Mathematical Modelling of Covid-19 Pandemic with Vaccination in Kaduna State, Nigeria

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Abstract
A study is made into the outbreak of the Corona Virus (Covid-19) disease pandemic, which the world had been battling since 2019. The disease is caused by the novel SARS-COV 2 highly virulent strain of flu, which infects the human respiratory system, and can lead to death. The virus was discovered in December 2019 where it began in a damp animal market in Wuhan city, Hubei province, China. This research work presents a COVID-19 transmission mathematical model that incorporates vaccination and other non-pharmaceutical measures like quarantine, and also provides a theoretical analysis of the model. The research has also estimated the free and endemic equilibrium points of COVID-19 as well as the vaccine reproduction number were estimated. For disease eradication to be successful, the basic reproduction number $R_0<1$, and the resulting vaccination reproduction number must be highly effective. Also, if more than one dose of the vaccine is taken, there is a much lower chance of getting sick from the disease. The results of the simulations indicate that the COVID-19 vaccines have been effective worldwide, but there was a skepticism about it in Kaduna State. But non-pharmaceutical interventions have been seen to be very effective in combating Covid-19. It is recommended that more public health awareness be created in order to effectively tackle future outbreaks and spread of the virus and other epidemics, and the simulation results be used to predict future spread of outbreaks.

Keywords: Basic Reproduction Number, Corona Virus (Covid-19), Epidemic, Mathematical Modelling, Pandemic, Vaccination.

INTRODUCTION
For over one year, the world had been battling with the Corona Virus (Covid-19) disease, which is caused by the novel SARS-COV 2 highly virulent strain of flu, which infects the human respiratory system, and can lead to death. The virus was discovered in December 2019 where it began in a damp animal market in Wuhan city, Hubei province, China. But its actual anthropological and vector origins and metamorphoses are still a subject of debate. This disease, as has been novel, has continued to cause a major burden on public health and safety, and the socio-economic life of the world (Iboi *et al.*, 2020). The World Health Organization (WHO) declared Covid-19 a pandemic on March 11th, 2020, (Cucinotta & Vanelli, 2020).

In the build-up to the global spreading of the illness, it was found that there was a need to develop a highly effective vaccine to contain the spread of the virus. Scientists were mobilized worldwide to begin the search for an effective vaccine against the virus, which would hopefully lessen the virus's ability to propagate and further flatten the curve of its morbidity. So many countries were initially skeptical about the effectiveness of developing a vaccine at such a very short period, because the vaccines go through a clinical trial period of not less than 10 years to be certified safe and effective to be administered in humans. But, the story of the Covid-19 vaccine subsequently became a success story, when scientists were able to produce a vaccine within a record period of nine (9) months and subsequently began to administer it on humans. This further boosted the confidence in science and scientific discoveries as a bulwark for human advancement and development (Lockey E., 2020; El-Bagourya *et al.*, 2021).
As at the 5th August 2021, the global infection of Covid-19 is over 200,840,180 with about

4,265,903 confirmed deaths and 3,984,596,440 vaccine doses have been administered. While in Nigeria, as at 3rd August 2021 there were 176,577 confirmed cases of Covid-19, 2,178 deaths and 3,938,945 doses of vaccines have been administered (WHO, 2021). From the data on Nigerian Centers for Disease Control (NCDC), Kaduna State is the 3rd highest with Covid 19 infections standing at 9,158 and deaths at 65, (NCDC, 2021).

Despite the overwhelming awareness of the effects of the Covid 19 disease and its dangers to human health, a vast population of Nigerian citizens, and Kaduna State, have been skeptical about its existence. Even with the discovery of a Vaccine for the virus, a good number of people are still in doubt about the existence of the virus, l*et al*one of an antidote for it. Hence the need for a study into the rate of awareness of Covid 19 Vaccine administration and prevention strategies using Kaduna State as a case study

Most research works and studies on Covid 19 have been on control strategies of usage of non-pharmaceutical interventions. There are very few studies that look into vaccination strategies as a control measure, such as (Wu *et al.*, 2014). Hence, this study intends to capture the gaps inherent in the lack of awareness of vaccination as a long-term control strategy for Covid 19 and other flu-related viral diseases.

This main aim of this research is to develop a mathematical model of Covid-19 pandemic and vaccination administration in Kaduna State by incorporating the Vaccination parameter to the SEIR model. This model was tested and analyzed in order to predict the spread of future outbreaks of the virus, based on the rate/efficacy of vaccination, and also proffer long term prevention, control and mitigation measures.

REVIEW OF RELATED LITERATURE

Mathematical Modelling

A mathematical model is a system description that uses mathematical ideas and terminology. Making a mathematical model is the process of mathematical modeling (Kin, 2012). This definition is strengthened by Kaur and Dindyal (2010), who opined that making and enhancing a mathematical model to describe and address real-world issues is known as mathematical modeling. By concentrating on the key components of a disease, establishing threshold levels for illness survival, and assessing the impact of certain control techniques, mathematical modeling can be useful in quantifying potential disease control strategies (van den Driessche, 2017).

Epidemiological Models

Epidemiology

Epidemiology is a method used in communities to determine the underlying causes of diseases and other health problems. In epidemiology, every member of the population is viewed as a patient. The scientific, rigorous, and information-driven study of the incidence, prevalence, patterns, causes, and risk factors linked with health in different demographics (neighborhood, school, city, state, country, global) is known as epidemiology. Additionally, this study's usefulness to the prevention and treatment of health issues (Dicker *et al.*, 2006).

An Epidemiological Model

According to standard definitions, an epidemiological model is "a mathematical and/or logical description of the epidemiology of disease transmission and its related processes." (Dubé *et al.*, 2007).

Application of Mathematical Models in Epidemiology

Since quite some time, mathematical models have been applied to the study of infectious illnesses. (Okuonghae & Omame, 2020).Daniel Bernoulli used mathematical life table analysis to illustrate the effects of smallpox variolation, a form of immunization, on life expectancy in a 1766 essay (Dietz & Heesterbeek, 2002). But the nonlinear dynamics of infectious illness transmission weren't well recognized until the 20th century (Kretzschmar & Wallinga, 2009).

Kermack and McKendrick used a set of differential equations to define the kinematics of disease propagation in a series of articles released in 1927 (Kermack and McKendrick 1991a; Kermack and McKendrick 1991b; Kermack and McKendrick 1991c). They developed the idea of a threshold value that would divide several dynamic regimes. An infectious illness can only affect a population if its "fundamental reproduction number" rises over a particular threshold. This gives birth to

the idea of "herd immunity" in the context of vaccination, which maintains that an infectious illness may be eradicated without vaccinating every member of the community. This idea was shown to be true during the 1970s smallpox eradication campaign.

It wasn't until the end of the 20th century that public health policy was informed by mathematical modeling. Modeling techniques were used more and more in the first two decades of the AIDS pandemic to predict the future course of the disease and identify the best preventive strategies.

However, mathematical modeling's biggest impact on public health came when it became necessary to evaluate intervention choices for recently developing and reemerging illnesses. Fear of a smallpox-related bioterrorist attack spurred the first use of mathematical modeling to combine historical data from smallpox outbreaks with questions about vaccination in modern civilizations (Ferguson *et al.,* 2003). Subsequently, the SARS virus pandemic caused by an emerging pathogen led to the application of mathematical modeling to assess real-time data analysis on infectious disease outbreaks and the efficacy of intervention strategies (Wallinga & Teunis, 2004).

While investigation of previous influenza A pandemic data, the fundamental reproduction quantity of influenzas has been low in prior outbreaks, the serial interval is short, which is a significant insight brought about by epidemics (Mills *et al.*, 2004). This suggests that while swift action is required for effective steps to be taken, an influenza outbreak can theoretically be controlled with moderate levels of intervention. In contrast, a sickness with a high basic reproduction number, like the measles, requires very high levels of vaccination coverage. The formulation of effective intervention policies and the evaluation of current interventions both greatly benefit from these mathematical analysis-derived insights.

The Susceptible-Infected-Recovered/Susceptible-Exposed-Infected-Recovered (SIR/SEIR) Model

In 1911, Sir Ronald Ross created the SIR/SEIR Model to investigate, evaluate, comprehend, and forecast infectious illnesses (Weiss, 2013). According to their illness condition, people within a closed population are divided into mutually exclusive groups, or compartments, in the SIR/SEIR paradigm. Each individual is assumed to be in one compartment at any given moment (t), however they are free to switch between compartments based on the model's parameters. The SIR model, so named for its three (3) compartments, is one of the most fundamental compartmental models (susceptible, infected, and recovered). According to this hypothesis, the infection process starts when a vulnerable person comes in touch with an infected person. Following an initial phase of infection during which the person is thought to be contagious, the person advances to a noncontagious state known as recovery, but this stage may involve isolation or even death (Tolles & Luong, 2020).

Rodrigues (2016) elaborated on the applications of SIR epidemiological models, and expressed the significance of epidemiological models in foretelling the progression of a disease, its effect on the populace, and the health systems' use of both human and material resources. Due to their shortcomings, these models, in Rodrigues (2016) opinion, might be used as a first tool to attempt when a new problem arises. Even so, they are a big assistance in defining new research steps and emergency responses to crises when there is little time to prepare.

The modeling and analysis of an SEIR model with various nonlinear treatment rates, was studied by Dubey *et al.*, (2013), where they conducted stability analyses for both endemic and disease-free equilibriums. They noticed that the fundamental reproduction number determines R_0 as well as on treatment rate whether a certain endemic equilibrium exists.

Mitigation and Containment Strategies

The modelling of ways to control and reduce the SARS epidemic in the absence of a quick diagnostic test, treatment, and vaccination was detailed and presented as early as 2004 (Gumel *et al.*, 2004). Using a deterministic model that closely resembles the data for cumulative infected cases and SARS-related deaths in the first three locations, they mathematically investigated the effect of isolation and quarantine on the containment of SARS during the epidemics in Toronto, Hong Kong, Singapore, and Beijing. The findings showed that reducing the incidence of contact between susceptible and ill people by isolating the latter is a crucial tactic that can limit SARS

epidemics with or without quarantine. A critical threshold value-based isolation program requires prompt deployment under strict sanitary safeguards.

A large-scale stochastic simulation model was developed and used by Timothy *et al.,* (2006) to study pandemic influenza mitigation strategies in the United States. They looked at how a pandemic strain of the influenza virus would spread among the 281 million people who make up the country's population for R_0 (the basic reproductive number), which ranges from 1.6 to 2.4. Timothy *et al.'s,* (2006) research model predicts that with $R_0 < 1.9$, quick vaccine manufacturing and distribution, even if they are insufficiently matched to circulating strains, might dramatically reduce disease transmission and keep the number of ill to <10% of the population, especially if children are given vaccination preference. They also recommended utilizing the following intervention techniques aggressively;

(i) Socially targeted antiviral prophylaxis (TAP), in which those with symptoms and the majority of their close contacts are treated or prevented with antiviral medications, respectively;

(ii) Dynamic mass vaccination, using different manufacturing and distribution rates, commencing at different times, and including either a random sample of people from the whole population or a predilection for children;

(iii) Shutdown of all schools, including playgroups and preschools, and

(iv) Social estrangement brought on by voluntarily altered social conduct or by legally required travel restrictions or quarantine programs.

