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A MATHEMATICAL MODEL FOR NON-PHARMACEUTICAL INTERVENTIONS IN THE TRANSMISSION OF COVID-19

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Abstract. South Africa is one of the African countries most affected by the Corona pandemic, with total numbers of 1536801 confirmed cases, 1462110 cured cases and 52082 deaths since the onset of the virus until March 20, 2021. This paper aims to provide a mathematical model to predict the transmission dynamics of MERS-CoV and the impact of non-pharmaceutical interventions on disease spread in South Africa using data from May 26, 2020, to March 20, 2021 that cover periods of two epidemic waves. The basic reproduction number (BNR) R_0 and the effective reproduction number R_{eff} are calculated. Based on the Covid 19 datasets, the model's parameters are estimated and sensitivity analyses for three parameters of the model that are related to the BNR are carried out, where two of the parameters showed significant effects on the BNR. Numerical simulations of the model are performed using the data of the first and second waves, where the transmissions of MERSCoV in the two waves are compared. The numerical simulations indicates that following nonpharmacological precautions including full or partial lock of the country has a major role in controlling the epidemic and limiting its spread. The model predicts that the infection contact rate is directly proportional to the number of epidemic cases, resulting in the total number

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of infected cases at the epidemic climax becomes very large. Also, when the closure is implemented earlier and for longer period, it effectively reduces the spread of the epidemic.

Keywords: COVID-19; mathematical model; sensitivity analysis; the effective reproduction number; Hazard rate of infection.

2010 AMS Subject Classification: 93A30.

1. INTRODUCTION

Corona virus is a large class of viruses that can infect animals and humans alike. They cause respiratory diseases, whether they are mild such as the common cold or severe such as pneumonia [1]. Corona virus disease is the result of a new type of Corona viruses that was previously called ncov-2019 (https://apps.who.int/iris/handle/10665/331221), which is the seventh member of the Corona viruses family, along with the Severe Acute Respiratory Syndrome (SARS), which spread between 2002-2003.

The National Institute of Infectious Diseases (NICD) in South Africa (NICD) confirmed that the first South African case was identified on March 5, 2020 as an imported case from Italy, a state of national disaster was declared on March 15, 2020. Travel to and from high-risk countries was banned, and schools were closed immediately.

A complete lockdown of South Africa started on March 26, 2020 and lasted on May 2020. Then, the easing of restrictions began with reducing the degree of national preparedness to fourth level. Then, effecting from June 1, the restrictions were reduced to degree 3.

As the second wave of COVID-19 reached its climax in January 2021, the South African government decided on a partial lockdown. Restrictions were imposed on the sizes of gatherings, and a daily curfew was imposed from 9 pm to 4 am. On July 12, 2021, a complete lockdown was imposed for 14 days while maintaining the ban on gatherings due to the third wave of the Corona virus, which emerged due to the highly contagious and rapidly spreading delta strain.

Mathematical models are proved to be useful in analyzing various scenarios of COVID-19 disease development, and to predict the best possible outcomes when public health policies are incorporated. Many researcher used mathematical models to study the dynamics of the ongoing Covid-19 in South Africa, for instance we refer to [2, 3, 4, 5, 6].

The COVID 19 timelines in South Africa are summarized in Table 1.

Date	Restriction/event		
5 Mar 2020	Minister of Health had confirmed the spread of the virus to South Africa		
15 Mar 2020	The President of South Africa declared a national state of disaster		
23 Mar 2020	A national lockdown was announced, starting on 26 March		
27 Mar 2020	The first local death from the disease		
1 May 2020	The begin phased easing of the lockdown restrictions level to 4		
1 Jun 20200	The national restrictions were lowered to level 3		
17 Aug 2020	The restrictions were lowered to level 2		
21 Sep 2020	Restrictions were lowered to level 1		
Dec 2020	South Africa experienced a second wave of Corona virus		
29 Dec 2020	The lockdown was tightened to level 3.		
1 Mar 2021	The lockdown was lowered to an adjusted level 1		
8 May 2021	The emergence of local cases infected with the highly contagious Delta		
	strain.		
31 May 2021	The country was moved to an adjusted alert level 2, due to a third wave		
	of infections		

Mathematical models are proved to be useful in analysing various scenarios of COVID-19 disease development, and to predict the best possible outcomes when public health policies are incorporated[7, 8]. Many researcher used mathematical models to study the dynamics of the ongoing Covid-19 in South Africa. In particular, Nyabadza et. al [2], proposed a model to illustrate the effect of social distancing on the transmission dynamics of corona virus in South Africa. Garba et. al [3] presented a model that incorporated the role of environmental contamination by Corona virus. The model also accounted for social-distancing effectiveness and community lockdown. Mushayabasa et. al [4] proposed a mathematical model incorporated all the relevant biological factors as well as the effects of individual behavioral reaction and government action to the spread of the epidemic. Mukandavire et. al [5] used a mathematical

model to study the Covid-19 transmission in South Africa and exploring vaccine efficacy scenarios and critical vaccination coverage to control the corona virus. Kassa et. al [6], proposed a mathematical model that takes into the account the behavior of individuals that results from the increase in the number of cases.

