread difficult without the formal structure of a mathematical model (Cosma, 2018; Becker et al., 2016).

In the study of infectious diseases, mathematical models have been used for decades, since since Sir Ronald Ross and Kermack-work McKendrick's in the 1900s (Kermack et al., 1927). Compartmental epidemiological models, such as the SIS model, are often used to mathematically model the spread of infectious diseases. These models divide a population into compartments, such as susceptible and infected individuals, and use ordinary differential equations or a stochastic framework to predict the spread of the disease through the population. SIS models specifically track the flow of individuals between the susceptible and infected compartments. (Galbadage et al., 2020). In the case of COVID-19, several models have been created to better understand the dynamics of disease transmission and available control options. The agent-based model developed by Ferguson et al. is one example of such a model. It was used to evaluate the impact of non-pharmaceutical interventions (NPIs) on COVID-19 mortality. According to their worst-case scenario forecasts, their model anticipated unacceptably high cumulative mortality in the US (2.2 million deaths) and the UK (510,000 deaths) in the absence of public health initiatives (i.e., the predicted COVID-19-induced mortality for the US was in the millions, while that of the UK was in the hundreds of thousands). Understanding the fundamental dynamics of the genesis, management, and mitigation of COVID-19 requires the use of mathematical models.

Eikenberry et al. (2020) utilized a multi-group Kermack-McKendrick-type epidemic model to evaluate the impact of public mask-wearing on the transmission of COVID-19 in the US. Their study demonstrated that the widespread use of face masks by the public has the potential to significantly reduce the impact of the pandemic and community transmission. The study also found that the use of face masks in combination with other non-pharmaceutical interventions (such as social distancing) and high compliance across the nation is likely to have the greatest positive effects on a community.

Using a stochastic model, Hellewell et al. (2020) showed that COVID-19 can typically be effectively contained within 3 months with highly effective contact tracing and isolation. Another stochastic model was used by Kucharski et al. (2020) to examine the COVID-19 trajectory in the Chinese city of Wuhan from January to February 2020. Their research demonstrated that the introduction of travel restrictions can result in a decrease in COVID-19 transmission.

Li et al. (2020) utilized a model for evaluating the impact of widespread influenza vaccination on the transmission of COVID-19 and other influenza-like viruses co-circulating during an influenza season to show that increasing the number of people who receive the influenza vaccine or improving public health initiatives will make it easier to control outbreaks of respiratory infections during the peak flu season.

To evaluate the effect of non-pharmaceutical treatments (NPIs) on the prevalence of COVID-19 in the general population, Ngonghala et al. (2020) created a thorough mathematical model. While early relaxation or lifting of social-distancing and community lockdown measures (as well as the wearing of face masks in public) is likely to cause a second wave, they discovered that prolonged implementation of these measures (as well as the wearing of face masks in public) can significantly lower COVID-induced mortality in the US generally and the state of New York in particular.

Mizumoto and Chowell (2022) used a mathematical model to examine the potential for an outbreak of COVID-19 on the Diamond Princess cruise ship, which saw a significant COVID-19 epidemic in January and February of 2020. They found that the model had a high reproduction rate, leading to significant outbreaks and that as the ship's isolation and quarantine measures became more effective, the reproduction rate significantly decreased.

Iboi et al. (2020) developed a mathematical model to determine whether a hypothetical vaccine with an expected efficacy of 80% could lead to the eradication of COVID-19 in the United States, assuming high vaccination coverage.

However, while many studies has examined the progression and transmission dynamics of COVID-19 using several compartmental models, they have not been able to factor into account the fact that COVID-19 does not seem to confer long-term mmunity and that individuals becomes susceptible after infection. This study aims to utilize SIS compartmental modelling and predictive analysis to examine the progression and transmission dynamic of COVID-19 in Nigeria, China, South Africa, and the United States. This is imperative since SIS compartmental model is best for diseases that do not confer long-term immunity. To achieve this aim, this study pursued the following objectives: (1) To utilize S-I-S compartmental modelling and predictive analysis to understand the progression of COVID-19 in selected countries around the world. (2) To determine the growth rate and ultimate death toll of the COVID-19 pandemic. (3) To predict the ultimate regional peaks of the pandemic. (4) To estimate the fatality rate of the disease in selected countries. (4) To analyze and estimate the effect of preventive measures adopted against COVID-19.

II. LITERATURE REVIEW

2.1 COVID-19

COVID-19 is a contagious disease caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). SARS-CoV-2 is a positive-sense single-stranded RNA virus that belongs to a group of related viruses known as coronaviruses (Uddin et al.,

2020). According to Khan, M. et al., (2021) the first coronavirus infection in humans was reported in 1960, although it was mistaken for a normal cold. However, the first deadly coronavirus-induced illness was seen in the world in 2002. However, SARS-CoV, also known as severe acute respiratory syndrome, was first identified in Foshan, China while Middle Eastern respiratory syndrome (MERS-CoV), another coronavirus infection outbreak, was later reported in Saudi Arabia in 2012, ten years later (Khan, M. et al. 2021).