The necessity of an efficient immunization plan was stated in (Tuite *et al.,* 2010). Model simulations suggest that high-risk groups of any age should receive immunizations first, followed by age groups with a larger likelihood of disastrous outcomes. The effects of vaccination depend on the dynamics of the epidemic, the timing of program rollout, and vaccine uptake, although the benefits may considerably lower morbidity and death owing to influenza.

An influenza model including treatment and vaccination and two preventative scenarios, a rise in vaccine uptake and a reduction in vaccine uptake, was subjected to an optimum control and sensitivity analysis by Tchuenche *et al.,* (2011). They found that when an outbreak first starts, full treatment efforts should be made while immunization rates are raised. The model, however, did not account for the interval before vaccination or the impact of seasonal fluctuation and climatic change on the dynamics of the illness.

Studies by Wu *et al.,* (2014) examined the effects of a widespread vaccination program against the H1N1 influenza pandemic in Taiwan in 2009. They came to the conclusion that widespread influenza vaccination was a successful preventative approach and that, both before and during an influenza pandemic, school-aged children should receive higher priority for immunization than adults. The creation of a successful vaccination program was identified as the most crucial medicinal defense against the flu virus.

Saunders-Hastings *et al.,* (2017) highlighted the necessity for a targeted early vaccine distribution to high-risk persons and locations and listed the requirement for an inter-wave vaccination as a technique to buffer against the consequences of a flu pandemic crisis.

It is impossible to overstate the importance of public health in raising awareness and providing healthcare palliatives. Weiss (2013), The SIR Model and the Foundations of Public Health, and Levy *et al.,* (2013) both covered this. They underlined the need to lower an epidemic's fundamental reproduction number to $R_0<1$.

An investigation of the clinical effects of the influenza virus on a patient who had not received vaccinations was conducted by (Harmon *et al.,* 2019). Children and the elderly should be protected against the influenza virus, and the severity of the illness should not be overlooked across all demographic groups.

More recently, a model was developed to show how vaccination affects the dynamics of an infectious illness like pneumonia (Rahman *et al.,* 2020). The study made the claim that pneumonia's infectious rate, a fictitious symptom of Corona, might be eliminated if the disease's effective reproduction number could be brought down to less than unity. It went on to suggest the use of additional preventative controls, such as those that would regulate the variables that significantly affect the number of reproductions.

Different pieces of literature have modeled and recommended a variety of control techniques

and strategies; (Algaissi *et al.*, 2020; Daniel Deborah, 2020; Kouidere *et al.*, 2020; Mumbu & Hugo, 2020; Zakary *et al.*, 2020)

METHODS

Description of the Study Area

The study area considered is Kaduna State. Kaduna State, which is located in the North-Western region of Nigeria. It has a population size of 6,113,503 (*State Population, 2006 - Nigeria Data Portal*, NPC.2006), which is the third highest in Nigeria. But as at 2021 it was estimated to have a population of 9,048,000 (Kaduna State Government Website)

Study Design

The study design is both analytic, experimental and quantitative.

Study Population

The study population is from all Covid – 19 infections and treatment. These included but was not limited to the actual and assumed/projected population of Kaduna State as at the time of conducting the research.

Data Collection

The data for the study was obtained from the National Center for Disease Control (NCDC), which is the major coordinating body for all Covid – 19 related activities in Nigeria.

Figure 1 is the graphical representation of the weekly confirmed Covid-19 infections in Kaduna State from 28th March, 2020 to 17th September, 2022.

Also, Tables 1 – 3 gives the weekly breakdown of the Covid-19 Infections, recoveries and deaths in Kaduna State from 29th February, 2020 to 6th November, 2022.

The data can be verified from the website of the NCDC (https://ncdc.gov.ng)

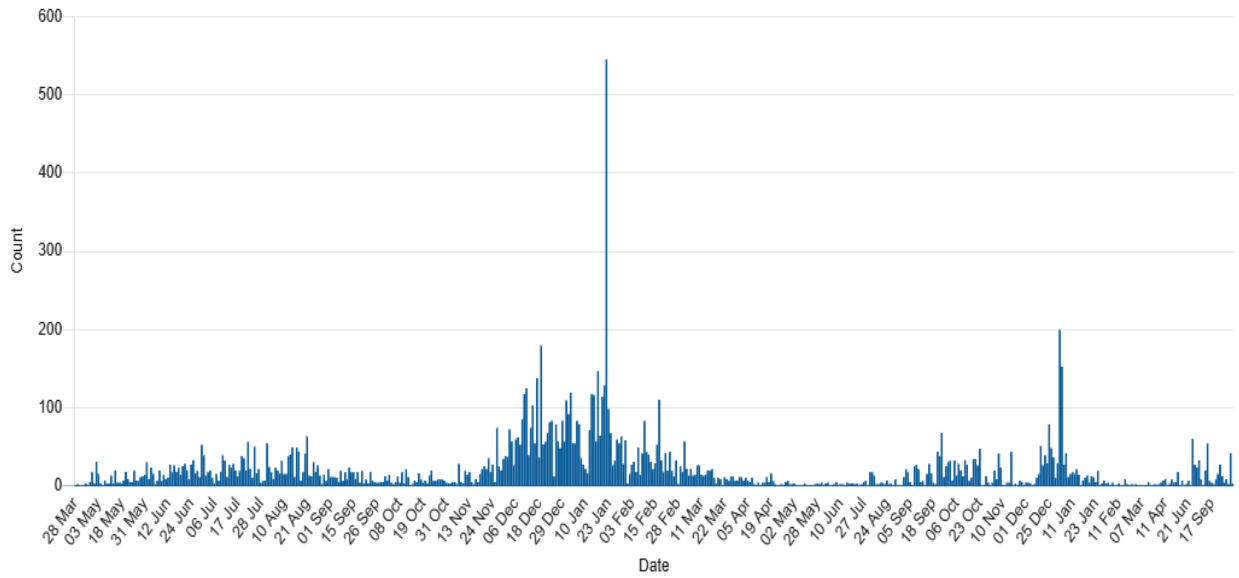

Figure 1: Confirmed COVID-19 Cases in Kaduna State from 28th March, 2020 to 17th September, 2022

(Source: https://covid19.ncdc.gov.ng/state/)

Table 1: Weekly breakdown of the Covid-19 Infections, recoveries and deaths in Kaduna State from 29th February, 2020 to 3rd January, 2021

WEEK	PERIOD	INFECTIONS		RECOVERIES		DEATHS	
		CUMMULATIVE TOTAL	TOTAL (NEW WEEKLY CASES)	CUMMULATIVE TOTAL	TOTAL	CUMMULATIVE TOTAL	TOTAL
Week 9	29 Feb 2020	0	0	0	0	0	0
Week 10	7 Mar 2020	0	0	0	0	0	0
Week 14	4 Apr 2020	6	0	0	0	0	0
Week 18	2 May 2020	66	31	6	0	1	0
Week 23	6 Jun 2020	337	2	205	8	10	0
Week 27	4 Jul 2020	855	20	570	0	12	0
Week 31	1 Aug 2020	1,457	0	1,176	0	12	0
Week 36	5 Sep 2020	2,189	5	2,086	15	32	0
Week 40	3 Oct 2020	2,440	14	2,345	11	40	1
Week 44	1 Nov 2020	2,655	38	2,567	49	43	1
Week 49	6 Dec 2020	3,387	323	3,048	222	47	0
Week 51	20 Dec 2020	4,504	637	3,877	548	48	1
Week 52	27 Dec 2020	4,940	436	4,443	566	50	2
Week 53	3 Jan 2021	5,447	507	4,708	265	53	3

(Source: https://covid19.ncdc.gov.ng/state/)

Table 2: Weekly breakdown of the Covid-19 Infections, recoveries and deaths in Kaduna State from 10th February, 2021 to 2nd January, 2022

WEEK	PERIOD	INFECTIONS		RECOVERIES		DEATHS	
		CUMMULATIVE TOTAL	TOTAL (NEW WEEKLY CASES)	CUMMULATIVE TOTAL	TOTAL (RECOVERIES)	CUMMULATIVE TOTAL	TOTAL (NEW WEEKLY DEATHS)
Week 1	10 Jan 2021	5,801	354	5,420	712	55	2
Week 5	7 Feb 2021	7,818	157	7,505	443	57	0
Week 9	7 Mar 2021	8,658	182	8,424	98	65	3
Week 13	4 Apr 2021	8,960	46	8,837	47	65	0
Week 17	2 May 2021	9,061	21	8,981	11	65	0
Week 22	6 Jun 2021	Data Not Available (Data Estimated)					
Week 25	27 Jun 2021	9,113	8	9,035	0	65	0
Week 26	4 Jul 2021	9,121	8	9,040	5	65	0
Week 30	1 Aug 2021	Data Not Available (Data Estimated)					
Week 34	29 Aug 2021	9,225	22	9,132	9	66	0
Week 35	5 Sep 2021	9,280	55	9,147	15	66	0
Week 39	3 Oct 2021	9,685	94	9,419	28	73	1
Week 44	7 Nov 2021	10,100	74	9,951	81	81	2
Week 48	5 Dec 2021	10,182	9	10,029	8	82	1
Week 52	2 Jan 2022	10,579	123	10,240	142	86	0

(Source: https://covid19.ncdc.gov.ng/state/)

Table 3: Weekly breakdown of the Covid-19 Infections, recoveries and deaths in Kaduna State from 9th February, 2022 to 6th November, 2022

WEEK	PERIOD	INFECTIONS		RECOVERIES		DEATHS	
		CUMMULATIVE TOTAL	TOTAL (NEW WEEKLY CASES)	CUMMULATIVE TOTAL	TOTAL (RECOVERIES)	CUMMULATIVE TOTAL	TOTAL (NEW WEEKLY DEATHS)
Week 1	9 Jan 2022	11,010	431	10,780	540	87	1
Week 5	6 Feb 2022	11,193	8	11,088	15	89	0
Week 9	6 Mar 2022	11,223	2	11,133	8	89	0
Week 13	3 Apr 2022	11,253	15	11,153	9	89	0
Week 17 - Week 18	8 May 2022	11,277	19	11,187	20	90	0
Week 21 - Week 22	5 Jun 2022	11,306	3	11,216	8	90	0
Week 25 - Week 26	3 Jul 2022	11,313	0	11,222	5	90	0
Week 31 - Week 32	14 Aug 2022	11,464	39	11,364	83	90	0
Week 35 - Week 36	11 Sep 2022	11,549	37	11,431	43	90	0
Week 39 - Week 40	9 Oct 2022	11,578	21	11,463	18	90	0
Week 43 - Week 44	6 Nov 2022	11,616	16	11,513	21	90	0

(Source: https://covid19.ncdc.gov.ng/state/)

Formulation of the Model

The model that will be used in this study is an expansion of the model in (Iboi *et al.*, 2020 and Riyapan *et al.*, 2021). The model in (Iboi *et al.*, 2020) was constructed using the SEIR model, and it consists of six (6) compartments, with three categories in the infected compartment. The model, developed by Riyapan *et al.*, 2021, is an expansion of the one developed by Iboi *et al.*, 2020. The model in this research, however, includes nine (9) compartments that are mutually exclusive. To achieve this, divide N(t), the total population at time(t), into;

Susceptible individuals – S(t); Exposed Individuals – E(t); Symptomatically-Infectious Individuals – I_s ; Asymptomatically-Infectious Individuals – I_a ; Quarantined or Hospitalized Individuals – Q(t); Recovered Individuals – R(t); Death Compartment – D(t); and the two new compartments; Vaccinated individuals – V(t); Susceptible with failed vaccination - $V_s(t)$ The following assumption is made that, the vaccine is highly effective and gives some level of immunity to the virus. This is to cater for low rate of failed vaccination.