Despite the effort that has been taken, South Africa is the most affected country by Covid-19 in the African continent with a total cases of 3.66M and 98,804 deaths. There are challenges, particularly in applying recommended strategies in above mentioned studies. This paper aims to study the ongoing epidemic for different choices of parameters in the model, which reflect the decisions government must make when implementing policies, such as social distancing, partial or full lockdown, etc. We propose an SEIRCD model with a time-varying infection strength to to assess the impact of non-pharmaceutical preventive measures on disease prevalence in South Africa. The model estimates the effective reproduction number \Re_{eff} , which depends on a timevarying infection strength, to examine the effect of the Government actions on disease spread.

The rest of this paper is organized as follows. In Section 2 we describe the proposed SEIRCD model. Estimation of the model's parameters and sensitivity analysis are discussed in Section 3. Then, numerical simulations are carried-out to illustrate the performance of the model. In Section 5 are the discussions and conclusions.

2. MODEL FORMULATION

We consider an SEIRCD epidemic model, where the total human population at any time t is denoted by N(t). The model subdivides human population into six compartments depending on the disease status. These compartments are Susceptible individuals S(t) those who have not been infected by the corona virus, Exposed E(t) those who are infected by the virus and still in the incubation period. Therefore, they cannot transmit it to others yet, infected individuals I(t)(confirmed infected), individuals in the Intensive Care Unit (ICU) C(t), recovered individuals R(t), dead individuals D(t) those who died because of the corona virus.

In this model, we assumed that the natural death and birth rates are constants, and we assumed that susceptible individuals move to the exposed individuals compartment E(t) after contact with infected individuals from compartment I(t) at the rate of $\gamma\beta(t)$ infection transmission, and the individual in compartment E(t) becomes infectious after the incubation period of the disease, which ranges from 3 to 5 days [9],[10], and is transferred to the compartment I(t) at a rate η . Infected individuals I(t) are transferred to the compartment R(t), at a rate $\delta \alpha$, by recovery from the disease, and are transferred to the compartment of ICU, at a rate $\delta(1 - \alpha)$, After the cases becomes critical. Infected individuals in ICU are transferred to the compartment R(t) or D(t), at a rate λ by recovery from the disease or at a rate μ by Death due to disease Covid-19.

Here $\beta(t)$, the infectious communication rate is a parameter for capturing the impact of public health interventions and state policies implemented in South Africa through the Woods-Saxon function [11]. This function is designed mathematically to describe and characterize transformations in terms of their scale or strength, smoothness or surprise, thickness (duration), and tipping point where $a_0, Z, t_{\text{Turning}}, b_{\text{Duratin}}$, are the fitting parameters used to describe the reduction in the rate of infectious contacts. Thus,

$$N(t) = S(t) + E(t) + I(t) + C(t) + R(t) + D(t).$$

The model for Covid-19 transmission dynamics in a population is given by the following system of deterministic non-linear differential equations 1.

(1)

$$\frac{dS}{dt} = -\frac{\gamma\beta(t)S(t)I(t)}{N}$$

$$\frac{dE}{dt} = \frac{\gamma\beta(t)S(t)I(t)}{N} - \eta E(t)$$

$$\frac{dI}{dt} = \eta E(t) - \delta I(t)$$

$$\frac{dC}{dt} = \delta (1 - \alpha)I(t) - (\mu + \lambda)C(t)$$

$$\frac{dR}{dt} = \delta \alpha I(t) + \lambda C(t)$$

$$\frac{dD}{dt} = \mu C(t)$$

where $\beta(t)$ is given by

$$\beta(t) = a_0 \left(1 + \frac{Z}{\exp\left(t - t_{\text{Turning}}/b_{\text{Duratin}}\right)} \right)$$

subject to the initial conditions:

$$S(0) = S_0 \ge 0, E(0) = E_0 \ge 0, I(0) = I_0 \ge 0, C(0) = C_0 \ge 0, R(0) = R_0 \ge 0, D(0) = D_0 \ge 0.$$

parameters	Descriptions
N	The total population
γ	Effective transmission rate
β	infectious communication rate or Hazard rate of infection
η	The incubation rate
δ	The estimated duration or illness
α	Recovery rate without being in ICU
λ	Recovery rate of ICU patient
μ	Death rate due to disease Covid-19 for individuals in the C(t)

The basic reproduction number \mathscr{R}_0 of model (1) is given as

(2)
$$\mathscr{R}_0 = \frac{\gamma \beta_0}{\delta},$$

whereas the effective reproduction number \mathcal{R}_{eff} is given as

(3)
$$\mathscr{R}_{eff} = \frac{\gamma \beta(t) S(t)}{\delta N},$$

3. PARAMETER ESTIMATION AND SENSITIVITY ANALYSIS

This sections aims at estimating the model's parameters and do sensitivity analysis on some of them. It is divided into three subsections, the first describes the data set, the second discusses the estimation of the parameters and in the third is sensitivity analysis.

3.1. Data. Corona virus epidemic data were obtained from the National Institute of Infectious Diseases in South Africa (NICD), the World Health Organization 2020 https://Covid.observer /,https://apps.who.int/iris/handle/10665/331221, Department Of Health Statements in South Africa, and Covid aster za and the data includes confirmed cases, deaths, and critical cases in (ICU), daily and cumulative. These data can be found in the websites of the South African Covid19 data repository https://github.com/dsfsi/Covid19za,and the COVID 19 ZA South Africa Dashboard https://bitly.com/Covid19za-dash.

