Continuous time stochastic model for the COVID-19 pandemic in Nigeria

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The rapid surge in cases of the novel coronavirus disease (COVID-19), caused by the new strain of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), remains a critical health concern in Nigeria and a global challenge. In this study, we propose an epidemic SVEnEpIQR model that incorporates the behavior of exposed individuals towards COVID-19 protocols and guidelines, as well as the effectiveness of quarantine and vaccination measures. Our model employs a Continuous Time Birth and Death process, presenting transition probabilities, establishing the Kolmogorov master equation, and utilizing the probability generating function approach to derive the expectation equation for each compartment. We conducted stochastic simulations and visualizations for each compartment, and the results align with epidemic response patterns observed in other models that rely on detailed population-level data. The predicted epidemic curve closely resembles the actual situation in Nigeria. Our findings indicate that an increase in the transmission intensity, quarantine and recovery rates leads to a rise in the number of secondary cases of infection. Moreover, we discovered that relying solely on quarantine and treatment of active COVID-19 cases will reduce the number of infected individuals but not the duration of virus spread. Importantly, we conclude that an increased vaccination rate among susceptible individuals not only reduces the number of infected individuals but also curtails the duration of the COVID-19 pandemic in Nigeria.

Keywords: stochastic; COVID-19; modeling; Markov chain; simulation

1. Introduction

The emergence of COVID-19 pandemic turned the world upside down. The Virus originated from the Asian country of China, in the city of Wuhan, and spread to more than 210 countries around the world. Every aspect of human behavior was impacted in one way or the other, the economic and social aspects of human lives being the most affected. How we interact with one another, how we communicate and our social activities were all affected by the pandemic.

One of the largest epidemics in a hundred years is the COVID-19, caused by SARS-CoV-2 which is a single-strand RNA-containing strain of SARSr-CoV of the genus, beta coronavirus, first genetically detected in 2019 in a sample of a patient with SARS pneumonia in Wuhan, China. According to the World Health Organization (Binti Hamzah *et al.*, 2020), the transmission of this virus from person to person happens by airborne droplets within the families of patients, which causes a fairly rapid spread of outbreaks (Yakovyna and Shakhovska, 2021).

Nigeria, the most populous country in Africa with an estimated population of about 200 million was the most affected country in the continent. Nigeria, like the entire countries of the world, had to fight the COVID-19 pandemic and contained the spread of the disease.

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Stopping the uncontrolled spread of the virus requires a coordinated strategy, clear messaging and social solidarity. The economic stability of the nations as well as individuals were tested, the mental strength to adapt to a new normal way of living was questioned and the ability of the most socialized species to adopt to a new restricted social order was also challenged. With neither the vaccine nor pharmaceutical medication to combat the COVID-19 pandemic, many countries were reduced to taking decisive actions to mitigate the pandemic. Bars, clubs, stadiums, places of worshiping (mosques and churches), offices, banks and even market places were shut down at some stages. Traveling restrictions were declared and even families were instructed to keep a certain social distance.

As vaccination of the population began and the creation of effective collective immunity would take some time, social distancing and quarantine restrictions, remained the only effective means of curbing the rate of infection. In such a situation, the role of modeling and predicting the COVID-19 spread, the maximum position and its duration grow. The results of such modeling and predictions are the basis for sound governmental decisions concerning appropriate measures and resources allocation, including pulmonary ventilation systems or dedicated hospitals (Yakovyna and Shakhovska, 2021).

Despite the many intervention strategies adopted by the government, the number of positive coronavirus cases kept increasing on a daily basis. It therefore became imperative to use continuous time stochastic modeling to analyze the spread of the coronavirus pandemic, the rate of contact, the rate of infection and the distribution.

2. Literature Review

Humanity has endured many diseases of variable lethality since its birth. Ebola, HIV and Lassa fever are just a few of them. Ebola is a devastating disease that is transmitted to humans from carrier non-human primates, named fruit bats, and which destroyed races of humankind. HIV is transferred from cross-species of chimpanzee to humans. In the earlier 19th century, it was unknown. It spread rapidly to all continents of the world, killing 300,000 people, including children and women, because its signs and symptoms did not accompany any transmission. Lassa fever has its severity and history of destroying humankind. It is transmitted to humans via rats. Not only this fever, but many other diseases, are also present that prove themselves devastating for the living being. Therefore, scientists tried very hard to build instruments to encounter the adverse effects of ailments and to produce possible treatment via vaccine or medicine. Among several other vicious diseases, COVID-19 has uprooted humanity by killing many people and is still consuming many lives to date (Shatanawi *et al*., 2020)

In December 2019, first cases of a novel pneumonia of unknown cause were reported from Wuhan, the seventh largest city in China. In the meantime, these cases had been identified as infections with a novel strain of coronavirus, called SARS-CoV-2 and the disease is called coronavirus disease 2019 (COVID-19) (Daniyal *et al*., 2020). Götz and Heidrich (2020) reported that patients may develop pains and aches, running nose with nasal congestion, diarrhea, and sore throat; some individuals had developed these as mild symptoms, while others might show their severe forms, and those affected with mild symptoms recovered through special treatment.

As the number of cases grew nationwide in Nigeria and local transmission surged relative to the number of imported cases, there became a need to focus on more local measures to decrease the spread of COVID-19. In addition to the lockdown, social distancing rule was enforced by cancelling mass gatherings, closing businesses except for providers of essential goods and services such as food and pharmaceutical entities and restriction of local travels (Ibrahim and Oladipo, 2020). In response to the COVID-19 pandemic, several countries adopted measures of social distancing to different degrees. For many countries, after successfully curbing the initial wave, lockdown measures were gradually lifted (Coletti *et al*., 2020).