Hence, we can make the following assumption, that;

$$N(t) = S(t) + V(t) + V_s(t) + E(t) + I_s(t) + I_a(t) + Q(t) + R(t) + D(t) \quad (1)$$

People who reside in the nation or have just crossed the border before it was closed make up the vulnerable compartment. The COVID-19-exposed people who are exhibiting symptoms are transferred to the infectious compartment for those with symptoms. People who don't exhibit any symptoms, however, are transferred to the infectious compartment for asymptomatic people. Due to the fact that they take preventative measures like keeping a distance from others, using masks, and avoiding large gatherings or meetings, the chance of infection for those who are in the sensitive compartment is decreased. Recovery from the quarantined and infectious compartments is required before people may proceed to the recovery compartment. Now, the vaccinated compartment comprises all the population that have been vaccinated. If at the onset the whole susceptible population have been vaccinated, then it is assumed there will be no infections, which is impossible, because there must be at least one infective. Also, if at any point a member of a particular

compartment is vaccinated, then the member returns to the susceptible compartment, but with partial immunity. This brings us to the concept of herd immunity, as captured in (Weiss, 2013). The Failed vaccinated compartment captures the individuals that have been vaccinated, but lost immunity due to the inefficacy of the vaccine.

Table 4: Variables in the Model

Variables in the Model	Description
S	Susceptible compartment
V	Vaccinated compartment
V_s	Vaccination Failed compartment
E	Exposed compartment
I_s	Symptomatic Infectious compartment
I_a	Asymptomatic Infectious Compartment
Q	Quarantined/Hospitalized compartment
R	Recovered Compartment
D	Death compartment

Table 5: Parameters Used in the Model and their meaning

Model Parameters	Description
ρ	Rate of Recruitment into Susceptible compartment
β_s	Real contact rate
β_a	Efficiency of Social distancing
ϕ	Rate of vaccination of susceptible individuals
σ	Vaccine efficiency/efficacy
ω	Rate of vaccine-based immunity waning
ψ	Measure of individuals using face mask
ξ	Effectiveness of face masks
$1-\theta$	Fraction individuals exposed and showing clinical symptoms after the incubation period
φ	Exposure rate from the exposed compartment to the infectious compartment
α_s	Rate of individuals in the symptomatically infected compartment
λ_s	Rate of recovery of individuals in the symptomatically exposed compartment
δ_s	Rate of mortality from Covid-19 for individuals in the infectious compartment
α_a	Rate of Isolation of asymptomatically infectious individuals
λ_a	Rate of recovery of asymptomatically infectious individuals
λ_q	Rate of recovery of individuals in the quarantined compartment
δ_q	Rate of Covid – 19 disease mortality for individuals in the quarantined compartment
μ	Natural mortality rate

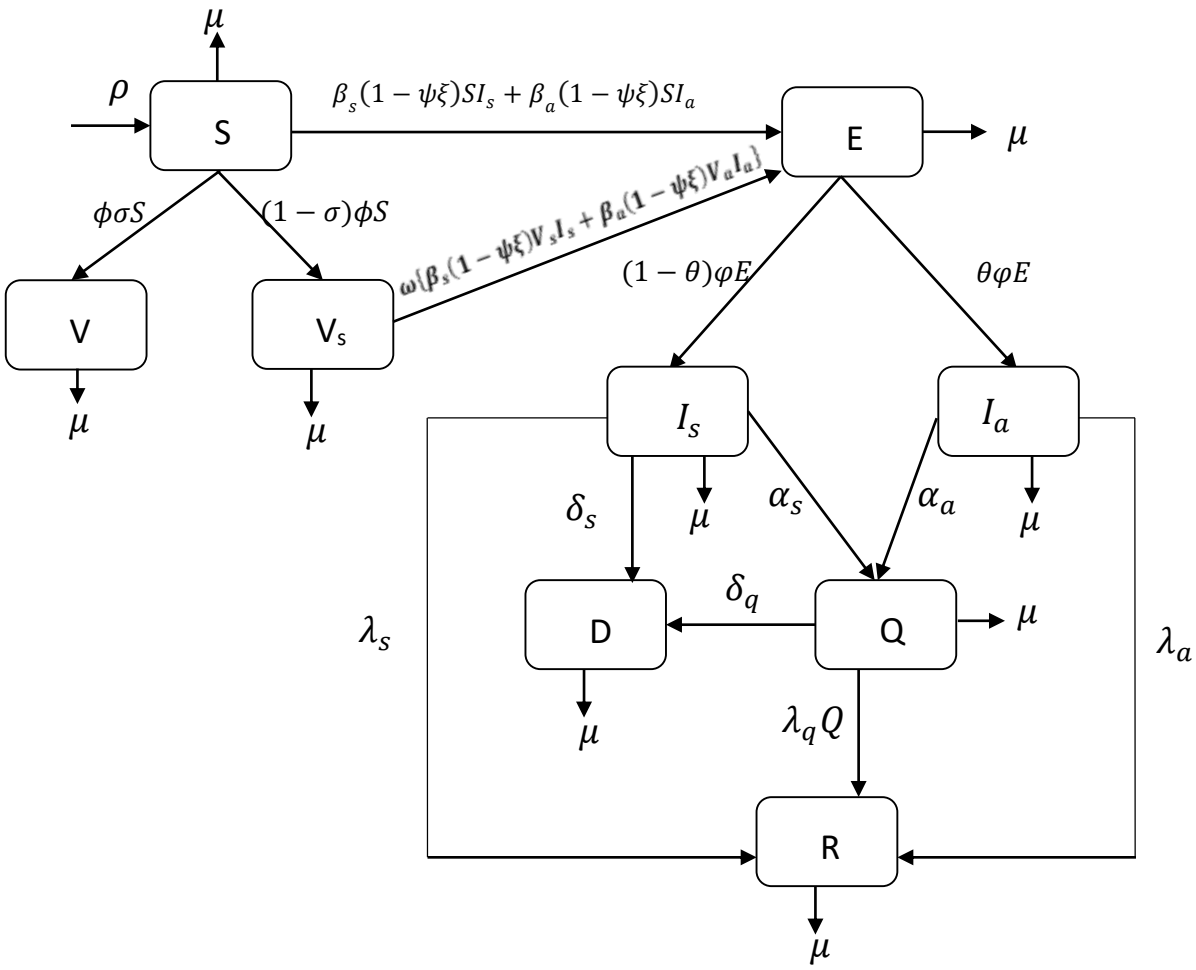

Figure 2: Flowchart of the formulated model

The following variables will be used to express the model provided in equation (1) above;

The parameters β_S and β_a, respectively, indicate the effective contact rate (contacts capable of transmitting COVID-19) for people in the infectious with symptoms and infectious without symptoms compartments. The percentage of people in a community that appropriately don face masks is indicated as $0 < \psi \leq 1$ while $0 < \xi \leq 1$ indicate the anticipated reduction in the risk of infection brought on by the usage of the face mask. The progression rate of those who have been exposed is expressed as φ. At the conclusion of the incubation period, a proportion $0 < \theta \leq 1$ of exposed people had no clinical signs of COVID-19 (and had moved to compartment I_a). The remainder, 1 - θ, displays clinical signs and transfers to the Is compartment. The recovery rates for people in the compartments I_S, I_a and Q, are represented by the parameters λ_S, λ_a and λ_q respectively. The rate of individual isolation is represented similarly by α_S and α_a. The values δ_S and δ_q, respectively, indicate the COVID-19-induced death rate for those living in the confined and asymptomatic infected compartments.

Standard values of the group contact rate parameter will be used as the basis for calculating the impact of social isolation and community lockdown measures in this study. Figure 2 depicts the flowchart of the model that was developed utilizing all the presumptions mentioned previously. In addition, Tables 4 and 5, which are presented in turn, provide descriptions of all the parameters and the meanings of all the variables. A system of nine differential equations with non-negative starting conditions may be formed from the aforementioned hypotheses and variables as follows;

$$\left.\begin{aligned}
\frac{dS}{dt} &= \rho - \beta_s(1-\psi\xi)SI_s - \beta_\alpha(1-\psi\xi)SI_\alpha - \phi S - \mu S && (2a)\\
\frac{dV}{dt} &= \phi\sigma S - \mu V && (2b)\\
\frac{dV_s}{dt} &= (1-\sigma)\phi S - \omega\{\beta_s(1-\psi\xi)V_sI_s + \beta_a(1-\psi\xi)V_sI_a\} - \mu V_s && (2c)\\
\frac{dE}{dt} &= \beta_s(1-\psi\xi)SI_s + \beta_a(1-\psi\xi)SI_a \\
&\quad +\omega\{\beta_s(1-\psi\xi)V_sI_s + \beta_a(1-\psi\xi)V_sI_a\} - (\varphi+\mu)E && (2d)\\
\frac{dI_s}{dt} &= (1-\theta)\varphi E - (\alpha_s + \delta_s + \lambda_s + \mu)I_s && (2e)\\
\frac{dI_a}{dt} &= \theta\varphi E - (\alpha_a + \lambda_a + \mu)I_a && (2f)\\
\frac{dQ}{dt} &= \alpha_s I_s + \alpha_a I_a - (\lambda_q + \delta_s + \mu)Q && (2g)\\
\frac{dR}{dt} &= \lambda_s I_s + \lambda_a I_a + \lambda_q Q - \mu R && (2h)\\
\frac{dD}{dt} &= \delta_s I_s + \delta_q Q && (2i)
\end{aligned}\right\} \quad (2)$$

Equation (2) is a system of nine (9) linear differential Equations. Since the total population is;

$$N(t) = \frac{dS}{dt} + \frac{dV}{dt} + \frac{dV_s}{dt} + \frac{dE}{dt} + \frac{dI_s}{dt} + \frac{dI_a}{dt} + \frac{dQ}{dt} + \frac{dR}{dt} + \frac{dD}{dt} \quad (3)$$

Then;

$$N(t) = \rho - \mu N \quad (4)$$

From equation (3), *N(t)* would approach a carrying capacity $\frac{\rho}{\mu}$ as $t \to \infty$.

Model (2) is a description of a human population; hence, the model variables can be proven be nonnegative for all time $t \geq 0$ and hence all solutions of the model (2) will remain positive for all time $t \geq 0$. Therefore, equations (2) is mathematically well-posed, and its dynamics can be considered in the region below:

$$\Omega_{Cvd19} = \left\{(S, E, V, V_s, I_s, I_a, Q, R, D) \in \Re_+^9 : S + E + V + V_s + I_s + I_a + Q + R + D \leq \frac{\rho}{\mu}\right\} \quad (5)$$

Data Analysis

The data for the given research was analyzed by solving the resulting differential equations analytically, and then using the Matrix Laboratory Software (MATLAB) to solve the for numerical values of the problems.