2.2 COVID-19 VIROLOGY

According to Mohamadian et al. (2020), coronaviruses are virions that have viral envelopes and a diameter of 120 nm. The crown-like structure on the surface of these virions is created by cloverleaf structures such as glycoproteins and proteins. Due to their crown-like form, these viruses are also referred to as coronaviruses. Within the genetic makeup of the virus is the nucleocapsid, which is composed of proteins wrapped with capsids. The nucleocapsid of the coronavirus contains a genomic genus of RNA that is spiral- or ring-shaped. The coronavirus genome is made up of a single strand of positive RNA with a methylation warhead in each of its 50 sections and a high concentration of adenine nucleotides at the end of its 3' region. The coronavirus genome encodes a protein known as replicase enzyme, which copies the virus genome and makes new copies using the capacities of the host cell.

2.3 SYMPTOMS

According to Dhama et al. (2020) and Zhou et. Al 2020, the symptoms of COVID-19 can vary greatly among patients, with some individuals remaining asymptomatic. Fever, a dry cough, and weariness, however, are the signs of infection that are most frequently present in the early stages. Other, less frequent signs and symptoms include nauseousness or vomiting, pain in the muscles or joints, sore throat, loss of taste or smell, nasal congestion, conjunctivitis, headache, different kinds of skin rashes, diarrhoea, shivering, and dizziness. Patients may have acute shortness of breath, hypoxia (low blood oxygen levels), lung damage, and organ malfunction as the condition worsens. In more severe COVID-19 cases, uncommon neurological side effects such stroke, encephalitis, psychosis, and nerve damage have also been recorded (Salahshoori et al., 2021). The typical signs and symptoms of COVID-19 are shown in Figure 1.

Figure 1: The most minor and major symptoms of COVID-19 (Salahshoori et. al 2021).

2.4 TRANSMISSION ROUTE

The transmission of SARS-CoV-2, the virus responsible for COVID-19, has been identified to occur through close contact and respiratory droplets, as well as through contaminated surfaces and potentially through airborne and faecal-oral routes (Sharf, 2020; Mackenzie et al., 2020; Falali and Kenarkoohi, 2020). It has been found in various organs of infected individuals, including the eye, nasopharynx, saliva, alveolar lavage fluid, blood, intestine, and faeces (Mackenzie et al., 2020). The primary settings for human-to-human transmission are communities, healthcare facilities, and within households (Mackenzie et al., 2020). The high transmission rate and uncertainty surrounding the main modes of transmission pose significant challenges for infection control and prevention efforts, highlighting the importance of measures such as social distancing and mask-wearing, as well as hand hygiene and handwashing to prevent transmission through contaminated surfaces and touching of the face's T-zone (Falali and Kenarkoohi, 2020).

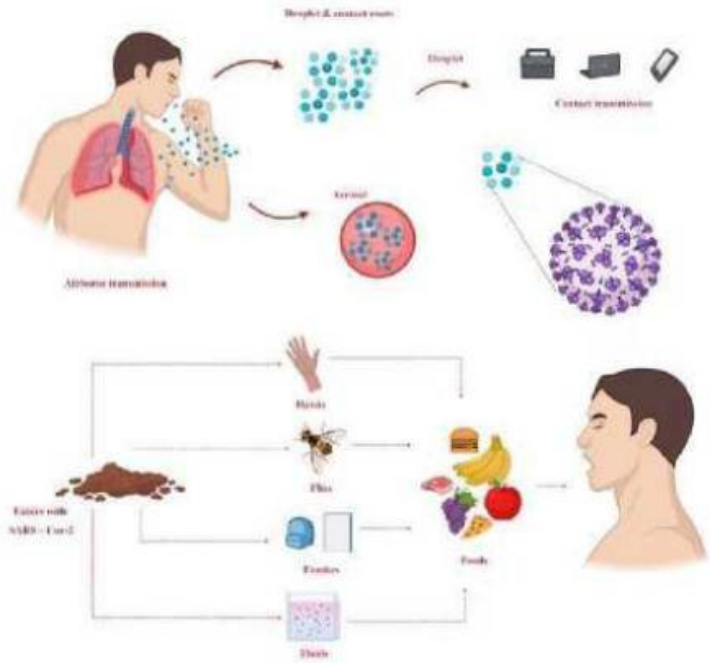

Figure 2. Schematic representation of SARS-CoV-2 Transmission Routes (Salahshoori et. al 2021).

2.3 EPIDEMIOLOGY
CHARACTERISTICS OF COVID-19

COVID-19 is generally a highly contagious disease, and most people are susceptible to it. The severity of the disease tends to increase with age and the presence of underlying conditions such as hypertension, diabetes, and cardiovascular disease. According to a study by Xu et al., (2020) the median age of onset for COVID-19 is around 55 years old. The global death-to-case ratio for COVID-19, according to data from Johns Hopkins University, is 1.29% as of March 20, 2022.