There exist scarce studies on the dynamism of the novel Coronavirus pandemic in Africa in general and Nigeria in isolation. Most of the studies were conducted whence the COVID-19 originated and where the most cases were recorded. Early studies failed to account for the behavior of the exposed individuals; most of the studies were carried out before the emergence of the COVID-19 vaccines; previous studies mainly focused on the symptomatic and the asymptomatic behaviours of the infected individuals. The purpose of this research is to fill these gaps. Therefore, the aim of this study is to model, using transition probabilities of continuous time stochastic model, the COVID-19 pandemic and its dynamics in Nigeria.

3. Methodology

In this study, the spread of COVID-19 pandemic was modeled using the Susceptible-Vaccinated-Exposed-Infectious-Quarantined-Recovered (SVEIQR) model. Using the modified version of Susceptible-Exposed-Infectious-Recovered (SEIR) model, unlike the previously modified versions of SEIR adapted currently by a few research groups, the COVID-19 spread was simulated. Our approach exploits the division of the Exposed compartment class into those that adhere to COVID-19 protocols; that is, those that show positive behaviour to COVID-19 protocols, E_p, and those that do not adhere to COVID-19 protocols; that is, those with negative behaviour towards COVID-19 protocols, E_n.

3.1 Model Formulation

We provided below the comprehensive details on the mathematical modeling of the Coronavirus infection and its background results. The model was developed by splitting the total human population at time, t, denoted by N(t), into the mutually exclusive compartments of the susceptible class, denoted by S(t). The compartment of the vaccinated individuals is denoted by V(t), the compartment of the exposed class that comply to Covid19 protocols is denoted by $E_p(t)$, the compartment of the Exposed individuals that doesn't comply to Covid19 protocols is denoted by $E_n(t)$, the compartment of the infected class is denoted by I (t). The compartment of the quarantined class is denoted by Q(t) while the compartment of the recovered class is denoted by R(t).
Thus,

$$N(t) = S(t) + V(t) + E_N(t) + E_p(t) + I(t) + Q(t) + R(t)$$

3.2 Conceptual framework

The conceptual framework is given in Figure 1.

Potentially infected population (Susceptible S)

It is a population that is still free from COVID-19 virus and has never interacted with active COVID-19 sufferers. This population will increase if there is birth and will decrease if there is death. This population also decreases when there is an interaction between the Susceptible and the Infectious population, which makes it a potential entry into either the exposed population with negative behaviour towards COVID-19, or the compartment of the exposed individuals with positive behaviour towards COVID-19 virus. This population will also decrease when the susceptible individuals that are fully vaccinated and make their entry into the vaccinated compartment. Population movement into or out of the designated compartments will also increase and decrease this population, but in this case, population movement is assumed to be non-existent.

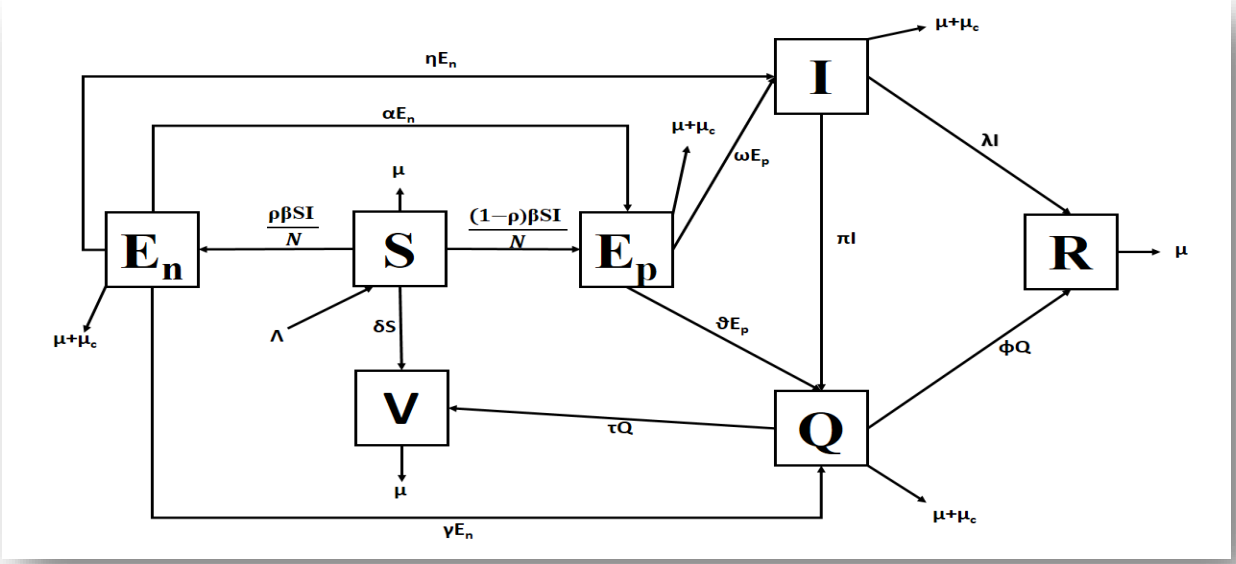

Figure 1: Schematic diagram of the COVID-19 model

Mathematically, this explanation can be written as;

$$\frac{\delta S}{\delta t} = \Lambda - \left(\frac{\beta I}{N} + \delta + \mu\right) S. \qquad (1)$$

Population Vaccinated (V)

This is the compartment of the vaccinated individuals. This population increases when individuals from the susceptible compartment are fully vaccinated and move into the vaccinated compartment; the population increase when quarantine individuals that tested negative to COVID-19 are vaccinated. The decline in this population is only due to natural mortality. In this case, it is assumed that individuals who are fully vaccinated have gained immunity and are no longer exposed to COVID-19 virus. Mathematically, this explanation can be written as;

$$\frac{\partial V}{\partial t} = \delta S + \tau Q - \mu V \qquad (2)$$

Exposed (Negative) population (E_n)