According to South Africa's statistics, the population in the middle of the 2020 was (59,308,690) and these statistics are very important in estimating individuals vulnerable to infection with the Coronavirus at the beginning of the epidemic.

This data changes rapidly and does not reflect to the some of the cases recorded either because some centers did not publish the data at the same time it was collected, or because the time period for data collection is different in the centers, or the data was not updated on a daily basis, and the data was automatically entered into a repository Data after the result was approved, and duplicate results for tests were excluded.

Data collection of confirmed cases, deaths and recoveries began at the beginning of March 2020, and data collection of intensive care cases began on May 27, 2020. South Africa ranked first in terms of the number of coronavirus cases in Africa.

3.2. Parameter Estimation. Parameters in the model and their estimated values from the daily cases and the cases in intensive care of Covid-19 in the first wave, and the daily cases of Covid-19 only in the second wave. All parameters of the model were estimated and presented in Table 3.

parameters	Estimated value (first wave)	Estimated value (second wave)	Reference
γ	0.0824	0.061	Fitted
η	0.2	0.2	$\left[\frac{1}{3} - \frac{1}{5}\right]$ [12]
δ	0.162	0.162	$\left[\frac{1}{18} - \frac{1}{5}\right]$ [12], [10]
α	0.964	0.495	Fitted
λ	0.0219	0.437	Fitted
μ	0.011	0.02	Fitted
a_0	1	1	Assumed
Z.	2.30	3.06	Fitted
$t_t u$	46.6	55.28	Fitted
b	5.019	1	Fitted

TABLE 3. Estimated values from the data COVID-19

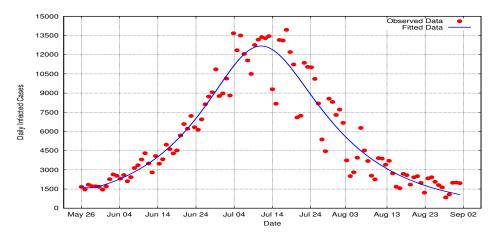


FIGURE 1. Model fit of the daily cases of COVID-19 cases in the first wave.

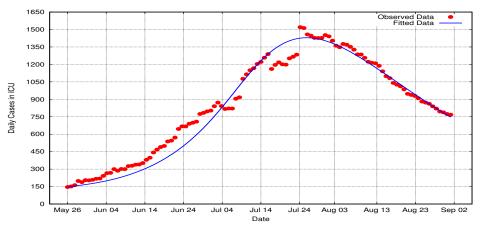


FIGURE 2. Model fit of the daily cases of COVID-19 in the Intensive Care Unit in the first wave.

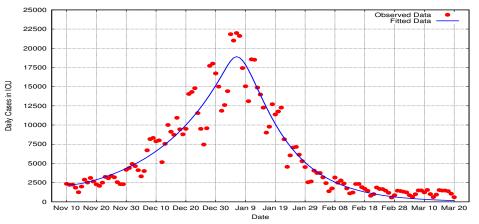


FIGURE 3. Model fit of the COVID-19 daily cases in second wave between 10 Nov 2020 to 20 Mar 2021.

In figures 1, 2 and 3 the daily cases of COVID-19 infections are represented by points and the model that fits these data is represented by a solid line. The figures illustrate how the model fits the daily and ICU cases of Covid 19 in the first and second waves, respectively, in South Africa. We will use the estimated parameter values to calculate the value of \mathscr{R}_0 and $\beta(t)$, and make forecasts for current measurements and other scenarios.

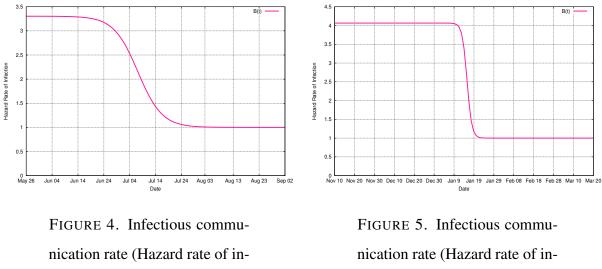
The start of the corona virus outbreak, the effective transmission rate was $\gamma = 0.082$, the infectious communication rate was $\beta_0 = 3.303$, and the basic reproduction number was $\Re_0 = 1.682$. After the first wave of the Corona pandemic ended, scientists were able to learn more about the disease and how it spreads, educating people about the seriousness of the virus and drawing their attention to the fact that it has become a global pandemic.

Preventive measures such as closure, wearing masks, sterilization and social distancing were followed, all of these measures did not prevent the emergence of a second wave of the Corona virus in South Africa. But those precautions reduced the effective transmission rate of the Corona virus γ to 0.061, the basic reproduction number \Re_0 to 1.528. The infectious contact rate β_0 increased to 4.06 with the end of the lockdown period as a result of people returning to their normal lives and mingling with others.

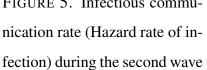
The rate at which Corona patients recover without entering the intensive care unit α was estimated to be 0.94, which means that most patients who contracted Corona disease were treated without their cases becoming critical in the first wave. This ration decreased in the second wave to $\alpha = 0.495$, due to the second mutated version of the Corona virus, which made it more contagious, threatening and faster spreading, and led to the emergence of new, more deadly symptoms that caused increased pressure on the health system, and an increase in the death rate α .