Analysis and Solutions of the Model

Here, a detailed analysis of the model is presented, by showing some dynamical properties of the model.

Positivity of the Solutions to the Model

Theorem 1:

If $\mathrm{S}(0) > 0, \mathrm{V}(0) > 0, V_S(0), E(0) > 0, I_S(0) > 0, I_a(0) > 0, Q(0) > 0, R(0) > 0, D(0) > 0$ then the solutions $(\mathrm{S}(t) > 0, \mathrm{V}(t) > 0, V_S(t), E(t) > 0, I_S(t) >$

Since model (1) depicts a human population, it is necessary that the model is meaningful and all states of the variables are non-negative for all time $t > 0$. This is seen by using Theorem 1 to show the positiveness of the solutions of model (1).

$0, I_a(t) > 0, Q(t) > 0, R(t) > 0, D(t) > 0)$ are positive for all time $t > 0$.

Proof:

From the first equation of the model (2), we see that;

$$\frac{dS}{dt} = \rho - \beta_s(1-\psi\xi)SI_s - \beta_\alpha(1-\psi\xi)SI_\alpha - \phi S - \mu S$$
$$\geq \beta_s(1-\psi\xi)SI_s - \beta_\alpha(1-\psi\xi)SI_\alpha - \phi S - \mu S \quad (6)$$

By the technique of variable-separable method, $\frac{dS}{dt}$ can be decomposed to;

$$\frac{dS}{dt} \geq -\beta_s(1-\psi\xi)SI_s - \beta_\alpha(1-\psi\xi)SI_\alpha - \phi S - \mu S \quad (7)$$

Equation (7) can be integrated to obtain the solution;

$$S(t) \geq S(0)e^{-\int_0^t(\beta_s(1-\psi\xi)I_s - \beta_\alpha(1-\psi\xi)I_\alpha + \phi + \mu)} > 0 \quad (8)$$

Since the initial value *S(0)*, and the corresponding exponential functions in Equation (8) are always positive, hence *S(t)*, is positive.

By using the same techniques, it can be seen that the other equations of model (2) satisfy the conditions; $V(t) > 0, V_S(t), E(t) > 0, I_S(t) > 0, I_a(t) > 0, Q(t) > 0, R(t) > 0, D(t) > 0$

Boundedness of the Non-Negative Solutions of the Model

We now show that all positive solutions to the solutions of equations (2) are bounded.

Theorem 2:

All positive solutions to model (2) defined in Theorem (1) are bounded.

Proof:

Summing the equations of equation (2), we obtain;

$$\frac{dN(t)}{dt} = \frac{d}{dt}\big(S(t) + V(t) + V_s(t) + E(t) + I_s(t) + I_a(t) + Q(t) + R(t) + D(t)\big) \quad (9)$$
$$= \rho - \mu N \quad (10)$$

Solving the above by method of Integration of Linear Equations with Integrating factor, between 0 and *t*, we obtain;

$$\int_0^t \frac{dN(t)}{dt}\,dt = \int_0^t (\rho - \mu N)\,dt \quad (11)$$

which gives;

$$N(t) = \frac{\rho}{\mu} - \left(\frac{\rho - \mu N(0)}{\mu}\right)e^{-\mu t} \quad (12)$$

It can be observed, from equation (12), that $N(t) \to \frac{\rho}{\mu}$ as $t \to \infty$

Therefore, the non-negative solutions to model (2) are bounded.

Equilibrium Points of the Model

The equilibrium points are the points where the equations (2) are equal to zero. Equating all the equations of (2) to zero, we obtain;

$$\left.\begin{aligned}
\rho - \beta_s(1-\psi\xi)SI_s - \beta_\alpha(1-\psi\xi)SI_\alpha - \phi S - \mu S &= 0 \quad (12a)\\
\phi\sigma S - \mu V &= 0 \quad (12b)\\
(1-\sigma)\phi S - \omega\{\beta_s(1-\psi\xi)V_sI_s + \beta_a(1-\psi\xi)V_sI_a\} - \mu V_s &= 0 \quad (12c)\\
\beta_s(1-\psi\xi)SI_s + \beta_a(1-\psi\xi)SI_a & \\
+\omega\{\beta_s(1-\psi\xi)V_sI_s + \beta_a(1-\psi\xi)V_sI_a\} - (\varphi+\mu)E &= 0 \quad (12d)\\
(1-\theta)\varphi E - (\alpha_s + \delta_s + \lambda_s + \mu)I_s &= 0 \quad (12e)\\
\theta\varphi E - (\alpha_a + \lambda_a + \mu)I_a &= 0 \quad (12f)\\
\alpha_s I_s + \alpha_a I_a - (\lambda_q + \delta_s + \mu)Q &= 0 \quad (12g)\\
\lambda_s I_s + \lambda_a I_a + \lambda_q Q - \mu R &= 0 \quad (12h)\\
\delta_s I_s + \delta_q Q &= 0 \quad (12i)
\end{aligned}\right\} (12)$$

Equation (12) is a system of equations, that when simplified, can give so many solutions. In any case, with respect to this research work, only two solutions will be considered;

(i) The Disease-Free Equilibrium State (DFES); and,
(ii) The Endemic Equilibrium State (EES).
(iii) The DFES is when the equations of model (2) are set to be equal to zero. This implies that there is no infection, hence the assumption that $I_s$and I_a are equal to zero. We denote the DFES in this study by;

$$\mathrm{K}^* = (S^*, V^*, V_s^*, E^*, I_s^*, I_a^*, Q^*, R^*, D^*)$$

where;

$$S^* = \frac{\rho}{\phi+\mu}; \quad V^* = \frac{\phi\sigma\rho}{\mu(\phi+\mu)}; \quad V_s^* = \frac{(1-\phi)\sigma\rho}{\mu(\phi+\mu)}; \quad E^* = 0; \quad I_s^* = 0;$$
$$I_a^* = 0; \; Q^* = 0; \quad R^* = 0; \quad D^* = 0$$

a

(ii) The EES is obtained by finding the values of $(S, E, V, V_s, I_s, I_a, Q, R, D)$ in their corresponding equations from equations $(12a - 12i)$ respectively.

Let the EES be denoted by;

$$\mathrm{K}^{**} = (S^{**}, V^{**}, V_s^{**}, E^{**}, I_s^{**}, I_a^{**}, Q^{**}, R^{**}, D^{**})$$

then;

$$S^{**} = \frac{\rho}{\beta_s(1-\psi\xi)I_s^{**} + \beta_a(1-\psi\xi)\, I_a^{**} + \phi + \mu}$$

$$V^{**} = \frac{\phi\sigma S^{**}}{\mu}$$

$$V_s^{**} = \frac{(1-\sigma)\phi S^{**}}{\omega\{\beta_s(1-\psi\xi)I_s^{**} + \beta_a(1-\psi\xi)I_a^{**}\} + \mu}$$

$$E^{**} = \frac{\beta_s(1-\psi\xi)S^{**}I_s^{**} + \beta_a(1-\psi\xi)S^{**}I_a^{**} + \omega\{\beta_s(1-\psi\xi)V_s^{**}I_s^{**} + \beta_a(1-\psi\xi)V_s^{**}I_a^{**}\}}{\varphi + \mu}$$

$$I_s^{**} = \frac{(1-\theta)\varphi E^{**}}{(\alpha_s + \delta_s + \lambda_s + \mu)}$$

$$I_a^{**} = \frac{\theta\varphi E}{(\alpha_a + \lambda_a + \mu)}$$

$$Q^{**} = \frac{\alpha_s I_s^{**} + \alpha_a I_a^{**}}{(\lambda_q + \delta_s + \mu)}$$

$$R^{**} = \frac{\lambda_s I_s^{**} + \lambda_a I_a^{**} + \lambda_q Q^{**}}{\mu}$$

$$D^{**} = 0$$

The Basic Reproduction Number of the Model

The Basic Reproduction Number (BRN), usually denoted by is defined as the expected number of secondary cases can be directly generated by one primary case in a susceptible infectious population.

Let us denote the BRN of our model by; $\mathcal{R}_0$.

Computation of the Basic Reproduction Number (BRN)

The BRN is computed using the Next Generation Matrix approach (Diekmann and Hesterbeek, 2009)

This is done by defining two square matrices, *F* and *V*, such that;

$F = \frac{\partial \mathcal{F}_i(x_0)}{\partial x_j}$ and $V = \frac{\partial \mathcal{V}_i(x_0)}{\partial x_j}$, where; $\mathcal{F}_i(x_0)$ and $\mathcal{V}_i(x_0)$ are the rates of new infections and the different ways of movements between the compartments in the diseased classes i.e. the compartments $x_j (j = 1,2,\ldots, n \in \mathbb{N})$, which represent the infected/diseased compartments of model (2).

We form the Next Generation Matrix from the diseased classes, thus;

$$\frac{dE}{dt} = \beta_s(1-\psi\xi)SI_s + \beta_a(1-\psi\xi)SI_a + \omega\{\beta_s(1-\psi\xi)V_sI_s + \beta_a(1-\psi\xi)V_sI_a\} - (\varphi+\mu)E$$

$$\frac{dI_s}{dt} = (1-\theta)\varphi E - (\alpha_s + \delta_s + \lambda_s + \mu)I_s$$

$$\frac{dI_a}{dt} = \theta\varphi E - (\alpha_a + \lambda_a + \mu)I_a$$

From G(X) = F(X) -V(X)

where F(X) represents the Infectious classes, I_s and I_a, and V(X) represents the Exposed classes. We obtain matrices $\mathcal{F}$ and $\mathcal{V}$ for S and $E, I_s and\ I_a$ respectively.

$$\mathcal{F} = \begin{pmatrix} \beta_s(1-\psi\xi)SI_s + \beta_a(1-\psi\xi)SI_a \\ 0 \\ 0 \end{pmatrix}$$

$$\mathcal{V} = \begin{pmatrix} -\omega\{\beta_s(1-\psi\xi)V_sI_s + \beta_a(1-\psi\xi)V_sI_a\} - (\varphi+\mu)E \\ -(1-\theta)\varphi E - (\alpha_s + \delta_s + \lambda_s + \mu)I_s \\ -\theta\varphi E - (\alpha_a + \lambda_a + \mu)I_a \end{pmatrix}$$

Solving the above we obtain our R_0 to be;

$$R_0 = \frac{\beta_s S T_2 T_4 T_5 - \beta_a S\theta\psi T_2 T_3}{T_4\{T_1 T_3 - \omega\beta_s V_s T_2 T_5\}}$$

where; $T_1 = \psi + \mu$ $T_2 = 1 - \psi\xi$ $T_3 = \alpha_s + \delta_s + \lambda_s + \mu$

$T_4 = \alpha_a + \lambda_a + \mu$ $T_5 = (1-\theta)\varphi$

RESULTS AND DISCUSSIONS

RESULTS

Here we present numerical simulations of the developed Model by using baseline values of the parameters presented in Table 4. These values are presented in Table 6.