This is the compartment of the exposed individuals with negative behaviour towards COVID-19 protocols. This population increases due to the interaction between Susceptible and Infected populations, which has the potential to make an exposed population. The active COVID-19 case is due to decreasing this population makes its entry into the compartment of infected individuals, change of behaviour from negative to positive and adherence to COVID-19 protocols also reduces this population as the individuals enter the Exposed category with positive behaviour compartment. The rate of compulsory test and quarantine of the exposed individuals also decreases this compartment. The decline due to death in this population is not only when there is natural death but also when symptoms of COVID-19 infection appear in latent individuals. Mathematically, it can be written as

$$\frac{\partial E_N}{\partial t} = \frac{\rho\beta SI}{N} - (\eta + \gamma + \alpha + \mu + \mu_C)E_N \quad (3)$$

Exposed (Positive) population (E_p)

This is the compartment of the exposed individuals with positive behaviour towards COVID-19 protocols. This population increases due to the interaction between Susceptible and Infected populations, which has the potential to make an exposed population. The active COVID-19 case is due to a decrease in this population which makes its entry into the compartment of infected individuals. The rate of voluntary COVID-19 testing by the individuals in this compartment and quarantine either at home or at government approved quarantine centers also decreases this compartment. The decline due to death in this population is not only when there is natural death but also when symptoms of COVID-19 infection appear in latent individuals. Mathematically, this explanation can be written as;

$$\frac{\partial E_P}{\partial t} = \frac{(1-\rho)\beta SI}{N} + \alpha E_N - (\upsilon + \omega + \mu + \mu_C)E_P \quad (4)$$

Population Infected (I)

This is the compartment of the infected individuals with active COVID-19 virus. The infected population increases from exposed individuals with negative behaviour, who have symptoms of infection by COVID-19 virus, which indicates that COVID-19 virus is active. The compartment also increases when the exposed individuals with positive behaviour shows symptoms of COVID-19 virus which indicates that they are infected while the reduction in this population occurs when there is natural recovery from the virus, or through quarantined procedure. Death naturally and/or from the disease complication also reduces this infected population. Mathematically, this explanation can be written as;

$$\frac{\partial I}{\partial t} = \eta E_N + \omega E_P - (\lambda + \pi + \mu + \mu_C)I \quad (5)$$

Quarantine Population (Q)

This is the population of the quarantined individuals. The increase in this population comes from Population Infected who is active COVID-19 sufferers. The population also increases when individuals from the exposed population with positive behaviour volunteer for COVID-19 test. The population also increases due to the rate of compulsory test for the individuals in the Exposed category with negative behaviour compartment. The treatment that is being undertaken in the quarantine may not stop until it is completely declared free from COVID-19, thus decreasing the compartment and entering into the recovered

compartment. This population also decreases when the test result of the quarantined individuals is negative (free from COVID-19); they can be vaccinated and moved into the Vaccinated compartment. The decline in this population due to death is not only caused by natural death but also by death due to COVID-19 complications. Mathematically, this explanation can be written as ;

$$\frac{\partial Q}{\partial t} = \gamma E_N + \upsilon E_P + \pi I - (\phi + \tau + \mu + \mu_C)Q \quad (6)$$

Population Recovered (R)

This is the compartment of the recovered individuals. The increase in this compartment is due to recovery; that is, those that recover naturally from the infected compartment and those that recover through quarantine medication from the Quarantined compartment. The only thing that makes this population decline is natural mortality. In this case, it is assumed that individuals who have recovered have gained immunity and are no longer exposed to COVID-19 virus. Mathematically, this explanation can be written as;

$$\frac{\partial R}{\partial t} = \lambda I + \phi Q - \mu R \quad (7)$$

since $N(t) = S(t) + V(t) + E_N(t) + E_p(t) + I(t) + Q(t) + R(t)$

Then, by taking the partial derivative with respect to t on both sides, the following equation is obtained

$$\frac{\partial N}{\partial t} = \frac{\partial S}{\partial t} + \frac{\partial V}{\partial t} + \frac{\partial E_N}{\partial t} + \frac{\partial E_P}{\partial t} + \frac{\partial I}{\partial t} + \frac{\partial Q}{\partial t} + \frac{\partial R}{\partial t}$$

Substituting the previous equations into N*, we shall obtain

$$\frac{\partial N}{\partial t} = \Lambda - (S + V + E_N + E_P + I + Q + R)\mu - (E_N + E_P + I + Q)\mu_C.$$

Table 1: Definition of Parameters and Symbols

S/No.	Parameter	Interpretation
1	Λ	Input rate (birth rate).
2	β	Contact rate.
3	ρ	Proportion of individuals that become exposed to COVID-19 virus.
4	α	Proportion of individuals from the E_n class that becomes compliant to protocols.
5	γ	Rate of compulsory COVID-19 test and quarantine of individuals from the E_n class.
6	δ	Rate of vaccination of Susceptible individuals.
7	η	Proportion of individuals from the E_n class that become active COVID-19 patients.
8	φ	Proportion of quarantined COVID-19 patients that recovers from the virus.
9	λ	Proportion of active COVID-19 patients that recovers naturally.
10	π	Proportion of active COVID-19 patients that are quarantined.
11	ω	Proportion of individuals from the E_p class that become active COVID-19 patients.
12	υ	Rate of voluntary COVID-19 test and quarantine of individuals from the E_p class.
13	τ	Rate of vaccination of the Quarantine individuals that tested negative to COVID-19.
14	μ	Natural death.
15	μ_c	Death due to COVID-19 complications.

3.3 Model Assumptions

The COVID-19 model for the spread of the coronavirus disease is developed based on the following assumptions.