A systematic review and meta-analysis published in December 2020 estimated the infection fatality rate (IFR) for the general population during the first wave of the pandemic to be between 0.5% and 1% in some areas, such as France, the Netherlands, New Zealand, and Portugal, and between 1% and 2% in other areas, such as Australia, England, Lithuania, and Spain. The IFR was estimated to be above 2% in Italy. It was discovered that these variations in IFR primarily correspond to variations in the population's age distribution and age-specific infection rates. For kids and younger people, the IFR was found to be extremely low (0.002 percent at age 10 and 0.01 percent at age 25), but it gradually rose to 0.4 percent at age 55, 1.4 percent at age 65, 4.6 percent at age 75, and 15 percent at age 85. These findings were also highlighted in a report issued by the World Health (Levin et al., 2020).

Table 1: Infection fatality rate (IFR) estimate per age group (to December 2020) (Levin et al., 2020).

Age Group	IFR (%)
0-34	0.004
35-44	0.068
45-54	0.23
55-64	0.75
65-74	2.5
75-84	8.5
85+	28.3

Most nations have higher COVID-19 case fatality rates for men than for women, although others, like Slovenia, India, Nepal, Vietnam, and Slovenia, have higher female fatality rates (Dehingia, 2021). With roughly 55 men and 45 women per 100 infections, a different meta-analysis indicated that men were more likely than women to get COVID-19 internationally (CI: 51.43-56.58). (Abate et al., 2020).

According to a meta-analysis published in November 2020, the virus's basic reproduction number (R0) ranges from 2.39 to 3.44, which means that in the absence of protection and preventive measures, each infection is anticipated to result in 2.39 to 3.44 more infections (Billah et al., 2020). R0, however, can be influenced by human behaviour as well as cultural and societal norms and may be higher in areas with high population density (Rockiov et al., 2020). For instance, one study discovered that Spain and the US had much higher R0 values than Sweden, Belgium, and the Netherlands, which had comparatively low R0 values of 3.5 and 5.9 to 6.4, respectively (Ke et al., 2021). The reproduction values of various SARS-CoV-2 variants are shown in Table 2.

Table 2: The Reproductive value R0 of SARS-Cov2 variants, (Liu et al., 2020; Davies et al., 2021; Liu et al., 2021).

Variant	R0
Reference/ancestral strain	~2.8
Alpha (B.1.1.7)	(40-90% higher than previous variants)
Delta (B.1.617.2)	~5 (3-8)

III. METHODOLOGY

SIS compartmental model which stands for susceptible, infected and susceptible compartmental epidemiology model was used. The SIS compartmental model is a model for diseases for which infection does not confer long-term immunity. It is called an SIS model since individuals return to the susceptible class when they recover from the infection.

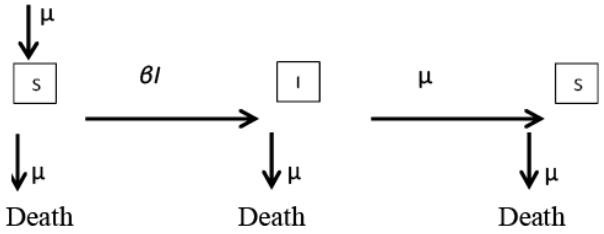

Figure 3. The compartmental diagram for an SIS model (Kamalu et. al., 2016)

In the compartmental diagram for an SIS model is given in Fig. 3, naturally occurring births and deaths (vital dynamics) are included, but the behaviour of solutions is similar when vital dynamics are not included. Additionally, in developing the model, the following assumptions were made: (1) The population under consideration is broken down into arbitrary classifications that change over time t. The susceptible class consists of people who are capable of contracting the illness but are not yet contagious, whereas the contagious class includes people who are spreading the illness to others. S(t) and I(t) stand for the percentages of the population that belong to each class, respectively. (2) The population under consideration has a constant size N, which is a big enough number to qualify the sizes of each class as continuous variables. (3) The population is mixing uniformly. (4) The entire human population at time t, represented as N(t), is divided into compartments of susceptible (S(t)), infectious (I(t)), and susceptible (S(t)) individuals. Thus, the SIS model equations as obtained from Kamalu et al. (2016)

$$I(t) = \frac{\mu(R_0-1)}{\beta+ae^{-\mu(R_0-1)}} \ldots \text{Eqn (1)}$$

$$(t) = \frac{a\mu^2(R_0-1)2_e{}^{-\mu(R_0-1)}}{[\beta+ae^{-\mu(R_0-1)t}]^{\ 2}} \ldots \text{Eqn (2)}$$

the peak time,

$$t_{pk} = \frac{1}{\mu(R_0-1)}\ In\ \frac{a}{\beta} \ldots \text{Eqn (3)}$$

3.2 COLLECTION OF DATA AND PARAMETER ESTIMATIONS

The COVID-19 data were obtained from a systematic search conducted on international scholars and credible databases including The World Health Organization, Nigeria centre for disease control (NCDC), Centre of disease control and prevention CDC, and Johns Hopkins Centre for System Sciences and Engineering (CSSE) for Nigeria, China, Unites States and South Africa. Keywords, such as "2019-nCoV," "2019 novel coronavirus," "nCoV," and "COVID-19 were used in the search to identify articles and data on COVID-19.