The state variables are provided with initial values given as; $N(0)$ = 9,048,000 (Population of Kaduna State) which is the total estimated population size as at the year 2020; and $S(0)$ = 1,000,000, $E(0)$ = 50, and $V(0)$ = 35. The infected populations are $I(0)$ = 32, $Q(0)$ = 10, and $R(0)$ = 15.

Table 6: Baseline values used for the Model Parameters in the Numerical Simulation

Model Parameters	Description	Values
N	Human Population	9.048 million
ρ	Rate of Recruitment into Susceptible compartment	25
β_s	Real contact rate	75%
β_a	Efficiency of Social distancing	55%
ϕ	Rate of vaccination of susceptible individuals	0.002
σ	Vaccine efficiency/efficacy	0.52
ω	Rate of vaccine-based immunity waning	0.0021
ψ	Measure of individuals using face mask	0.2
ξ	Effectiveness of face masks	0.5
$1-\theta$	Fraction individuals exposed and showing clinical symptoms after the incubation period	0.5
φ	Exposure rate from the exposed compartment to the infectious compartment	1/6 persons
α_s	Rate of individuals in the symptomatically infected compartment	0.2
λ_s	Rate of recovery of individuals in the symptomatically exposed compartment	1/5
δ_s	Rate of mortality from Covid-19 for individuals in the infectious compartment	0.00001
α_a	Rate of Isolation of asymptomatically infectious individuals	0.2
λ_a	Rate of recovery of asymptomatically infectious individuals	1/10
λ_q	Rate of recovery of individuals in the quarantined compartment	0.05
δ_q	Rate of Covid – 19 disease mortality for individuals in the quarantined compartment	0.015
μ	Natural mortality rate	$3.6529\text{x}10^{-5}$

The plotting of the individual compartments of the created model are in Figures 3 – 8. At first, the virus was spreading rapidly, but effective pharmaceutical and non-pharmaceutical controls were put in place, which successfully stopped the epidemic.

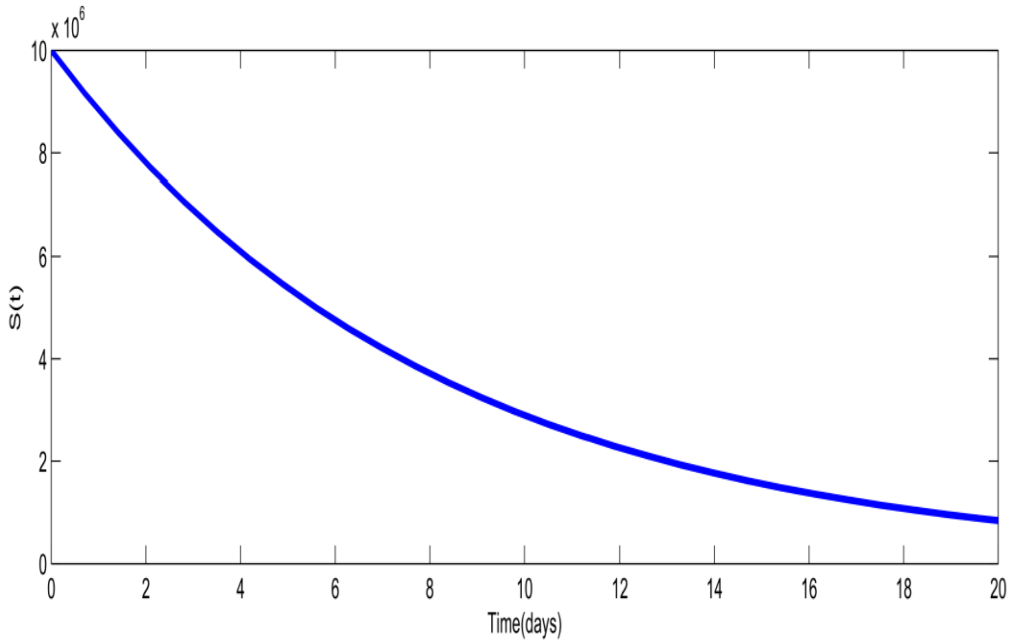

Figure 3: Dynamics of the susceptible class of Model (1).

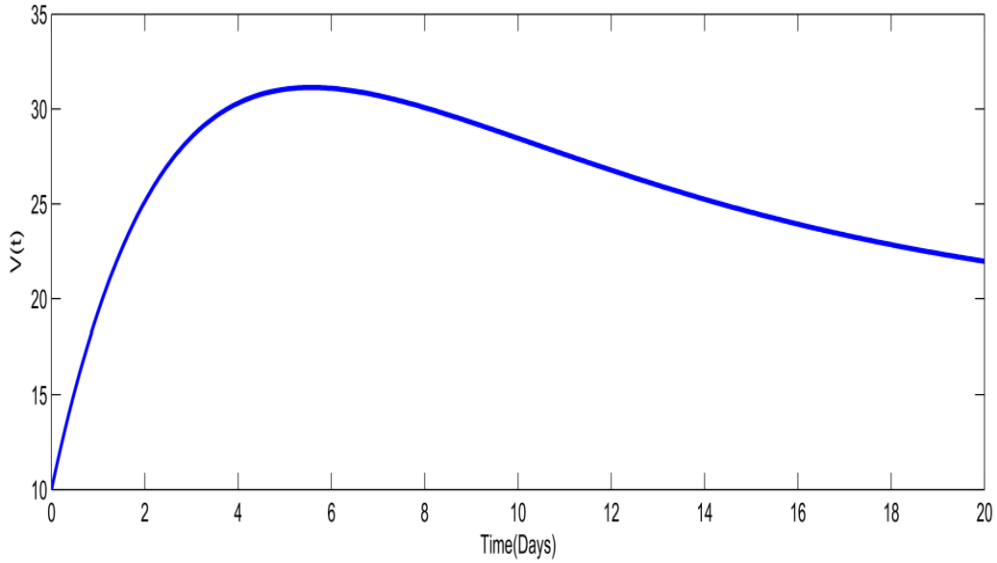

Figure 4: Dynamics of the vaccination class of Model (1).

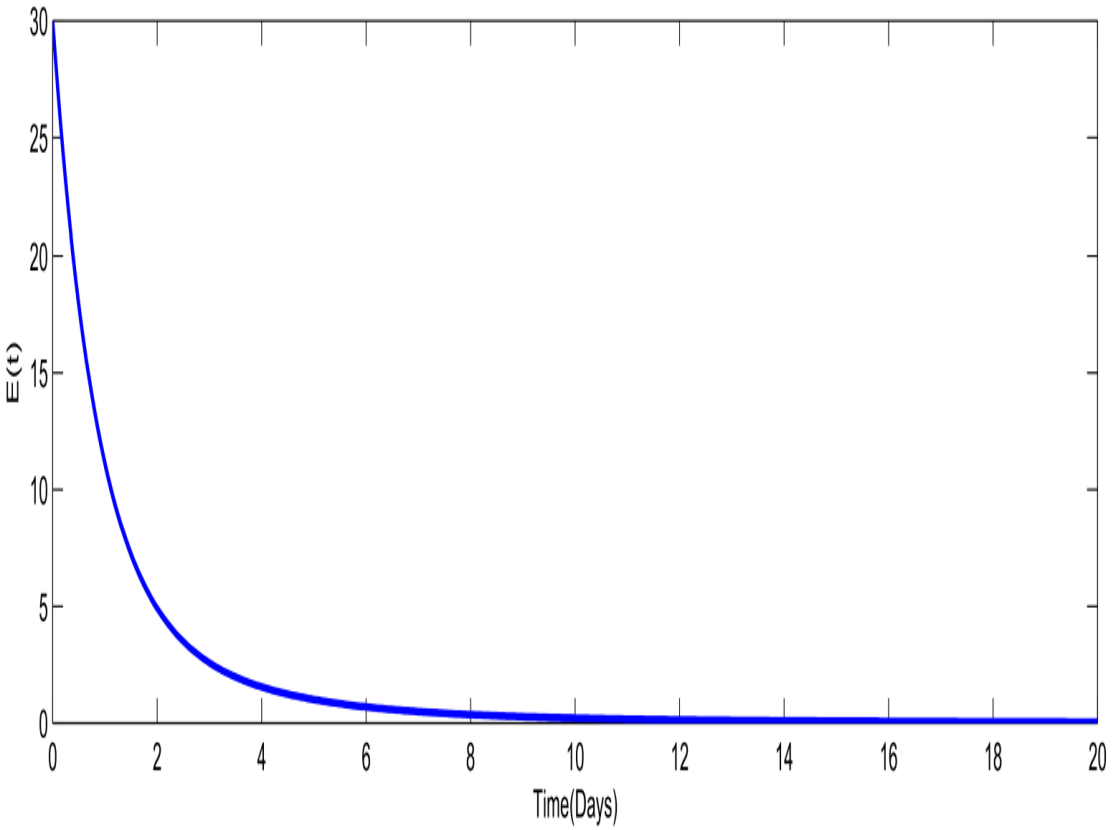

Figure 5: Dynamics of the exposed class of Model (1).

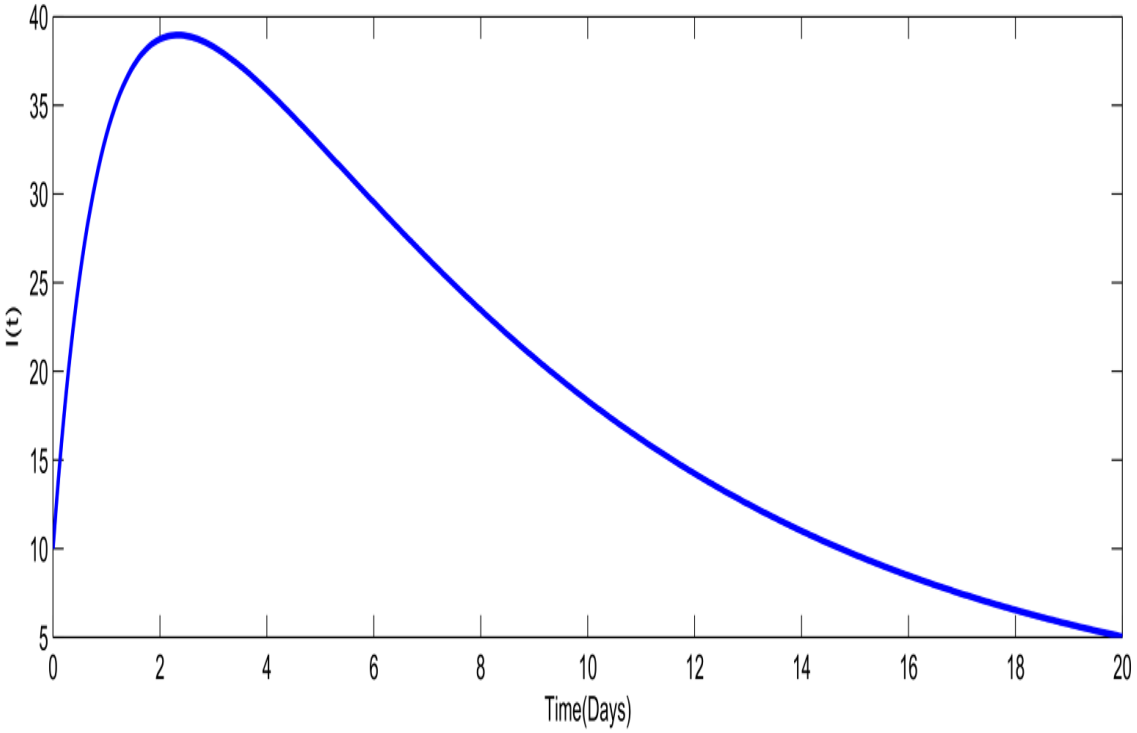

Figure 6: Dynamics of the infected class of Model (1).