1. There is natural death in all the compartments since certain individuals can die off naturally from any population.
2. That no individual in the susceptible population is immuned to contracting the COVID-19 virus.
3. There is proximity in the population and between humans to be specific, since human interacts with each other, through this contact, uninfected individuals can get infected.
4. The entire population is broken into a homogeneous sub-population, such that individuals in each compartment are distinguishable from each other.
5. That there is death due to disease complications in the infectious sub-populations, since certain individuals can die from the virus.
6. That fully vaccinated individuals in the compartment vaccinated (V) are immuned to contracting COVID-19.
7. That there is natural recovery from the COVID-19, which is asymptomatic individuals that contracted COVID-19 and did not undertake the COVID-19 test and did not go through quarantine and/or isolation who can recover naturally from the virus.
8. That recovered individuals are assumed to be fully recovered; they have gained a natural immunity in the process and thus cannot contract COVID-19 again.
9. That the contact rate of both the exposed classes (positive and negative behaviours) are assumed to be equal.
10. That the death rate in the infectious sub-systems is not only due to natural death but also due to diseases complications.
11. That the system is based on the ordinary differential equation describing the evolution numbers of individuals in each compartment.

3.4 Continuous Time Markov Chain

Definition: Let X*(t)* be the state at time, t ≥ 0, a stochastic process, X(*t*), $t \geq 0$, on state, S, is said to be a Continuous Time Markov Chain (CTMC), if for all *i*,*j* in S and $t \geq 0$
$P(X(s+t) = j/X(s) = i, X(u), 0 \leq u \leq s) = P(X(s+t) = j/X(s) = i)$.

Table 2: Transition Probabilities

Change	Probability	Description
$S \to S+1$	$\Lambda(\Delta t) + o\Delta t$	Birth of susceptible individuals
$S \to S-1$	$\mu S(\Delta t) + o\Delta t$	Death of susceptible individuals
$S \to S-1, E_N \to E_N+1$	$\frac{\rho\beta SI}{N}(\Delta t) + o\Delta t$	Movement of susceptible individuals to E_n class
$S \to S-1, E_P \to E_P+1$	$\frac{(1-\rho)\beta SI}{N}(\Delta t) + o\Delta t$	Movement of susceptible individuals to E_p class
$S \to S-1, V \to V+1$	$\delta(\Delta t) + o\Delta t$	Rate of vaccination of susceptible individuals
$E_N \to E_N-1, E_P \to E_P+1$	$\alpha E_N \Delta t + o\Delta t$	Change of behaviour from E_n to E_p class
$E_N \to E_N-1, I \to I+1$	$\eta E_N \Delta t + o\Delta t$	Rate of becoming infective of E_n class
$E_N \to E_N-1, Q \to Q+1$	$\gamma E_N \Delta t + o\Delta t$	Rate of compulsory testing on E_n class
$E_N \to E_N-1$	$\mu E_N(\Delta t) + o\Delta t$	Natural Death in E_n class
$E_N \to E_N-1$	$\mu_C E_N(\Delta t) + o\Delta t$	Death due to COVID-19 in E_n class

$E_P \to E_P - 1, I \to I + 1$	$\omega E_N \Delta t + o\Delta t$	rate of becoming infective of E_p class
$E_P \to E_P - 1, Q \to Q + 1$	$\upsilon E_N \Delta t + o\Delta t$	rate of voluntary testing in E_p class
$E_P \to E_P - 1$	$\mu E_p(\Delta t) + o\Delta t$	Natural Death in E_p class
$E_P \to E_P - 1$	$\mu_C E_p(\Delta t) + o\Delta t$	Death due to COVID-19 in E_p class
$I \to I - 1, Q \to Q + 1$	$\pi I \Delta t + o\Delta t$	Rate natural recovery in I class
$I \to I - 1, R \to R + 1$	$\lambda I \Delta t + o\Delta t$	Rate of quarantine of infectious individuals
$I \to I - 1$	$\mu I(\Delta t) + o\Delta t$	Natural Death in I class
$I \to I - 1$	$\mu_C I(\Delta t) + o\Delta t$	Death due to COVID-19 in I class
$Q \to Q - 1, R \to R + 1$	$\phi Q \Delta t + o\Delta t$	Rate of recovery in Q class
$Q \to Q - 1, V \to V + 1$	$\tau Q \Delta t + o\Delta t$	Rate of vaccination of quarantine individuals
$Q \to Q - 1$	$\mu Q(\Delta t) + o\Delta t$	Natural Death in Q class
$Q \to Q - 1$	$\mu_C Q(\Delta t) + o\Delta t$	Death due to COVID-19 in Q class
$V \to V - 1$	$\mu V(\Delta t) + o\Delta t$	Natural Death in V class
$R \to R - 1$	$\mu R(\Delta t) + o\Delta t$	Natural Death in R class

The CTMC is said to be Homogenous if for all t, $s \geq 0$ if, $P(X(s+t) = j/X(s) = i) = P(X(t) = j/X(s) = i)$

Let X(t) be the size of population in the compartment at time, t. Let λ(t) be the stochastic birth-rate, μ(t) be the stochastic death rate associated with the defined process. Then, the birth and death of individuals will be defined by:

$$P\big(X(t+\Delta t) - X(t)\big) = \begin{cases} \Lambda(t)\Delta t + o\Delta t, if,, j = i+1 \\ \mu(t)\Delta t + o\Delta t, if,, j = i-1 \\ 1 - (\Lambda(t)\Delta t + \mu(t)\Delta t + o\Delta t), j = 1 \\ o\Delta t, otherwise \end{cases}$$