3.2 CURVE FITTING

After careful extraction of the data, the cumulatives were calculated and numerical values in were plotted using the MATLAB toolbox package to obtain scatter diagrams. The models were then superimposed on the scatter diagrams after which the toolbox was asked to apply the models to the scatter diagrams. Profiles will be plotted showing the models following the scatter diagrams and simultaneously, the numerical values of the constants of the models will be declared with 95% confidence bound as well as their statistical goodness-of-fits.

Furthermore, we estimate the respective rates for each of the eight data sets. In particular, we fit the rate of the cumulative number of deaths and cases generated from the model in equation 4 to observe the rate of the death and confirmed cases respectively.

IV. RESULT DISCUSSION

The results of the study show that the COVID-19 pandemic has had different impacts in different in Nigeria, China, South Africa, and the United States, with varying numbers of cases and deaths, fatality rate and different reproductive numbers (the average number of people that one infected person will infect).

4.1. NIGERIA

In Nigeria, the COVID-19 pandemic has resulted in a relatively lower number of cases and deaths compared to other countries. The ultimate number of cases and deaths are 3936090 and 54841.1 with a reproductive number of R0 = 1.50. The peak rate of death and cases occur 20 months with 2900.39 deaths and 20 months with

229569 respectively, so that the peak fatality will be 1.26%. This suggests that the virus has had a relatively lower impact in Nigeria compared to other countries. Figures 4 and 5 are the Nigerian COVID-19 cumulative death versus time and the rate of Nigerian cumulative deaths versus time. Figures 6 and 7 are Nigerian COVID-19 Cumulative Cases versus time and the rate of Nigeria COVID-19 Cumulative Cases versus time.

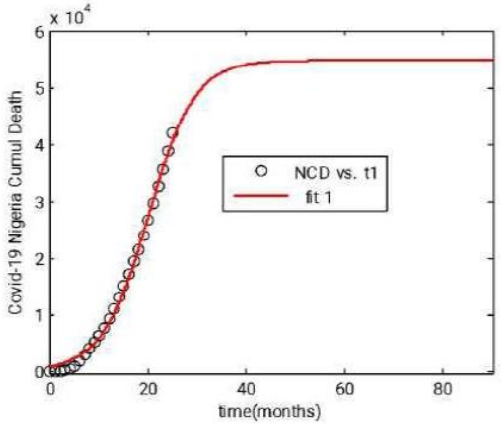

Fig 4: Nigerian COVID-19 Cumulative Death versus time (months)

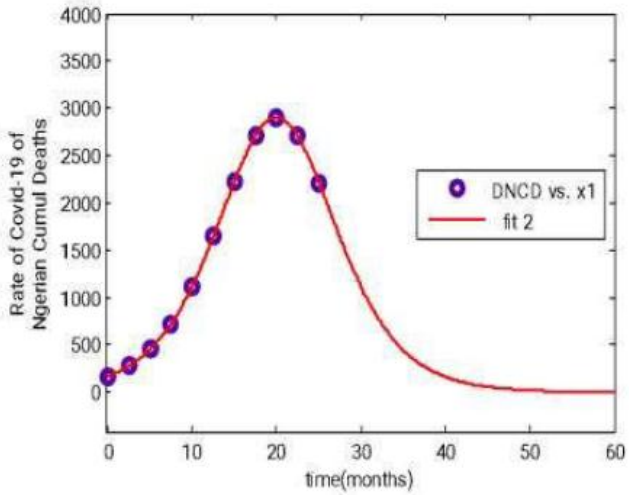

Fig 5: Rate of Nigerian COVID-19 Cumulative Deaths versus time (months)

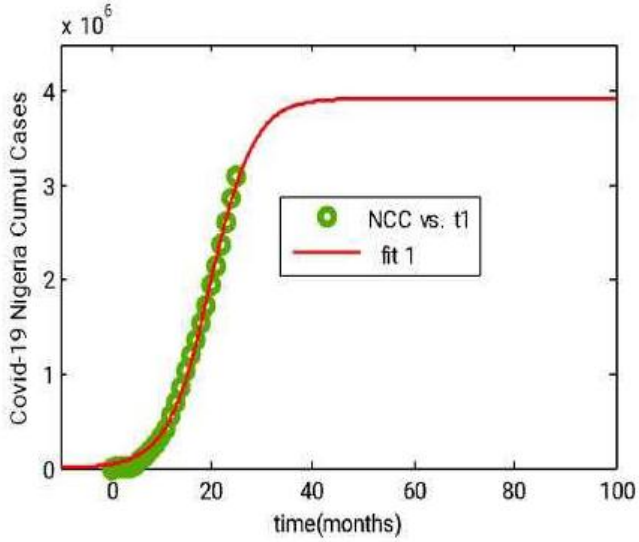

Fig 6: Nigerian COVID-19 Cumulative Cases versus time (months)