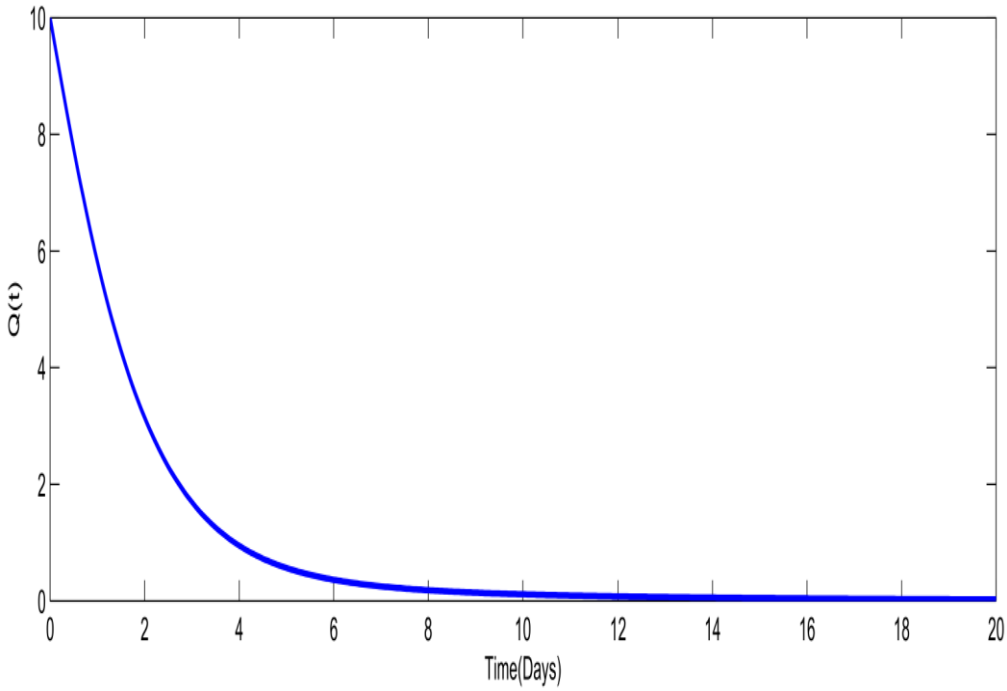

Figure 7: Dynamics of the quarantined class of Model (1).

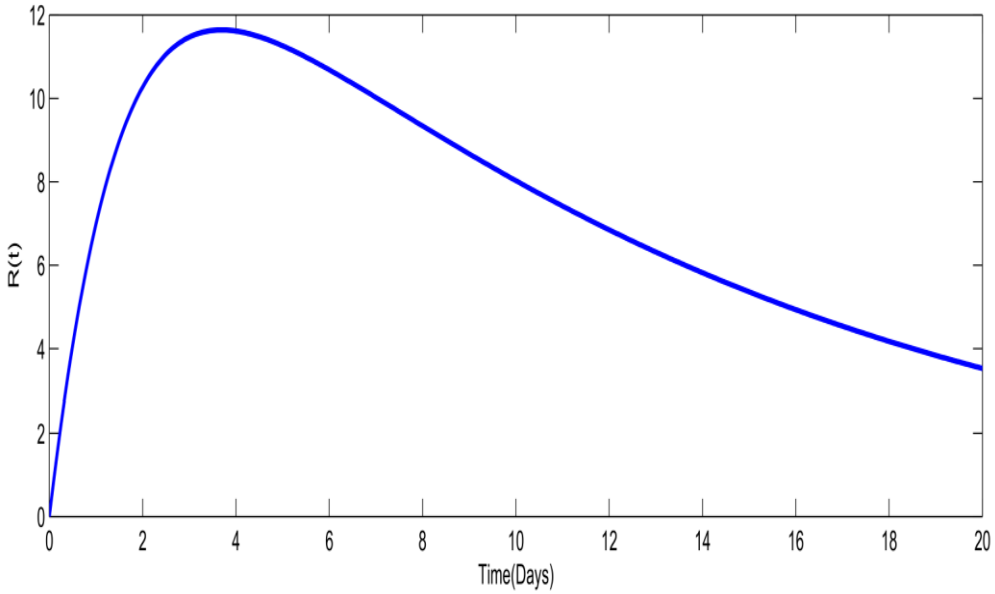

Figure 8: Dynamics of the recovered class of Model (1).

DISCUSSION

The suggested model's charting in Figure 9 depicts the dynamics of each compartment. Figures 10 and 11 make it abundantly evident that as vaccination efficacy and compliance increase, the value of the sick population decreases. Additionally, the value of R0 reaches zero and the illness will not transmit from one person to another if the vaccine is 100% successful in stopping disease transmission and is administered in sufficient numbers, i.e., $\delta = 1$.

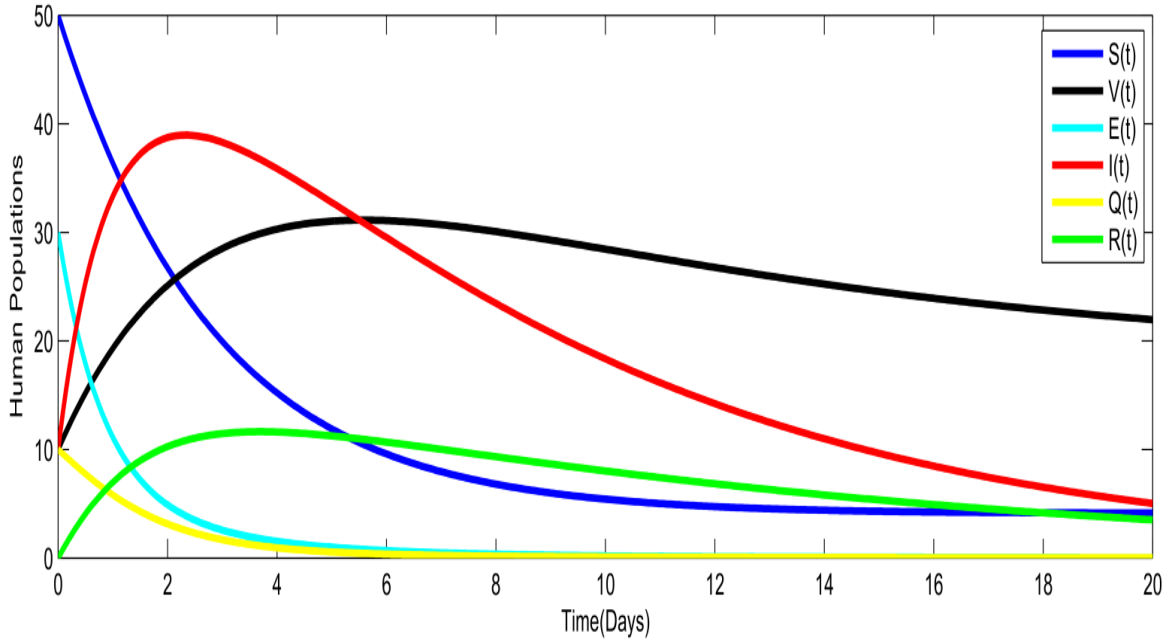

Figure 9: Dynamics of Model (1).

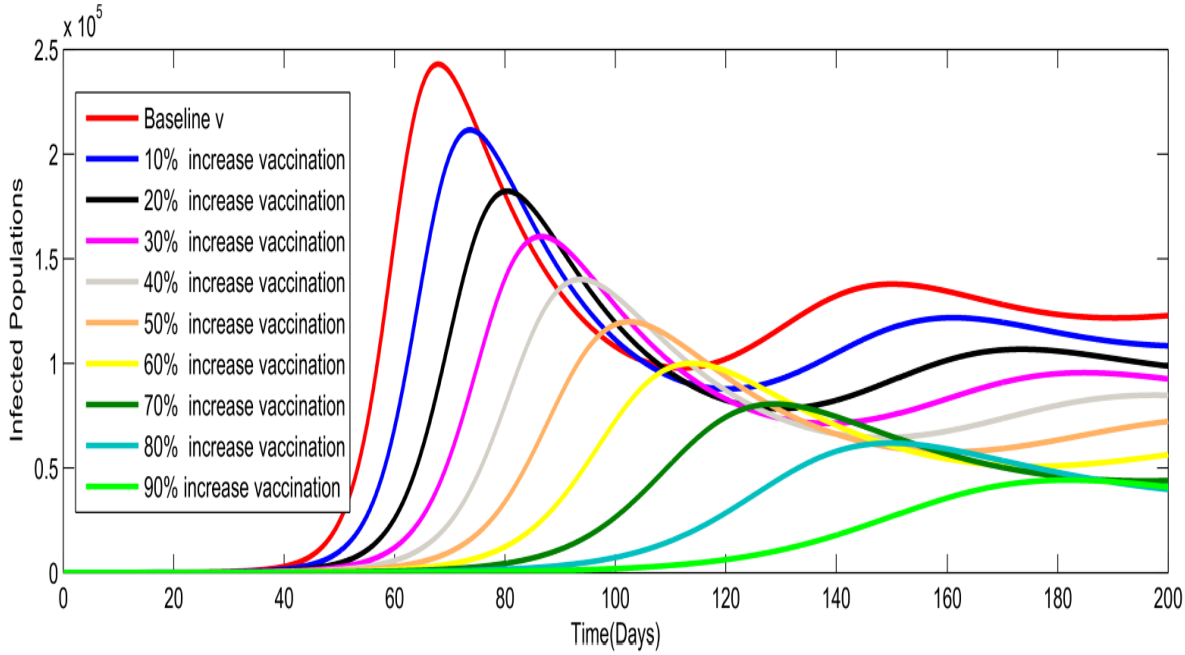

Figure 10: Dynamics of Model (1) with the effect of different rates of vaccination.