Define $\Delta S(t) = S\big(t + \Delta(t)\big) - S(t)$

From the transition probabilities generated, define:

$$P_{e1,e2,e3,e4,e5,e6,e7}(t+\Delta t)$$

$$= \begin{cases} \Lambda(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (1,0,0,0,0,0,0) \\ \frac{\rho\beta SI}{N}(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (-1,0,1,0,0,0,0) \\ \frac{(1-\rho)\beta SI}{N}(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (-1,0,0,1,0,0,0) \\ \delta S(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (-1,1,0,0,0,0,0) \\ \mu S(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (-1,0,0,0,0,0,0) \\ \alpha E_N \Delta t + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,-1,1,0,0,0) \\ \eta E_N \Delta t + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,-1,0,1,0,0) \\ \gamma E_N \Delta t + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,-1,0,0,1,0) \\ \mu_C E_N(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,-1,0,0,0,0) \\ \mu E_N(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,-1,0,0,0,0) \\ \omega E_N \Delta t + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,-1,1,0,0) \\ \upsilon E_N \Delta t + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,-1,0,1,0) \\ \mu_C E_p(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,-1,0,0,0) \\ \mu E_p(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,-1,0,0,0) \\ \lambda I \Delta t + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,0,-1,0,1) \\ \pi I \Delta t + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,0,-1,1,0) \\ \mu_C I(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,0,-1,0,0) \\ \mu I(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,0,-1,0,0) \\ \phi Q \Delta t + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,0,0,-1,1) \\ \tau Q \Delta t + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,1,0,0,0,-1,0) \\ \mu_C Q(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,0,0,-1,0) \\ \mu Q(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,0,0,-1,0) \\ \mu V(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,-1,0,0,0,0,0) \\ \mu R(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,0,0,0,-1) \\ 1 - \Omega(\Delta t) + o\Delta t, \rightarrow if\,(e_1,e_2,e_3,e_4,e_5,e_6,e_7) = (0,0,0,0,0,0,0) \\ 0, \rightarrow otherwise \end{cases}$$

where,

$$\Omega = \Lambda(t) + \frac{\rho\beta SI}{N}(t) + \frac{(1-\rho)\beta SI}{N}(t) + \delta S(t) + \mu S(t) + \alpha E_N(t) + \eta E_N(t) + \gamma E_N(t) + \mu_c E_N(t) + \mu E_N(t) + \omega E_p(t) + \upsilon E_p(t) + \mu_c E_p(t) + \mu E_p(t) + \lambda I(t) + \pi I(t) + \mu_c I(t) + \mu I(t) + \tau Q(t) + \phi Q(t) + \mu_c Q(t) + \mu Q(t) + \mu V(t) + \mu R(t).$$

Invoking the law of total probability to the transition probabilities generated, we can express $P_{(e1,e2,e3,e4,e5,e6,e7)}(t+\Delta t)$ in terms of probability at time t as follows:

$$P_{(e1,e2,e3,e4,e5,e6,e7)}(t+\Delta t) = \Lambda(\Delta t)p(e_1+1)(t) + \frac{\rho\beta SI}{N}(e_1-1)(e_3+1)(\Delta t)p(e_1-1,e_3+1)(t) + \frac{(1-\rho)\beta SI}{N}(e_1-1)(e_4+1)(\Delta t)p(e_1-1,e_4+1)(t) + \delta S(e_1-1)(e_2+1)(\Delta t)p(e_1-1,e_2+1)(t) + \mu(e_1-1)(\Delta t)p(e_1-1)(t) + \alpha(e_3-1)(e_4+1)(\Delta t)p(e_3-1,e_4+1)(t) +$$

$$\eta(e_3-1)(e_5+1)(\Delta t)p(e_3-1,e_5+1)(t)+\gamma(e_3-1)(e_6+1)(\Delta t)p(e_3-1,e_6+1)(t)$$
$$+$$
$$\mu_c(e_3-1)(\Delta t)p(e_3-1)(t)+\mu(e_3-1)(\Delta t)p(e_3-1)(t)$$
$$+\omega(e_4-1)(e_5+1)(\Delta t)p(e_4-1,e_5+1)(t)+$$
$$\upsilon(e_4-1)(e_6+1)(\Delta t)p(e_4-1,e_6+1)(t)+\mu_c(e_4-1)(\Delta t)p(e_4-1)(t)$$
$$+\mu(e_4-1)(\Delta t)p(e_4-1)(t)+$$
$$\pi(e_5-1)(e_6+1)(\Delta t)p(e_5-1,e_6+1)(t)+\lambda(e_5-1)(e_7+1)(\Delta t)p(e_5-1,e_7+1)(t)$$
$$+$$
$$\mu_c(e_5-1)(\Delta t)p(e_5-1)(t)+\mu(e_5-1)(\Delta t)p(e_5-1)(t)$$
$$+\tau(e_6-1)(e_2+1)(\Delta t)p(e_6-1,e_2+1)(t)+$$
$$\phi(e_6-1)(e_7+1)(\Delta t)p(e_6-1,e_7+1)(t)+\mu_c(e_6-1)(\Delta t)p(e_6-1)(t)$$
$$+\mu(e_6-1)(\Delta t)p(e_6-1)(t)+$$
$$\mu(e_2-1)(\Delta t)p(e_2-1)(t)+\mu(e_7-1)(\Delta t)p(e_7-1)(t)+(1-$$
$$\Omega)(\Delta t)P_{(e1,e2,e3,e4,e5,e6,e7)}+o(\Delta t).$$

From the equation above, we can derive the master differential equation, also known as Kolmogorov forward differential equation for the transition probabilities. We compute $\frac{[P_{(e1,e2,e3,e4,e5,e6,e7)}(t+\Delta t)-P_{(e1,e2,e3,e4,e5,e6,e7)}]}{(\Delta t)}$ and set $(\Delta t)=0$.