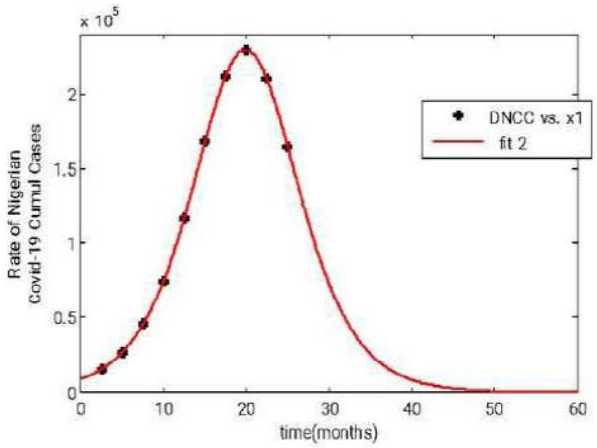

Fig 7: Rate of Nigerian COVID-19 Cumulative Cases versus time (months)

4.2 CHINA

In China, the COVID-19 pandemic has resulted in a moderate number of cases and deaths, with the ultimate number of cases and deaths amounting to 2807410 and 124794 at 86.5 and 86.8 months respectively. The reproductive number R0 =1.28 and the peak rate of death and cases occur 15 months with 5955.06 deaths and 15 months with 121682 respectively, so that the fatality rate FR = 4.89%. This suggests that the virus has had a moderate impact in China compared to the other countries in terms of the number of infected persons and death, China has the highest likelihood of death for every infected person. This is to say that for every infected person in China, there is a 4.8% chance of death. Figure 8 and 9 are
China COVID-19 Cumulative Deaths versus time and the rate of China COVID-19 Cumulative Deaths versus time. Figure 10 and 11 are China COVID-19 Cumulative cases versus time and the rate of China COVID-19 Cumulative cases versus time.

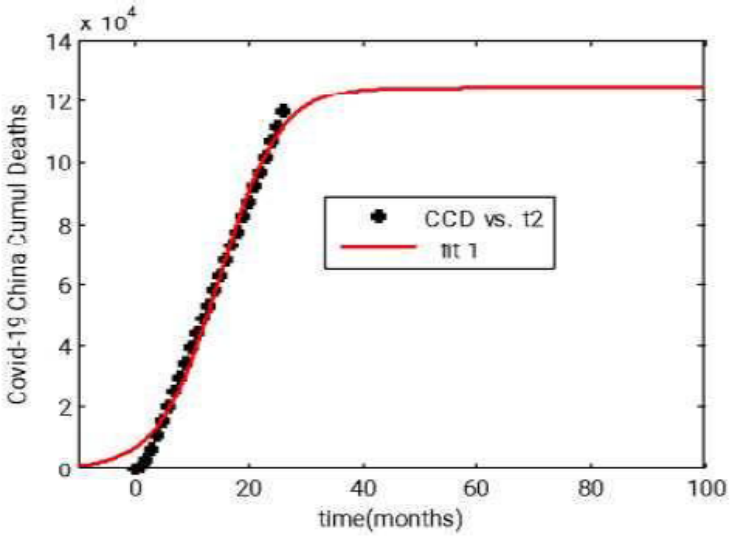

Fig 8: China COVID-19 Cumulative Deaths versus time (months)

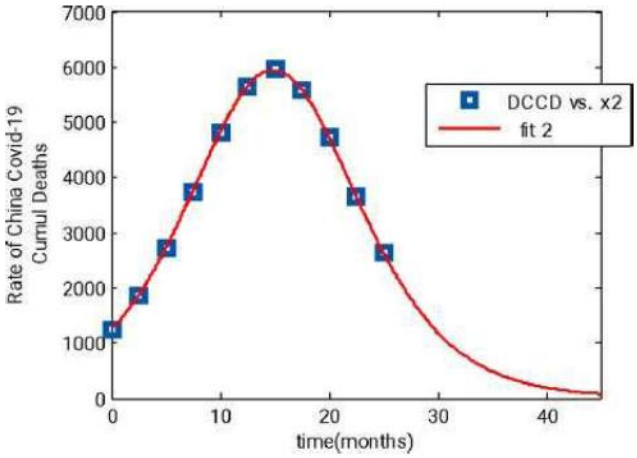

Fig 9: Rate of China COVID-19 Cumulative Death versus time (months)