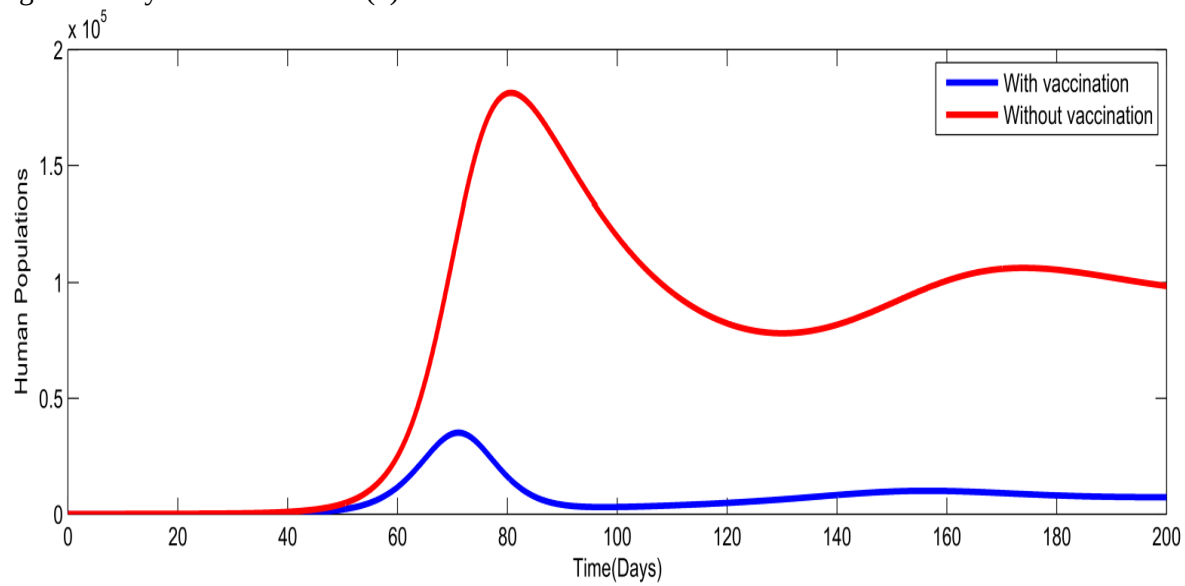

Figure 11: Dynamics of Model (1) with and without the effect of vaccination.

Figures 10 through 14 are provided to explore the dynamic influence of possible control strategies on the infection incidence in Kaduna State. Plotting of the simulation data across 200 and 300 days is done. In the visual findings that are displayed, we considered a number of non-pharmaceutical procedures together with their baseline values. The main areas of focus and study were the impact of vaccine V, the percentage of people who were exposed to and came into contact with COVID-19 patients, and lastly, the combined effect of the vaccination and quarantine on the infected cases. Figure 11 presents the resulting graphical interpretation, which indicates that an extra 15,000 COVID-19 infections were predicted during the height of the pandemic. Furthermore, Figure 11 shows that when vaccination effectiveness is increased above baseline values, there is a significant decrease in COVID-19 cases.

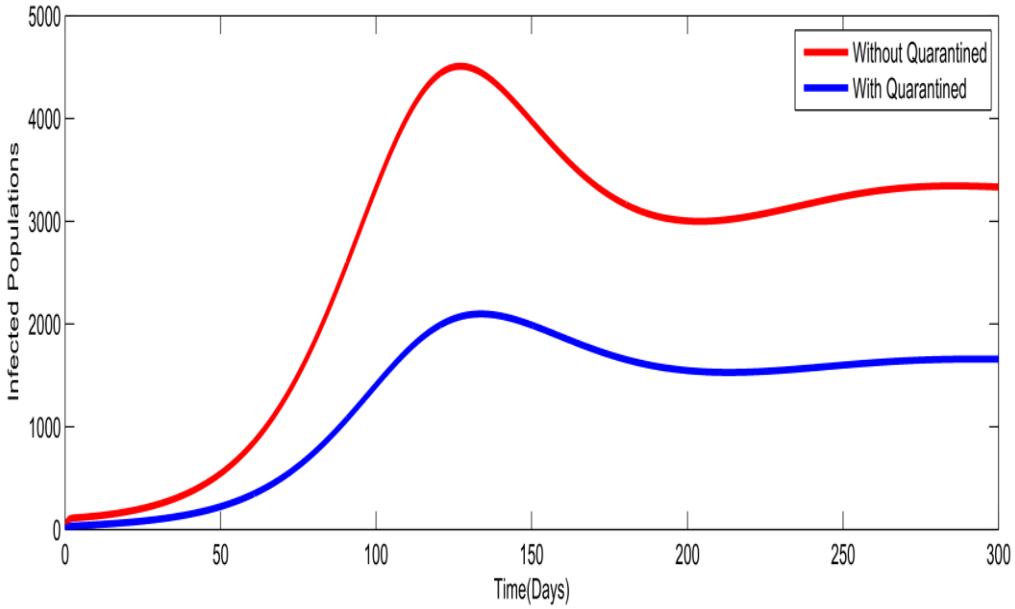

Figure 12: Dynamics of Model (1) with and without the effect of quarantine.

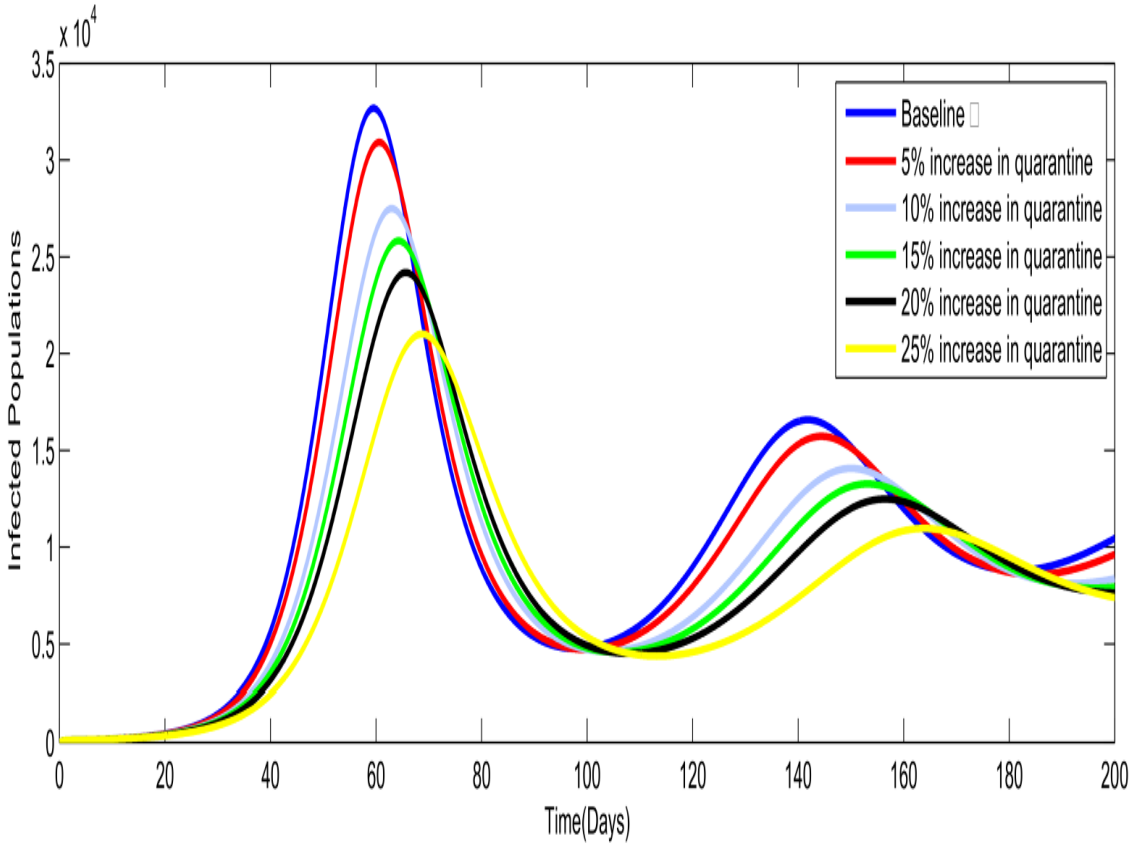

Figure 13: Dynamics of Model (1) with the increasing effect of the quarantine rate.

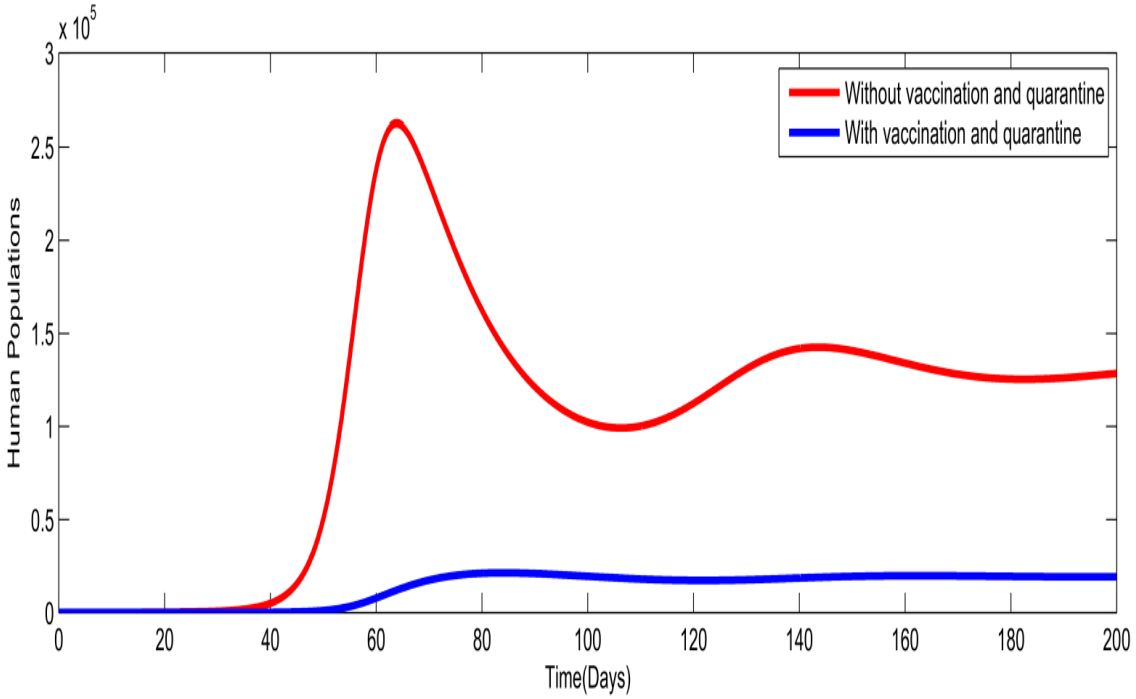

Figure 14: Dynamics of Model (1) with the effect of vaccination and quarantine.

Figures 11 and 13 show how newly infected COVID-19 patients behave both with and without a quarantine rate. Emphasizing that the situation is much worse without quarantine and that the number of infected patients has shockingly increased to over 300,000 is important. Nonetheless, there was a notable reduction in the peak number of new COVID-19 cases when quarantine rates were restricted to baseline values. In Figure 14, we track the trajectories of infected individuals with and without vaccination and quarantine in further detail. The highly efficient application of both vaccination and quarantine resulted in a considerable reduction in the number of reported instances of infection.

CONCLUSION

In this study, a vaccination model was created by including the vaccine class and additional elements that are essential for immunizing vulnerable individuals. Initially, we created the model and provided the precise model results. When $R_0 < 1$, the endemic equilibrium point was globally asymptotically stable, but when $R_0 > 1$, the model was locally asymptotically stable, according to our analysis of the model's stability at a disease-free equilibrium. To achieve the sensitivity analysis of the model, we employed the PRCC. Some important factors and their effects on the system were illustrated graphically. We have included some important information on immunization and quarantine so that you may better comprehend the significance of these traits. The effective use of immunization and isolation of confirmed sick individuals, which considerably reduced the number of infected people, is supported by the graphical interpretation. It should be noted that the illness situation was far worse and the number of infected patients rapidly increased in the absence of vaccinations and quarantines. Thus, the current research suggests that appropriate and successful application of these pharmaceutical and non-pharmaceutical interventions is still necessary to prevent or minimize COVID-19 infection.