$$P_{(e1,e2,e3,e4,e5,e6,e7)}(t+\Delta t)=\Lambda p(e_1+1)(t)+\frac{\rho\beta SI}{N}(e_1-1)(e_3+1)\,p(e_1-1,e_3+1)(t)+$$
$$\frac{(1-\rho)\beta SI}{N}(e_1-1)(e_4+1)\,p(e_1-1,e_4+1)(t)+\delta S(e_1-1)(e_2+1)\,p(e_1-1,e_2+1)(t)+\mu(e_1-1)\,p(e_1-1)(t)+$$
$$\alpha(e_3-1)(e_4+1)\,p(e_3-1,e_4+1)(t)+\eta(e_3-1)(e_5+1)\,p(e_3-1,e_5+1)(t)+\gamma(e_3-1)(e_6+1)\,p(e_3-1,e_6+1)(t)+$$
$$\mu_c(e_3-1)\,p(e_3-1)(t)+\mu(e_3-1)\,p(e_3-1)(t)+\omega(e_4-1)(e_5+1)\,p(e_4-1,e_5+1)(t)+$$
$$\upsilon(e_4-1)(e_6+1)\,p(e_4-1,e_6+1)(t)+\mu_c(e_4-1)\,p(e_4-1)(t)+\mu(e_4-1)\,p(e_4-1)(t)+$$
$$\pi(e_5-1)(e_6+1)\,p(e_5-1,e_6+1)(t)+\lambda(e_5-1)(e_7+1)\,p(e_5-1,e_7+1)(t)+\mu_c(e_5-1)\,p(e_5-1)(t)+\mu(e_5-1)\,p(e_5-1)(t)+$$
$$\tau(e_6-1)(e_2+1)\,p(e_6-1,e_2+1)(t)+\phi(e_6-1)(e_7+1)\,p(e_6-1,e_7+1)(t)+\mu_c(e_6-1)\,p(e_6-1)(t)+\mu(e_6-1)\,p(e_6-1)(t)+$$
$$\mu(e_2-1)\,p(e_2-1)(t)+\mu(e_7-1)\,p(e_7-1)(t)+(1-\Omega)P_{(e1,e2,e3,e4,e5,e6,e7)}-\Omega(\Delta t)P_{(e1,e2,e3,e4,e5,e6,e7)}$$

Therefore, the Master equation will be defined as;

$$\frac{P_{(e1,e2,e3,e4,e5,e6,e7)}(t+\Delta t)-P_{(e1,e2,e3,e4,e5,e6,e7)}}{(\Delta t)}$$
$$P_{(e1,e2,e3,e4,e5,e6,e7)}(t)=$$
$$P_{(e1,e2,e3,e4,e5,e6,e7)}(t+\Delta t)$$
$$=\Lambda p(e_1+1)(t)+\frac{\rho\beta SI}{N}(e_1-1)(e_3+1)p(e_1-1,e_3+1)(t)+$$
$$\frac{(1-\rho)\beta SI}{N}(e_1-1)(e_4+1)p(e_1-1,e_4+1)(t)$$
$$+\delta S(e_1-1)(e_2+1)p(e_1-1,e_2+1)(t)+$$
$$\mu(e_1-1)p(e_1-1)(t)+\alpha(e_3-1)(e_4+1)p(e_3-1,e_4+1)(t)+$$
$$\eta(e_3-1)(e_5+1)p(e_3-1,e_5+1)(t)+\gamma(e_3-1)(e_6+1)p(e_3-1,e_6+1)(t)+$$

$$\mu_c(e_3-1)p(e_3-1)(t)+\mu(e_3-1)p(e_3-1)(t)$$
$$+\omega(e_4-1)(e_5+1)p(e_4-1,e_5+1)(t)+$$
$$\upsilon(e_4-1)(e_6+1)p(e_4-1,e_6+1)(t)+\mu_c(e_4-1)p(e_4-1)(t)$$
$$+\mu(e_4-1)p(e_4-1)(t)+$$
$$\pi(e_5-1)(e_6+1)p(e_5-1,e_6+1)(t)+\lambda(e_5-1)(e_7+1)p(e_5-1,e_7+1)(t)+$$
$$\mu_c(e_5-1)p(e_5-1)(t)+\mu(e_5-1)p(e_5-1)(t)$$
$$+\tau(e_6-1)(e_2+1)p(e_6-1,e_2+1)(t)+$$
$$\phi(e_6-1)(e_7+1)p(e_6-1,e_7+1)(t)+\mu_c(e_6-1)p(e_6-1)(t)$$
$$+\mu(e_6-1)p(e_6-1)(t)+$$
$$\mu(e_2-1)p(e_2-1)(t)+\mu(e_7-1)p(e_7-1)(t)+(1-\Omega)P_{(e1,e2,e3,e4,e5,e6,e7)}$$
$$-\Omega(\Delta t)P_{(e1,e2,e3,e4,e5,e6,e7)}$$

The above is the Kolmogorov Master forward equation, which is of full dynamics. It should be noted that Λ and β could either be a constant or time-dependent. In this model, we assumed that Λ and β are dependent on time.

Define T_j as the time for the j^{th} jump. Then the time for $(j+1)^{th}$ jump will be given by

$$T_{J+1}=T_J+W_J$$

where W_j is the interevent time for j^{th} jump.