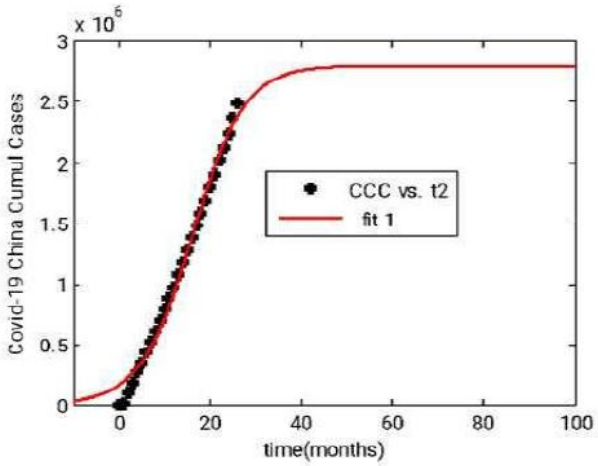

Fig 10: China COVID-19 Cumulative Cases versus time (months)

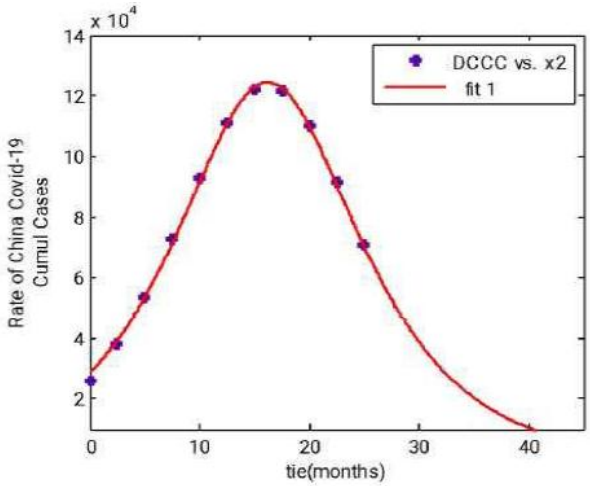

Fig 11: Rate of China COVID-19 Cumulative Cases versus time (months)

4.3 SOUTH AFRICA

In South Africa, the COVID-19 pandemic has resulted in a high number of cases and deaths. The ultimate number of cases and deaths are 53076000 and 1391180 with a reproductive number of R0 = 1.53. The peak rate of death and cases occur 20 months with 89157.7 deaths and 20.7 months with 3074750 respectively, so that the peak fatality will be 2.90%. This suggests that the virus has had a significant impact in South Africa compared to other countries. Figure 12 and 13 are South African COVID-19 Cumulative Deaths versus time and

the rate of South African COVID-19 Cumulative Deaths versus time. Figure 14 and 15 are South African COVID-19
Cumulative cases versus time and the rate of South African COVID-19 Cumulative cases versus time.

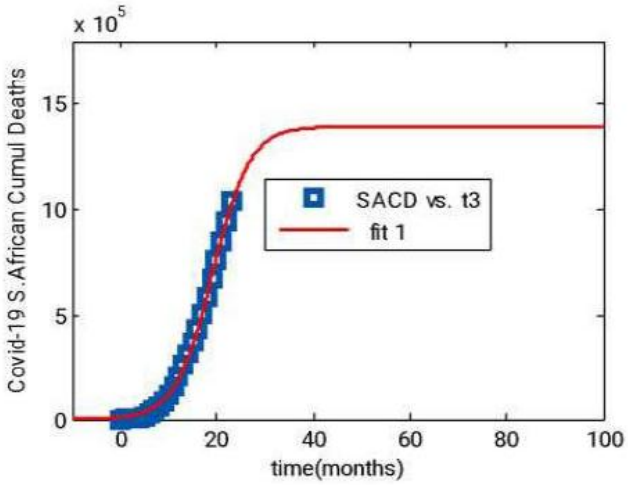

Fig 12: South African COVID-19 Cumulative Deaths versus time (months)

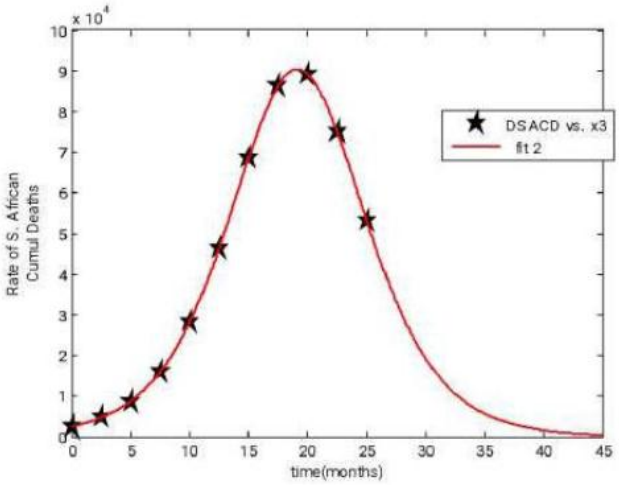

Fig 13: Rate of S. African Cumulative Deaths versus time (months)