RECOMMENDATIONS

The recommendations listed below are based on the study's findings. First and foremost, the government and its development partners have to step up their media efforts and provide health professionals more authority to promote the COVID-19 immunization. Second, considering that the studied families with insurance coverage were less likely to be reluctant to vaccinate, the government need to make health insurance more widely available. Finally, in order to improve vaccination uptake, information about the COVID vaccine should be directed towards Nigerian young, who make up the majority of the population. Finally, it is critical that a qualitative study be done in the future to evaluate the societal factors influencing vaccination reluctance in Nigerians.

REFERENCES

Algaissi, A. A., Alharbi, N. K., Hassanain, M., & Hashem, A. M. (2020). Preparedness and response to COVID-19 in Saudi Arabia: Building on MERS experience. *Journal of Infection and Public Health.* 13(6) pp. 834–838. doi.org/10.1016/j.jiph.2020.04.016

Cucinotta, D., & Vanelli, M. (2020). WHO declares COVID-19 a pandemic. *Acta Biomedica*. 91(1) pp.157–160. https://doi.org/10.23750/abm.v91i1.9397

Daniel Deborah, O. (2020). Mathematical Model for the Transmission of Covid-19 with Nonlinear Forces of Infection and the Need for Prevention Measure in Nigeria. *Journal of Infectious Diseases and Epidemiology*, *6*(5). https://doi.org/10.23937/2474-3658/1510158

Dicker, R.C., Coronado, F., Koo, D., & Parrish, R.G. (2006). *Principles of Epidemiology in Public Health Practice: An Introduction, Third Edition*. https://stacks.cdc.gov/view/cdc/6914/cdc_6914_DS1.pdf

Dietz, K., & Heesterbeek, J. A. P. (2002). Daniel Bernoulli's epidemiological model revisited. *Mathematical Biosciences*. 180 (2002) 1–21.http://www-history.mcs.st-andrews.ac.uk/history

Driessche van den, P. (2017). Reproduction numbers of infectious disease models. In *Infectious Disease Modelling*. 2(3), pp.288–303.

https://doi.org/10.1016/j.idm.2017.06.002

Dubé C., Garner G., Stevenson M., Sanson R., Estrada C. & Willeberg P. (2007). *The use of epidemiological models for the mangement of animal diseases.* In Proc. 75th General Session of the International Committee of the World Organisation for Animal Health (OIE), 20-25 May, Paris, 11.

Dubey, B., Patra, A., Srivastava, P. K., & Dubey, U. S. (2013). Modeling and analysis of an SEIR model with different types of nonlinear treatment rates. *Journal of Biological Systems*, *21*(3). https://doi.org/10.1142/S021833901350023X

ElBagourya M., Tolba M.M, Nasser H.A, Jabbar A., Elagouz A.M., Akthama Y. and Hutchinsone A. (2021). The Find of COVID-19 Vaccine Challenges and Opportunities. Journal of Infection and Public Health, 14(2021), 389–416

Ferguson, N. M., Keeling, M. J., Edmunds, W. J., Gani, R., Grenfell, B. T., Anderson, R. M., & Leach, S. (2003). *Planning for smallpox outbreaks*. www.nature.com/nature

Germann, T. C., Kadau, K., Longini, I. M., Macken, C. A., & Nair, G. B. (2006). *Mitigation strategies for pandemic influenza in the United States*. www.who.intcsrresourcespublications

Gumel, A. B., Ruan, S., Day, T., Watmough, J., Brauer, F., van den Driessche, P., Gabrielson, D., Bowman, C., Alexander, M. E., Ardal, S., Wu, J., & Sahai, B. M. (2004). Modelling strategies for controlling SARS outbreaks. *Proceedings of the Royal Society B: Biological Sciences*, *271*(1554), 2223–2232. https://doi.org/10.1098/rspb.2004.2800

Harmon, T. S., Olano, J. P., Nguyen, Q. D., Duran, C., & Patel, S. (2019). David Versus Goliath: The Clinical Consequences of an Influenza: A Viral Infection in an Unvaccinated Patient. *Cureus*. 11(5). https://doi.org/10.7759/cureus.4788

Iboi, E. A., Sharomi, O., Ngonghala, C. N., & Gumel, A. B. (2020). Mathematical modeling and analysis of COVID-19 pandemic in Nigeria. *Mathematical Biosciences and Engineering*, *17*(6), 7192–7220. https://doi.org/10.3934/MBE.2020369

Iboi, E., Sharomi, O. O., Ngonghala, C., & Gumel, A. B. (2020). Mathematical modeling and analysis of COVID-19 pandemic in Nigeria. *MedRxiv*. https://doi.org/10.1101/2020.05.22.20110387

Kaur, B. & Dindyal, J. (Eds.) (2010). Mathematical applications and Modelling: Yearbook 2010, Association of Mathematics Educators. Singapore: World Scientific. ISBN-13 978-981-4313-33-9.342

Kermack, W. O, & Mckendrick, A. G. (1927). A Contribution to the Mathematical Theory of Epidemics. *Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character*. 115(772) https://doi.org/10.1098/rspa.1927.0118

Kermack, W. O., & Mckendrick, A. G. (1933). Contributions to the mathematical theory of epidemics. III.—Further studies of the problem of endemicity. *Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character*. 141(843). https://doi.org/10.1098/rspa.1933.0106

Kermack, W. O., & Mckendrick, A. G. (1991). Society for Mathematical Biology Contributions to The Mathematical Theory of Epidemics-I. *Bulletin of Mathematical Biology*. 53(1).

Kermack, W. O., & Mckendrick, A. G. (1933). Contributions to the mathematical theory of epidemics. III.—Further studies of the problem of endemicity

Kin, H. W. (2012). *Mathematical Modelling - From Abstract to Practical*. N.T.U. National Institute of Education, Editor.

Kouidere, A., Khajji, B., Bhih, A. el, Balatif, O., & Rachik, M. (2020). A mathematical modeling with optimal control strategy of transmission of covid-19 pandemic virus. *Communications in Mathematical*

Biology and Neuroscience, *2020*, 1–23. https://doi.org/10.28919/cmbn/4599

Kretzschmar, M., & Wallinga, J. (2009). Mathematical Models in Infectious Disease Epidemiology *Modern Infectious Disease Epidemiology*. 2010, 209–221. doi: 10.1007/978-0-387-93835-6_12.

Lockey E. (2020). Covid-19: The Race for a Vaccine. *Journal of the Renin-Angiotensin-Aldosterone System*, April-June, 2020: 1–3

Mills, C. E., Robins, J. M., & Lipsitch, M. (2004). Transmissibility of 1918 Pandemic influenza. *Nature*, *432*(7019), 904–906. https://doi.org/10.1038/nature03063

Mumbu, A., Rahman J., & Hugo, A. K. (2020). Mathematical modelling on COVID-19 transmission impacts with preventive measures: a case study of Tanzania. *Journal of Biological Dynamics*, *14*(1), 748–766. https://doi.org/10.1080/17513758.2020.1823494

National Population Commission – Providing Demographic Data For Social and Economic Planning For National Development. (2021). Retrieved August 16, 2021, from https://nationalpopulation.gov.ng/

NCDC. (2020). NCDC Coronavirus COVID-19 Guidelines. In *Ncdc*. https://covid19.ncdc.gov.ng/report/%0A https://covid19.ncdc.gov.ng/guideline/

Okuonghae, D., & Omame, A. (2020). Analysis of a mathematical model for COVID-19 population dynamics in Lagos, Nigeria. *Chaos, Solitons and Fractals*, *139*. https://doi.org/10.1016/j.chaos.2020.110032

Rahman, K. S., Mitkari, S. R., & Shaikh, S. (2020). Modeling the Impact of Vaccination, Screening, Treatment on the Dynamics of Pneumonia. *Journal of Scientific Research*, *12*(4), 525–536. https://doi.org/10.3329/jsr.v12i4.45815

Riyapan, P., Shuaib, S. E., & Intarasit, A. (2021). A mathematical model of COVID-19 pandemic: A case study of Bangkok, Thailand. *Computational and Mathematical Methods in Medicine*, *2021*. https://doi.org/10.1155/2021/6664483

Rodrigues, H. S. (2016). Application of SIR epidemiological model: new trends. *International Journal of Applied Mathematics and Informatics.* 10, pp92-97

Saunders-Hastings, P., Hayes, B. Q., Smith, R., & Krewski, D. (2017). National assessment of Canadian pandemic preparedness: Employing InFluNet to identify high-risk areas for inter-wave vaccine distribution. *Infectious Disease Modelling*, *2*(3), 341–352. https://doi.org/10.1016/j.idm.2017.06.005

National Population Commission State Population, Nigeria Data Portal. (2006). Retrieved August 16, 2021, from https://nigeria.opendataforafrica.org/ifpbxbd/state-population-2006

Tchuenche, J. M., Khamis, S. A., Agusto, F. B., & Mpeshe, S. C. (2011). Optimal Control and Sensitivity Analysis of an Influenza Model with Treatment and Vaccination. *Acta Biotheoretica*, *59*(1), 1–28.
1 https://doi.org/10.1007/s10441-010-9095-8

Tolles, J., & Luong, T. (2020). Modeling Epidemics with Compartmental Models. In *JAMA - Journal of the American Medical Association.* 323(24),2515–2516. https://doi.org/10.1001/jama.2020.8420

Tuite, A. R., Fisman, D. N., Kwong, J. C., & Greer, A. L. (2010). Optimal Pandemic influenza vaccine allocation strategies for the Canadian population. *PLoS ONE*, *5*(5). https://doi.org/10.1371/journal.pone.0010520

Wallinga, J., & Teunis, P. (2004). Different Epidemic Curves for Severe Acute Respiratory Syndrome Reveal Similar Impacts of Control Measures. *American Journal of Epidemiology*, 160. https://academic.oup.com/aje/article-abstract/160/6/509/79472

Weiss Sir Ronald Ross, H. (2013). The SIR model and the Foundations of Public

Health. *MATerials MATemàtics*, 2013(3), pp17

Wu, U. I., Wang, J. T., Chang, S. C., Chuang, Y. C., Lin, W. R., Lu, M. C., Lu, P. L., Hu, F. C., Chuang, J. H., Chen, Y. C., Hsieh, S. M., Chien, S. F., Chang, H. H., Chang, Y. Y., Lin, H. C., & Hong, M. C. (2014). Impacts of a mass vaccination campaign against pandemic H1N1 2009 influenza in Taiwan: A time-series regression analysis. *International Journal of Infectious Diseases*, *23*, 82–89. https://doi.org/10.1016/j.ijid.2014.02.016

Zakary, O., Bidah, S., Rachik, M., & Ferjouchia, H. (2020). Mathematical Model to Estimate and Predict the COVID-19 infections in Morocco: Optimal control strategy. *Journal of Applied Mathematics*, *2020*. https://doi.org/10.1155/2020/9813926