In the first wave, the recovery rate of patients at the ICU λ was estimated to be $\lambda = 0.0219$. This rate highly increased during the second wave to $\lambda = 0.437$. The reason for this significant improvement in the rate of recovery in intensive care units is that the treatment protocol was not known at the beginning of the Corona pandemic, as health units were focused on treating the symptoms of the disease. But the improvement in the treatment protocol during the second wave led to an improvement in the recovery rate of patients in the intensive care units.

Figures 4 and 5, show the estimation of the infectious communication rates during the first and second waves, respectively. It was found that $\beta_0 = 3.303$ in the first wave as appears in Figure 4, meaning that each person interacts with three individuals and transmits the disease to them. This rate is changed in the second wave, and was found to be $\beta_0 = 4.06$. At the end of the two waves this rate became $\beta^* = 1$, due to the preventive procedures that were imposed in South Africa.



fection) during the first wave



3.3. Sensitivity Analysis. It can be seen from Equation (2), the basic reproduction number \mathscr{R}_0 depends on three parameters, namely γ , β_0 and α . It does not depend on rest of the parameters (*i.e.* $\eta, \mu, \alpha, \lambda$).

To determine the relative importance of the model parameters for the initial transmission of Covid-19 and disease spread, it would be self-evident to study the sensitivity of the basic reproduction number \mathcal{R}_0 to changes in the parameters affecting it, and even more so to calculate the sensitivity index for each of these parameters.

Definition 1. The sensitivity index of \mathcal{R}_0 with respect to a parameter P is given by

$$C_P^{\mathscr{R}_0} = \frac{\partial \mathscr{R}_0}{\partial P} \times \frac{P}{\mathscr{R}_0}$$

These values are given in Table 4.

parameters	Sensitivity Index	Sensitivity Index
	(First wave)	(Second wave)
γ	+0.998	+1.000
eta_0	+0.998	+1.000
δ	-0.998	-1.000

TABLE 4. Sensitivity of basic reproductive number evaluated for the parameters value given in Equation (2)

It is worthy to note that the sensitivity index depends on the three parameters γ , β_0 and δ , and is independent of the parameters η , μ , α , λ . For example, the sensitivity index $\gamma = +1$ means that any change in γ will have a similar and in the same proportion effect on \mathcal{R}_0 , be it an increase or a decrease. In a similar fashion, the sensitivity index $\delta = -1$, means that any change in δ will have reverse effect and in the same proportion on \mathcal{R}_0 .

4. NUMERICAL SIMULATIONS

In this section we perform numerical simulation and epidemiological analysis using South African corona virus data and consider several scenarios by increasing and/or decreasing the value of the model parameters.

From Table 3, the effective transmission rate was estimated as $\gamma = 0.0824$ and $\gamma = 0.061$ in the first and second waves of the pandemic, respectively. Figures 6 and 7 show how how changing the parameter γ would change the dynamics of the infected population, in the first and second waves of the pandemic.

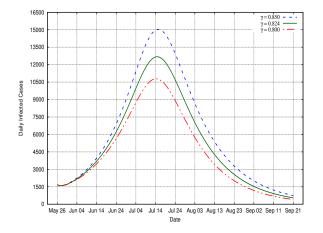
Figure 6 shows that for $\gamma = 0.0824$ the peak of the infected population would be at around 12680 in the first wave of the pandemic. In the case of decreasing γ to 0.08, the peak of the infected cases is predicted to be 10,680. In the case of increasing γ to 0.085, the peak of the infected cases is predicted to be 15030.

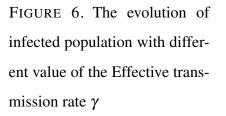
From the 1st of May 2020, a lockdown with restrictions of level 4 were applied in South Africa, due to the global first wave of Corona pandemic. These restrictions were lowered gradually in June, August and September to levels 3, 2 and 1 respectively. These policies led to a

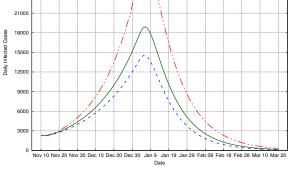
3000

27000

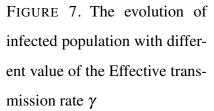
2400







 $\gamma = 0.058$ $\gamma = 0.061$ $\gamma = 0.065$



drop in the effective transmission rate γ when the second wave started, to $\gamma = 0.06$. Figure 7 simulates the dynamics of the infected population during the second wave of the pandemic. It shows that for $\gamma = 0.061$ then the peak size of the infected population in the second wave is at around 18900 patients. If γ is lowered to 0.058, the peak of the infected cases would drop to 14540 cases and if raised to 0.065, then the peak would raise up to around 29100 cases.

From Table 3, the recovery rates of the ICU patients were estimated as $\lambda = 0.0219$ and $\lambda = 0.495$ during the first and second waves of Corona pandemic. Figures 8 and 9 simulate the effect of changing the recovery rate λ of ICU patients on the dynamics of the ICU patients during the first and second waves.