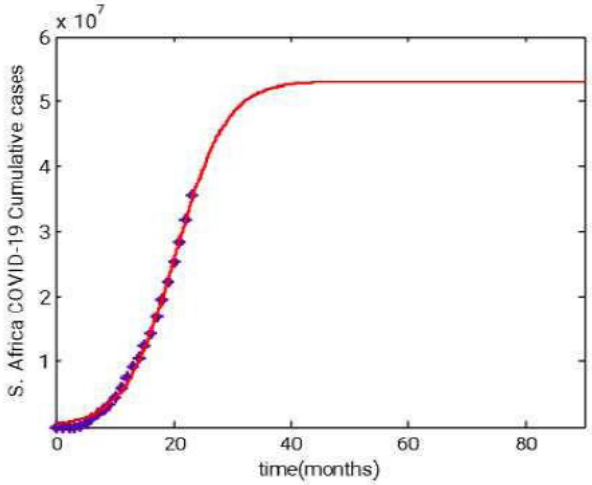

Fig 14; South African COVID-19 Cumulative Cases versus time(months)

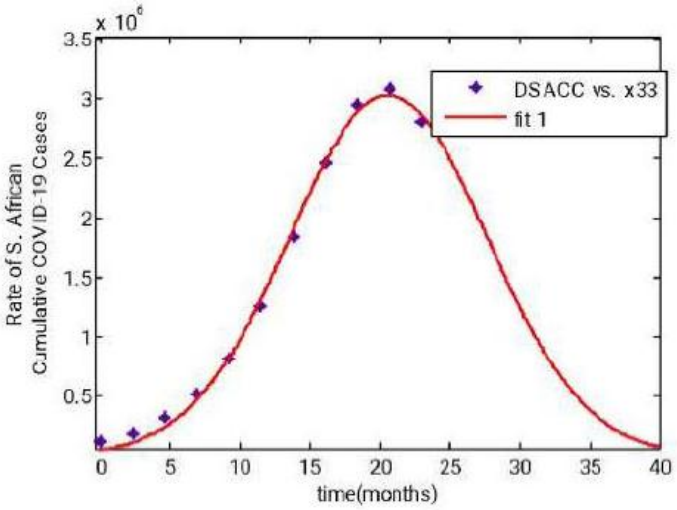

Fig 15: Rate of South African COVID-19 Cumulative Cases versus time (months)

4.4 UNITED STATES

In the United States, the COVID-19 pandemic has resulted in a high number of cases and deaths, with the ultimate number of cases and deaths amounting to 740725000 and 12440000 at 83.9 and 69.7 months respectively. The reproductive number R0 =1.48 and the peak rate of death and cases occur 19.2 months with 721291 deaths and 22.5 months with 43996400 respectively, so that the fatality rate FR =1.64%. This suggests that the virus has had a severe impact in the United States compared to other countries in terms of the total number of cases and deaths. However, in terms of the fatality rate, it is clear that the United States despite the high number of cases and deaths maintained a lower fatality rate slightly above Nigeria and below South Africa. Figure 16 and 17 are United State COVID-19 Cumulative Deaths versus time and the rate of United State COVID-19 Cumulative Deaths versus time. Figure 18 and 19 are United State COVID-19 Cumulative cases versus time and the rate of United State COVID-19 Cumulative cases versus time.

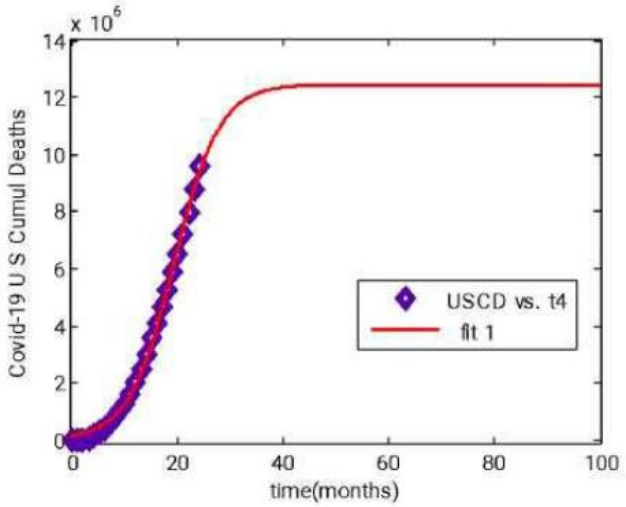

Fig 16: United States COVID-19 Cumulative Deaths versus time (months)