Now for $x(T_J)=(e_1,e_2,e_3,e_4,e_5,e_6,e_7)^T$ and $n=(e_1+e_2+e_3+e_4+e_5+e_6+e_7)$

We obtain the interevent time as, $W_J=\frac{ln\,U}{\upsilon(e_1,e_2,e_3,e_4,e_5,e_6,e_7)}$

where **U** is a uniformly distributed random variable on the interval [0,1] (Allen, 2010) and

$$\upsilon(e_1,e_2,e_3,e_4,e_5,e_6,e_7)$$
$$=\Lambda(t)+\frac{\rho\beta I}{N}(t)e_1e_3+\frac{(1-\rho)\beta I}{N}(t)e_1e_4+\delta(t)e_2+\mu(t)e_1+\alpha(t)e_4+$$
$$\eta(t)e_5+\gamma(t)e_6+\mu_c(t)e_3+\mu(t)e_3+\omega(t)e_5+\upsilon(t)e_6+\mu_c(t)e_4+\mu(t)e_4+\pi(t)e_6$$
$$+\lambda(t)e_7+$$
$$\mu_c(t)e_5+\mu(t)e_5+\tau(t)e_2+\phi(t)e_7+\mu_c(t)e_6+\mu(t)e_6+\mu(t)e_2+\mu(t)e_7$$

and

$$\frac{1}{\upsilon(e_1,e_2,e_3,e_4,e_5,e_6,e_7)}$$

is the mean of the exponentially distributed random variable W_j (Maiga, 2019).

5. Simulation of the Results and Discussion

Table 3: Parameter Values

S/No.	Parameter	Value	Value	Source
1	Λ	Input rate (birth rate)	0.01	Estimated
2	B	Contact rate	0.45	(Kinafa *et al*., 2020)
3	P	Proportion of individuals that become exposed to COVID-19 virus.	0.6	(NCDC, 2021)
4	A	Proportion of E_n class that becomes compliant to protocols	0.4	(Abioye *et al*., 2021)
5	Γ	Rate of compulsory COVID-19 test and quarantine in E_n class	0.02	(Iboi *et al*., 2020)
6	δ	Rate of vaccination of Susceptible individuals	0.000075	(NCDC, 2021)

7	η	Proportion of the E_n class that become active COVID-19 patients	0.09615	(Iboi *et al.*, 2020)
8	φ	Proportion of quarantined COVID-19 that recovers from the virus	0.714285	(Abioye *et al.*, 2021)
9	λ	Proportion of active COVID-19 patients that recovers naturally.	0.67	(Uchejeso *et al*., 2020)
10	π	Proportion of active COVID-19 patients that are quarantined	0.25	(Uchejeso *et al*., 2020)
11	ω	Proportion from the E_p class that become active COVID-19	0.001	(Kinafa *et al*., 2020)
12	υ	Rate of voluntary COVID-19 test and quarantine in the E_p class	0.005	(Iboi *et al*., 2020)
13	τ	vaccination of Quarantine class that tested negative to Covid19	0.2	(NCDC, 2021)
14	μ	Natural death	0.000005	(Daniyal *et al*., 2020)
15	μ_c	Death due to COVID-19 complications.	0.009995	(Iboi *et al*., 2020)
16	S	Susceptible Compartment	189000000	Estimated
17	V	Vaccinated Compartment	2710000	(NCDC, 2021)
18	E_n	Exposed Negative Compartment	2500000	(NCDC, 2021)
19	E_p	Exposed Positive Compartment	5000000	(NCDC, 2021)
20	I	Infectious Compartment	55000	(NCDC, 2021)
21	Q	Quarantine Compartment	214000	(NCDC, 2021)
22	R	Recovered Compartment	179000	(NCDC, 2021)

We derived the numerical scheme using the continuous time Markov chain model, Kolmogorov master equation, for the approximate solution of the model involving the derivative. Then, we particularized the scheme for our model by giving the scheme shown in figures visualized. As we take the recorded reported cases, the time unit considered in the numerical solution is in years. The respective values of the biological parameters involved in the model obtained through the real cases of Nigerian data shown in Table 2 is used for the simulation purpose.

The SVE_nE_pIQR model presented allots each member of its hypothetical population to one of the seven compartments. The number of times individuals in the various compartments interact with each other and their probability of transmitting infection at each interaction was varied in order to simulate the effect of interventions.