Figure 8 shows the dynamics of the ICU patients during the first wave. At the estimated value $\lambda = 0.0219$, the peak occurred on the first of August with around 1430 patients at the ICU. The simulations show that if λ is decreased to the value $\lambda = 0.01$ the peak will raise to around 1810 patients at the ICU, and if increased $\lambda = 0.03$ then the peak will go down to around 1250 patients. Similarly, in Figure 9, the simulation show that the peak of the ICU patients dynamics occurred on the 9th of January 2021. The actual number of the ICU patients corresponding to the estimated value $\lambda = 0.437$ had a peak of around 3300 patients. If λ is lowered to 0.3 then

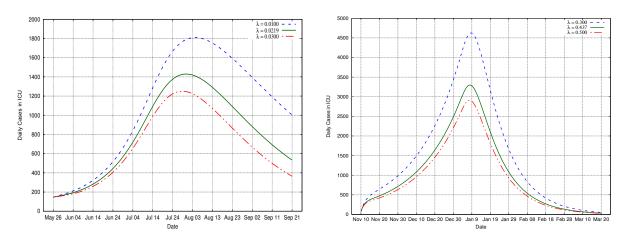


FIGURE 8. The evolution of infected population in ICU with different value of the Recovery rate of ICU patient λ

FIGURE 9. The evolution of infected population in ICU with different value of the Recovery rate of ICU patient λ

the peak would raise to around 4625 patients and if increased to $\lambda = 0.5$, then the peak would drop to around 2900 cases.

From Table 3, the recovery rates of infected population that are not in the ICU were estimated to be $\alpha = 0.964$ and $\alpha = 0.495$, during the first and second waves of the Corona pandemic, respectively. Figures 10 and 11 simulate the effect of changing the recovery rate of patients that are not in the ICU on the dynamics of infected population during the first and second waves of the infection.

Figure 10 shows that the peak size of infected population during the first wave was on the 1st of August 2020, with a total number of patients around 1430, for the estimated value of $\alpha = 0.964$. If α is decreased to 0.94, then the peak size of the infected population would be raised to around 2400 patients. If it is increased to 0.98, the peak size would be lowered to around 810 patients. Figure 11 shows that the peak on the number of infected population during the second wave was around 3300 on the 9th of January 2021, which was achieved for the estimated value $\alpha = 0.495$. If the value of α is decreased to the value 0.3, the peak in the size of infected population will be raised to around 4600 patients. If it is increased to 0.6 the peak size of the infected population would drop to around 2600 patients.

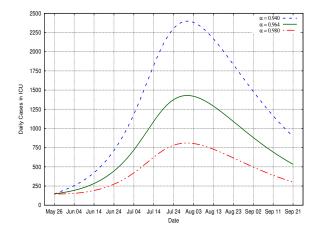
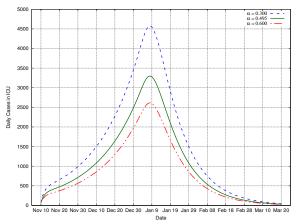
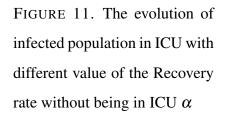


FIGURE 10. The evolution of infected population in ICU with different value of the Recovery rate without being in ICU α





Figures 12 and 13 show how changing the effective communication rate parameter $\beta(t)$ can affect the dynamics of the infected populations during the first and second waves of pandemic. Since the form of $\beta(t)$ involves a parameter Z, then, increasing or decreasing the value of Z leads to an increase or a decrease of the effective communication rate $\beta(t)$. From Table 3, the initial values of β are estimated as $\beta_0 = 3.3$ and $\beta_0 = 4.06$ in the first and second waves, respectively.

Figure 12 shows that for $\beta_0 = 3.3$, the peak size of the infected population in the first wave is around 12680. If β_0 is decreased to 2.3, the peak of the infected population would drop to around 2370. If β_0 is increased to 4.2, the peak size of the infected population would raise to around 57950 patients. Figure 13 shows that for $\beta_0 = 4.06$, the peak size of the infected population in the second wave is around 18900. If β_0 is decreased to 3.02 that would lower the peak size of the infected population to around 3900, whereas if β_0 is increased to 5.06, the peak size of the infected population would jump to around 76670 patients.

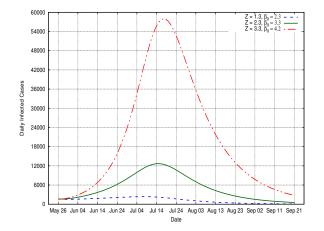
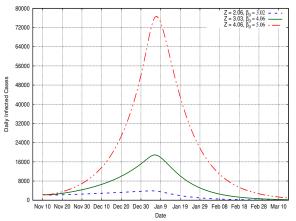
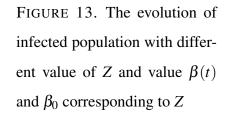


FIGURE 12. The evolution of infected population with different value of Z and value $\beta(t)$ and β_0 corresponding to Z





5. CONCLUSIONS

In this paper, we proposed an SEIRCD model with time-varying force of infection, developed to illustrate the dynamics of corona virus transmission. The model examines the nonpharmaceutical preventive policies on the spread of Corona pandemic in South Africa.