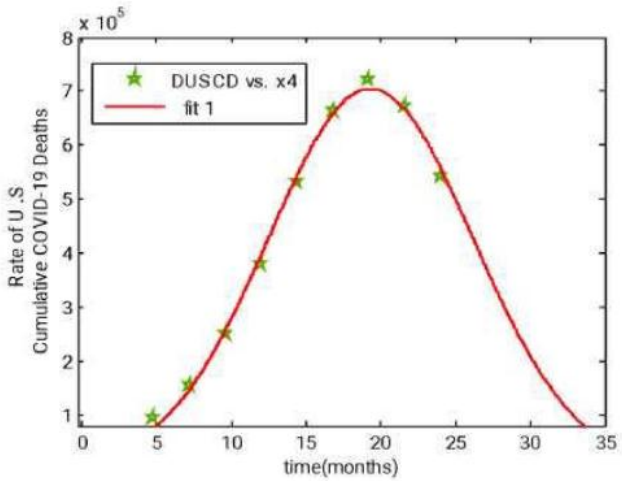

Fig 17: Rate of United States COVID-19 Cumulative Deaths versus time (months)

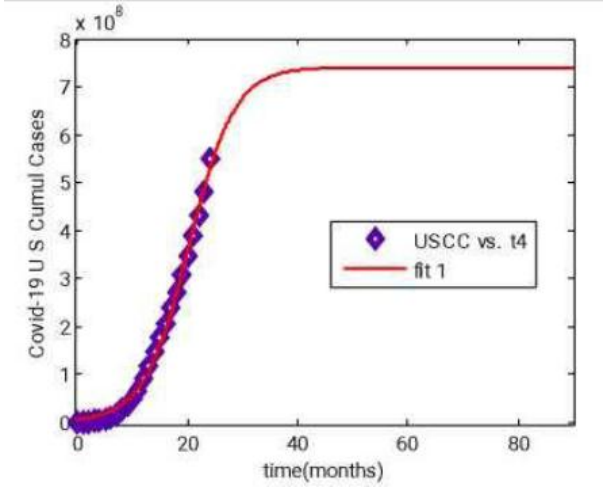

Fig 18: US covid-19 cumulative cases versus time (months)

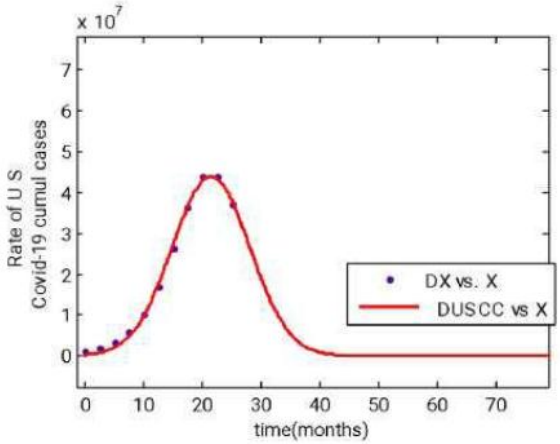

Fig 19: Rate of United States COVID-19 Cumulative cases versus time (months)

The results showed that the COVID-19 pandemic has had varying impacts in these countries, as indicated by the different cumulative numbers of cases and deaths, reproductive numbers, and fatality rates. The results also show that the R^2 were very impressive raging from 0.9903 to 0.9979. This shows that the model was almost perfect. The goodness of fit terms of coefficient of correlation (R^2) of the developed model on test data gives excellent validation. For Nigeria, R^2 is 0.9962 and 0.9968 for both death and cases test data respectively. For China, R^2 is 0.9903 and 0.9912 for both death and cases test data respectively. South Africa R^2 death and

cases test are 0.9979 and 0.9976 respectively. For United States, R^2 is 0.9975 and 0.99649 for both death and cases test data respectively.

V. CONCLUSION

In conclusion, this study analyzed the progression of COVID-19 in Nigeria, China, South Africa, and the United States using an SIS model and empirical data obtained from credible internet sources like Centre for Disease Control (CDC), Johns Hopkins Centre for Systems Sciences and Engineering, Nigeria Centre for Disease Control (NCDC), and World Health Organization (WHO). These findings add to our understanding of the COVID-19 pandemic and its varying impacts of the virus in different countries. Despite the staggering number of deaths and cases of COVID-19 in South Africa and the United State, they managed to maintain a low fatality rate which tells a lot about their healthcare system that is among the four countries. Nigeria has the lowest fatality rate of 1.26% followed by the United States with 1.64%, South Africa with 2.90%, and China with 4.98%. However, the results of this study may be limited by several factors, including the accuracy of the data used and the potential for missing relevant factors that could have impacted the progression of the pandemic. Future research should aim to address these limitations and provide a more comprehensive understanding of the COVID-19 pandemic and the effectiveness of different interventions. This information can inform policy decisions and help to better prepare for and respond to future pandemics. In addition and based on the results further research should be conducted to better understand the characteristics of COVID-19 and how it impacts different countries, including the potential for reinfection and the long-term effects of the virus on individuals. Efforts should be made to improve data collection and reporting on COVID-19 cases and deaths, including ensuring that all cases are accurately counted and classified. Clear, timely, and transparent communication is critical to effectively responding to the COVID-19 pandemic. Governments and health authorities should work to ensure that the public is informed about the risks and ways to protect themselves.

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