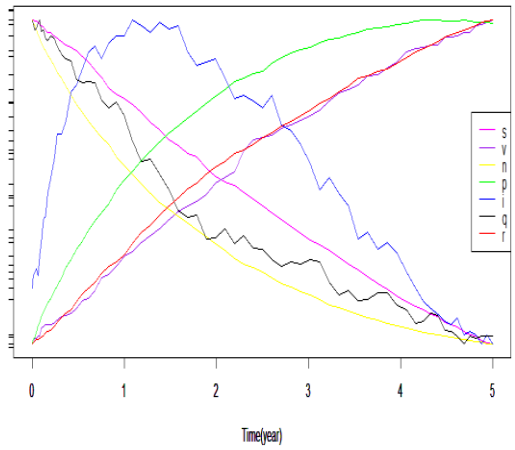

Figure 2: Visualization of the Compartmental values

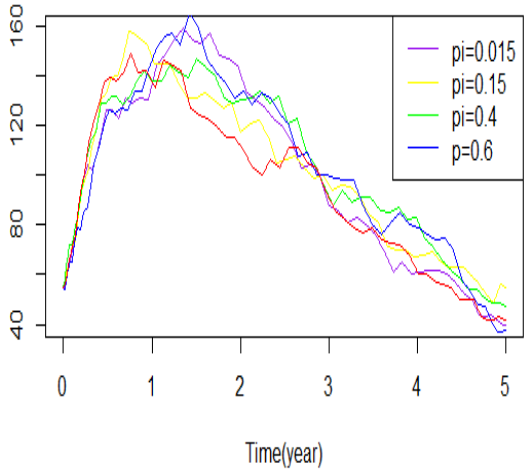

Figure 3: Infectious Class for Varying Pi

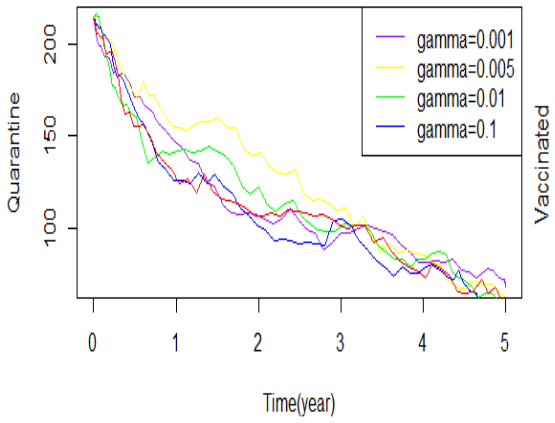

Figure 4: Quarantine Class for varying gamma

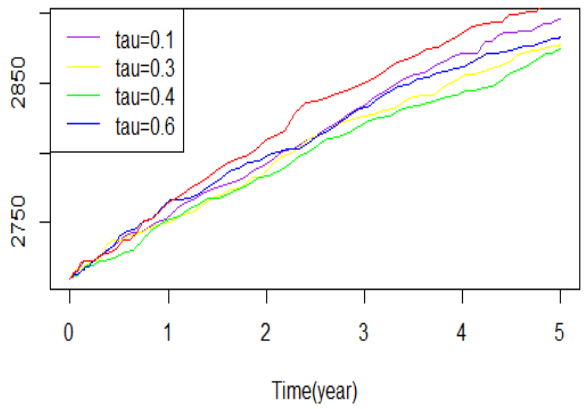

Figure 5: Vaccinated Class for varying tau

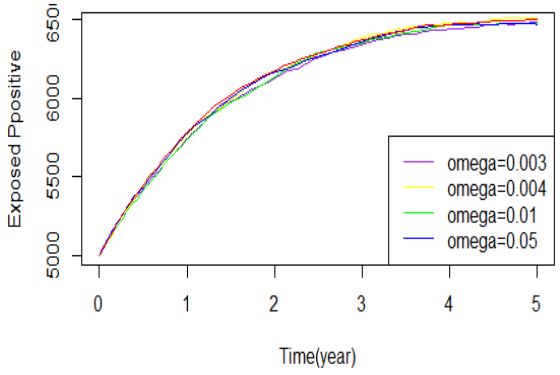

Figure 6: Exposed Positive Class for VaryingOmega

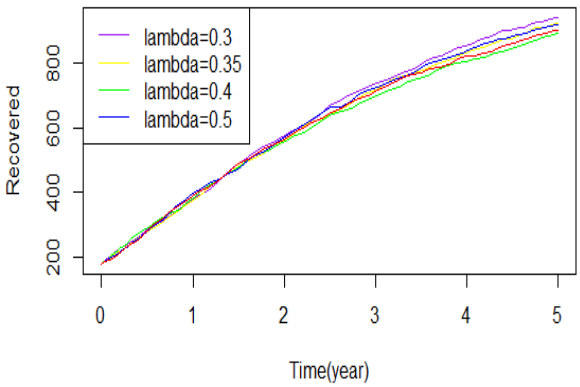

Figure 7: Recovered class for varying lambda

We observed, in Figure 2, that when the compliance with the intervention strategies is high and the contact rate is low there is decrease in the susceptibility, increase in the vaccination population, decreases in the exposed class with negative behaviour, and increase in the exposed class with positive behaviour. The infectious compartment increases, then

plummets over the years, then the quarantine compartment decreases, and increases in the recovered Compartment with positive behaviour towards the guidelines. Similarly, in Figure 3, the plot shows the visualization of the infectious class when the active COVID-19 cases are quarantined. Figure 4 shows that when the compulsory testing is higher in the Exposed compartment with negative behavior, the individuals are tested and quarantined early while the compartment decreases. Also, the infectious compartment decreases while the Quarantine compartment increases. Similarly, if the vaccination rate of the Quarantine compartment increases, then there will be decrease in the number of quarantine individuals and increase in the population of the vaccinated individuals. Early identification and quarantine of infected individuals reduces the contact rate; thus reducing the population of exposed individuals and subsequently leading to the decrease in the rising of new infections.

The result of this research also supported the work of Iboi *et al*. (2020) who reported that COVID-19 could be eliminated in Nigeria if social distancing and face masking were at least moderate. Therefore, based on the limiting testing facilities, lack of work force and poor vaccination rate, it will be easier to achieve strict compliance to the COVID-19 protocols in order to eradicate COVID-19 in Nigeria. We further affirm that the recovery rates will be increasing in the long run regardless of the various intervention measures compliance, testing rate and vaccination rates.

6. Conclusion

In the last few years, stochastic models have been used as a useful tool to understand the complex dynamics and to determine the future trend of an infectious disease. Although, the mathematical epidemic models developed via classical integer order differential systems have its own significance to explore disease dynamics. However, the stochastic models, designed through the continuous time Markov chains, are more useful than the ordinary case, due to data fitting, the memory effects, and time constrain etc. We studied a new stochastic model for understanding the complex dynamics of Coronavirus pandemic in Nigerians reported cases using continuous time Markov chain. We studied the model and provided its stochastic results in details. This study found out that the vaccination of the individuals in the susceptible compartment, as well as those in the quarantine compartment that tested negative to the coronavirus pandemic would help massively in the battle to contain the outspread of the virus. It is also found that the COVID-19 protocols; that is, Face masking, regular hand sanitizing and social distancing, will help in battling COVID-19 on the long run.

The proposed model parameters obtained through estimations are considered further to obtain its numerical results. We studied graphically the model equations solution with the Kolmogorov master equation and found that the solution fits the numerical COVID-19 data in Nigeria. We then varied the important sensitive parameters for different compartments. Increasing the strict adherence to the Non-Pharmaceutical interventions, the number of infective compartments decreases well. The results obtained in this paper through this continuous time stochastic model can be useful further for the scientists and researchers working on the COVID-19 infection in Nigeria. The results can be useful to having the policy for the future spread and control of Coronavirus in the country.

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