As seen in figures 1, 2 and 3, the model fits well with the daily infected cases and intensive care cases of Covid-19 in the first wave, and only with the daily infected cases in the second wave, which leads to an optimal estimate of the epidemiological parameters of the model in both waves in South Africa, as seen in Table 3. To find out which parameters have more impact on the dynamics of the infected populations in and out the ICUs during the first and second waves of the pandemic, sensitivity analyses were carried out on some of the models' parameters. Namely, the effective transmission rate parameter γ , the recovery rate λ of the ICU patients, the recovery rate α of infected cases not in the ICU and the infectious communication rate β . The sensitivity indices of such parameters were computed and displayed in Table 4.

Figures 6 and 7, 8 and 9, 10 and 11 and; 12 and 13 show the sensitivity of the infected population dynamics to changes on the parameters γ , λ , α and β_0 , respectively. By comparing the effects of these parameters on the infected population dynamics through the figures, we find

that the dynamics of the model is more sensitive to the change in parameter β_0 , followed by γ . It is also noted that the parameter α has more impact on the dynamics of infected population at the ICU than the parameter λ . We see that the two most effective parameters, β and γ are related to the basic reproduction number \Re_0 .

We conclude from these results that decreasing the effective transmission rate leads to a decrease in the number of infected individuals and delays the peak time of the epidemic. If preventive policies such as the implementation of complete lockdown once increases in the daily cases are noticed, this will lead to the delay of the peak time and therefore reduces the total number of infections at the peak. The study shows that reducing the infection transition rate between members of the population has a very positive effect in limiting the spread of Covid-19 in South Africa.

APPENDIX A. MODEL DIAGRAM

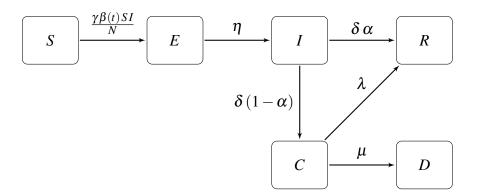


FIGURE 14. Schematic diagram of the proposed model given by system (1)

APPENDIX **B.** ANALYSIS OF THE MODEL

In the section, we seek to qualitatively study the dynamical properties of the infectious disease model(1), which quantifies disease Spread or extinction in a population.

Theorem 1. (positivity) suppose that related solution of the initial data

$$\{S(0), E(0), I(0), C(0), R(0), D(0)\} \in \mathbb{R}^6_+\}$$
 is $(S(t), E(t), I(t), C(t), R(t), D(t))$

. Then for the system of equation (1) the positively invariant set is R^6_+

Proof 1. *Consider the equations of system* (1), *substitute*

$$S = 0, E = 0, I = 0, C = 0, R = 0, D = 0$$

in the first, second, third, fourth, fiftieth, and sixth equations, respectively. Then we have

$$\begin{aligned} \frac{dS}{dt}\Big|_{S \to 0} &= 0 \\ \frac{dE}{dt}\Big|_{S \to 0} &= \frac{\gamma\beta(t)SI}{N} > 0 \\ \frac{dI}{dt}\Big|_{E \to 0} &= \eta E > 0 \\ \frac{dI}{dt}\Big|_{I \to 0} &= \delta(1-\alpha)I > 0 \\ \frac{dR}{dt}\Big|_{I \to 0} &= \delta\alpha I + \lambda C > 0 \\ \frac{dD}{dt}\Big|_{D \to 0} &= \mu C > 0 \end{aligned}$$

Positive invariant region that meets the model (1) is given by

$$\Omega = \{ (S(t), E(t), I(t), C(t), R(t), D(t)) \in \mathbb{R}_+^6 : N(t) \le N(0), \forall t \ge 0 \}$$

The coordinates of an Disease-free equilibrium point (S, E, I, C, R, D) the system of equation(1) obtained by the following equations:

(5)
$$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dC}{dt} = \frac{dR}{dt} = \frac{dD}{dt} = 0$$

therefore, the system of equation (1) indicates that The disease free equilibrium denoted by E_{dfe} , i.e.,

(6)
$$E_{dfe} = (S_0, E_0, I_0, C_0, \mathscr{R}_0, D_0) = (N, 0, 0, 0, 0, 0)$$

B.2. The basic reproduction number. The basic reproduction number is a baseline measure in epidemiology is denoted by \mathscr{R}_0 is the expected value of secondary infections rate per time unit. Based on the system of equation (1), We have three infected classes I(t), E(t), C(t).

$$\frac{dE}{dt} = \frac{\gamma\beta(t)S(t)I(t)}{N} - \eta E(t)$$
(7a)

$$\frac{dI}{dt} = \eta E(t) - \delta I(t)$$
(7b)

$$\frac{dC}{dt} = -\delta(1-\alpha)I(t) + (\mu+\lambda)C(t)$$
(7c)

We assume that the Hazard rate of infection is a constant $\beta(t)$ taking the maximum value $\beta(0) = \beta_0$ at t = 0 and the minimum value $\beta(t^*) = \beta^*$ at $t = t^*$. let x = (E, I, C) and rewrite the system of equation (7) for the susceptible and infected classes in the general from

(8)
$$\frac{dx}{dt} = f(x) - v(x)$$

where

(9)
$$f(x) = \begin{bmatrix} \frac{\gamma\beta(t)SI}{N} \\ 0 \\ 0 \end{bmatrix}, v(x) = \begin{bmatrix} \eta E \\ -\eta E(t) + \delta I(t) \\ \delta(1-\alpha)I(t) - (\mu+\lambda)C(t) \end{bmatrix}$$

Now the Jacobian of f(x) and v(x) of the disease free equilibrium point is

(10)
$$F = \begin{bmatrix} 0 & \gamma \beta_0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

(11)
$$V = \begin{bmatrix} \eta & 0 & 0 \\ -\eta & \delta & 0 \\ 0 & -(1-\alpha)\delta & \mu + \lambda \end{bmatrix}$$

Therefore

(12)
$$V^{-1} = \begin{bmatrix} \frac{1}{\eta} & 0 & 0\\ \frac{1}{\delta} & \frac{1}{\delta} & 0\\ \frac{(1-\alpha)}{(\mu+\lambda)} & \frac{(1-\alpha)}{(\mu+\lambda)} & \frac{1}{\mu+\lambda} \end{bmatrix}$$

The reproduction number of the system equation (1) is follows

(13)
$$\mathscr{R}_0 = \rho(FV^{-1})$$

Therefore

(14)
$$FV^{-1} = \begin{bmatrix} \frac{\gamma\beta_0}{\delta} & \frac{\gamma\beta_0}{\delta} & 0\\ 0 & 0 & 0\\ 0 & 0 & 0 \end{bmatrix}$$

The eigenvalues of FV^{-1} are

(15)
$$(\frac{\gamma\beta_0}{\delta}, 0, 0)$$

Thus

(16)
$$\mathscr{R}_0 = \rho(FV^{-1}) = \frac{\gamma\beta_0}{\delta}$$

and the effective reproduction number is given by

(17)
$$R_{eff} = \frac{\gamma \beta(t) S(t)}{\delta N}$$

Theorem 2. For the system of equation (1), then exist a unique postive endemic equilibrium point E_{en}^* if $\mathcal{R}_0 > 1$.

Proof 2. An endemic equilibrium $E^* = (S^*, E^*, I^*, C^*, R^*, D^*)$, with $S^*, E^*, I^*, C^*, R^*, D^* > 0$, satisfies

(18)
$$S^* = \frac{\delta N}{\gamma \beta^*}$$

(19)
$$E^* = N \left[1 - \frac{\delta}{\gamma \beta^*} \right] \left[\frac{\delta \left(\mu + \lambda \right)}{A} \right]$$

(20)
$$I^* = N \left[1 - \frac{\delta}{\gamma \beta^*} \right] \left[\frac{\eta \left(\mu + \lambda \right)}{A} \right]$$

(21)
$$C^* = N \left[1 - \frac{\delta}{\gamma \beta^*} \right] \left[\frac{\eta \, \delta \, (1 - \alpha)}{A} \right]$$

(22)
$$R^* = N\left[1 - \frac{\delta}{\gamma\beta^*}\right] \left[\frac{\delta\eta\left(\alpha(\mu+\lambda) - \lambda(1-\alpha)\right)}{A}\right]$$

(23)
$$D^* = N \left[1 - \frac{\delta}{\gamma \beta^*} \right] \left[\frac{\delta \eta \mu (1 - \alpha)}{A} \right]$$

where

$$A = \eta (\mu + \lambda) + \delta (\mu + \lambda)(\eta \alpha + 1) + \delta \eta (1 - \alpha) (1 - \lambda + \mu) + (\mu + \lambda) (\eta + \delta (1 + \eta \alpha))$$

B.3. Stability analysis of the model.

Theorem 3. the system of equation (1) is locally stable related to the free equilibrium point E_{dfe} if $\Re_0 < 1$ and unstable if $\Re_0 > 1$.

Proof 3. The Jacobian matrix [13] with respect to the system of equation (1) is given by :

(24)
$$J = \begin{bmatrix} -\frac{\gamma\beta(t)I}{N} & 0 & -\frac{\gamma\beta(t)S}{N} & 0 & 0 & 0 \\ \frac{\gamma\beta(t)I}{N} & -\eta & \frac{\gamma\beta(t)S}{N} & 0 & 0 & 0 \\ 0 & \eta & -\delta & 0 & 0 & 0 \\ 0 & 0 & \delta(1-\alpha) & -\mu-\lambda & 0 & 0 \\ 0 & 0 & \alpha\delta & \lambda & 0 & 0 \\ 0 & 0 & 0 & \mu & 0 & 0 \end{bmatrix}$$

At E_{dfe} , the jacbian matrix becomes

$$(25) J(E_{dfe}) = \begin{bmatrix} 0 & 0 & -\gamma\beta_0 & 0 & 0 & 0 \\ 0 & -\eta & \gamma\beta_0 & 0 & 0 & 0 \\ 0 & \eta & -\delta & 0 & 0 & 0 \\ 0 & 0 & \delta(1-\alpha) & -\mu-\lambda & 0 & 0 \\ 0 & 0 & \alpha\delta & \lambda & 0 & 0 \\ 0 & 0 & 0 & \mu & 0 & 0 \end{bmatrix}$$

Thus, we get the eigenvalues are

$$egin{aligned} \lambda_1 &= 0, \lambda_2 = 0, \lambda_3 = 0, \lambda_4 = -\mu - \lambda \ \lambda_5 &= -rac{(\delta+\eta)}{2} + K \ \lambda_6 &= -rac{(\delta+\eta)}{2} - K \end{aligned}$$

where

$$K = \frac{1}{2}\sqrt{4\gamma\beta_0\eta + \delta^2 - 2\delta\eta + \eta^2}$$

If $\frac{(\delta+\eta)}{2} > K$ implying that $\lambda_5 < 0$, then $\Re_0 < 1$, so the system of equation (1) is locallyasymptotically stable for $\Re_0 < 1$, and implying that $\frac{(\delta+\eta)}{2} < K$ then $\lambda_5 > 0$, we obtain that $\Re_0 > 1$, Hence the system of equation (1) is unstable for $\Re_0 > 1$.

Theorem 4. The endemic equilibrium E_{en}^* of the system equation (1) is locally-asymptotically stable if $\Re_0 > 1$.

Proof 4. The characteristic equation of the E_{en}^* is given by

(26)
$$m^{6} + (A_{1} + A_{2})m^{5} + (A_{3} + \delta\eta\lambda\mu A_{2})m^{4} + (A_{3} + A_{4})m^{3} + A_{2}A_{4}m^{2} = 0$$

Therefore

(27)
$$m^4 + (A_1 + A_2)m^3 + (A_3 + \delta\eta\lambda\mu A_2)m^2 + (A_3 + A_4)m + A_2A_4 = 0$$

where

$$A_{1} = \mu + \lambda + \delta + \eta$$

$$A_{2} = \beta^{*} \left[1 - \frac{\beta_{0}}{\beta^{*} \mathscr{R}_{0}} \right] \left[\frac{\eta \left(\mu + \lambda \right)}{A} \right]$$

$$A_{3} = \delta \lambda + \delta \mu + \eta \lambda + \eta \mu$$

$$A_{4} = \delta \eta$$

Since $A_1 > 0, A_2 > 0, A_3 > 0, A_4 > 0$ for $\mathcal{R}_0 > \frac{\beta_0}{\beta^*} > 1$ and $(A1 + A_2)(A_3 + \delta\eta\lambda\mu A_2) > (A_3 + A_4)$ $((A_1 + A_2)(A_3 + \delta\eta\lambda\mu A_2) - (A_3 + A_4))(A_3 + A_4) > (A_1 + A_2)A_2A_4$ Using Routh-Hurwitz Criterion, E_{en}^* is stable if and only if $\Re_0 > \frac{\beta_0}{\beta^*} > 1$.

DATA AVAILABILITY

The data used to support the work are either cited within the article as references, or hyperlinks to the data were given within the text.

CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

REFERENCES

- O.T. Kolebaje, O.R. Vincent, U.E. Vincent, P.V.E. McClintock, Nonlinear growth and mathematical modelling of COVID-19 in some African countries with the Atangana–Baleanu fractional derivative, Commun. Nonlinear Sci. Numer. Simul. 105 (2022), 106076.
- [2] F. Nyabadza, F. Chirove, C. Chukwu, et al. Modelling the potential impact of social distancing on the COVID-19 epidemic in South Africa, Comput. Math. Methods Med. 2020 (2020), 5379278.
- [3] S.M. Garba, J.M.S. Lubuma, B. Tsanou, Modeling the transmission dynamics of the covid-19 pandemic in South Africa, Math. Biosci. 328 (2020), 108441.
- [4] S. Mushayabasa, E.T. Ngarakana-Gwasira, J. Mushanyu, On the role of governmental action and individual reaction on COVID-19 dynamics in South Africa: A mathematical modelling study, Inform. Med. Unlocked. 20 (2020), 100387.
- [5] Z. Mukandavire, F. Nyabadza, N.J. Malunguza, et al. Quantifying early covid-19 outbreak transmission in South Africa and exploring vaccine efficacy scenarios, PloS One. 15 (2020), e0236003.
- [6] S.M. Kassa, J.B.H. Njagarah, Y.A. Terefe, Modelling COVID-19 mitigation and control strategies in the presence of migration and vaccination: the case of South Africa, Afr. Mat. 32 (2021), 1295–1322.
- [7] I. Ahmed, G.U. Modu, A. Yusuf, et al. A mathematical model of coronavirus disease (COVID-19) containing asymptomatic and symptomatic classes, Results Phys. 21 (2021), 103776.
- [8] H.M. Yang, L.P.L. Junior, F.F.M. Castro, et al. Mathematical modeling of the transmission of SARS-CoV-2evaluating the impact of isolation in são paulo state (brazil) and lockdown in spain associated with protective measures on the epidemic of COVID-19, PloS One. 16 (2021), e0252271.
- [9] Q. Lin, S. Zhao, D. Gao, et al. A conceptual model for the coronavirus disease 2019 (COVID-19) outbreak in Wuhan, China with individual reaction and governmental action, Int. J. Infect. Dis. 93 (2020), 211–216.
- [10] H. Wang, Z. Wang, Y. Dong, et al. Phase-adjusted estimation of the number of Coronavirus Disease 2019 cases in Wuhan, China, Cell Discov. 6 (2020), 10.

- [11] H.H. Ayoub, H. Chemaitelly, G.R. Mumtaz, et al. Characterizing key attributes of COVID-19 transmission dynamics in China's original outbreak: Model-based estimations, Glob. Epidemiol. 2 (2020), 100042.
- [12] I. Korolev, Identification and estimation of the SEIRD epidemic model for COVID-19, J. Econ. 220 (2021), 63–85.
- [13] P. Van den Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, Math. Biosci. 180 (2002), 29-48.