SIMULATION OF INFECTIOUS DISEASE MODEL AND ITS EFFECTS TO THE NIGERIAN ECONOMY

By

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Abstract

Corona virus of 2019 is an infectious disease that is making its impact felt in and around the whole world, hence a pandemic. Simulation technique has been used in investigating the sampling input and characterizing the daily uncertainty of the newly infected in the different geopolitical zones of the country. State space analysis of the transition probabilities of the susceptible-infective class have been carried out to model human - human - surface-human contact. A subinterval method for gathering statistical observation is the daily report by the Nigerian Centre for Disease Control (NCDC). Selected values of the disease updates is used to identify the trend, compare transmission rates and provide future patterns between regions. The data analysis has revealed that a higher percentage of the confirmed covid-19 patients are in the southwest region and of the working population. The cases have also shown that there is need for gradual reopening of the economy as many nations are gradually slipping into economic recession. The data was analyzed by means of Microsoft word and excel, 2010 edition. Noteworthy is the fact that the data is presented in tables, charts and graphs.

KEYWORDS: Simulation , Infectious disease, Susceptible-infective, Transition probability, Threshold process, Confirmed cases.

1. INTRODUCTION

For a century, the world has not seen anything like corona virus disease of 2019(Covid-19) pandemic. Covid-19 is a member of the family of Corona viruses that has affected over 200 countries worldwide. It has been reported that a higher percentage of covid-19 deaths was associated with elderly and those with serious underlying health situations like hypertension, diabetes and coronary artery diseases(Zhou et al[33]). Once in awhile, some nations have experienced one epidemic or the other like the Severe acute respiratory syndrome(SARS) outbreak in Canada or the MERS-COV outbreak in South Korea and in the west African subregions, the Ebola outbreak(Butler[2]) and the Pine wilt disease(Shah et al [25]). As covid-19 spreads, a large number of the population are becoming exposed to the virus. Many people see covid-19 as a myth, they do not believe in the existence. Others see it as ‘a big man disease’, while a few others believe in the reality of covid-19 because they have seen victims of the disease or know some people who lost their dear ones to the virus. The federal and state government agencies in Nigeria have gone on public enlightenment campaign to educate the populace on the new disease outbreak. The rapidly evolving situation has resulted in the ‘new normal lifestyle. The pandemic has also crippled a lot of businesses including small-scaled enterprises due to the prolonged lockdown. Covid-19 globally has adversely affected a lot of economies, bringing the super powers to their knees; affecting more of the rich than the poor, more of the educated than the ignorant, hence, in the local parlance, ‘big man disease’.

Generally, infectious diseases are major life threatening ailments to both individuals and public health. Covid-19 is a pandemic that has the tendency to wipe off entire human race if not properly handled. From the analysis given of the pattern of disease transmission pattern (Sun et al[26]) and the difficult challenges in the control of the outbreak(Pellis et al [22]); Kraemer et al[14]), covid-19 is a danger to our teaming population especially lives in the local communities. Most infectious respiratory diseases outbreak unlike covid19 were not transmitted by touching contaminated surfaces (Virlogeux et al[28]; Varia et al[27]). The early work of Kenmack and McKendrick[13] has been a strong motivating factor to many contributors in modeling epidemics and proffering mathematical solution to it. Mathematical models in different dimensions have been used to seek answers to certain questions on infectious diseases transmissibility rate, effects and numbers and incubation period(Lauer et al [15]; Yulian[32]). Statistical analysis(Linton et al[16]) has been a dependable bedrock for understanding many things about the outbreak of an infectious disease. A mathematical model based on numerical results have been studied. Techniques like Variational iteration method (Harir et al [9]), differential transformation methods(Kanth and Aruna, [11]), optimal control strategies of transmission dynamics(Kang et al. [10]; Edwards[7]), simulating model(Chen et al[3]) have been applied to provide solutions to the resulting nonlinear modeled equations. Many nations economy have been seriously affected as they enter into recession a second time in 5years (www.premiumtimesng.com 21 November,2020) after World Bank's prediction in June 25, 2020 (www.worldbank.org) .

2.0 **Mathematical Model Modeling**

There are several models of infectious diseases. We have the SEIR, SIR, MSER,SIS etc. and their various modifications commonest, among these is the SEIR model. The SEIR model according to Harir et al [9] is a model based on the dividing the population under study into four distinct compartments: susceptible (S) individuals, the exposed but not yet infectious (E), infectious (I)class and the recovered (R).

S denotes Susceptible: that is the population of those not infected but are likely to be infected.

E stands for Exposed: those exposed to the virus whether they are already infected, one cannot tell until after the incubation period which is between 2-14days. This is also the susceptible population-deaths.

I indicates Infective: this comprises the population of those confirmed to have the virus.

R is the Recovered/Removed: this constitute those who have recovered from the disease plus those who died as a result of the virus. For the purpose of this current work, SIR model has been selected where the 'E' in SEIR is collapsed into S. We re-define S as the susceptible including those exposed and those not yet exposed to the virus. The aim of adopting SIR model for simulation of covid-19 infections pattern is because of the fact that the model generates a univariate population when the various factors interact with

each other in a bivariate distribution (Nsoesie et al[18]; Osthus et al,[19]). SIR model is a tractable bivariate distribution extension of the birth/death process where the rates are allowed to be nonlinear in the sense that it can be easily managed. The spread of most infectious diseases apart from physical contact, can also be caused by human mobility rate. In this work, we will consider the modeling of the threshold process in part, the chain process and the transformational approach of the epidemic situation of covid-19 as it relates to Nigeria.

In each case of matrix exponentiation, Monte Carlo approximation or Bayesian approximation can be applied. This leads to generating transition probabilities which enable direct inferences of parameters in the model. The transition events of S→I→R populations are in strict compliance, hence the constant population. Few attempts have been made to compute the transition probabilities of their interactions. It was demonstrated in Keeling and Ross[24] that transition probabilities through matrix exponentials is achievable for modeling spread of infectious/transmissible diseases for small population. However, some researchers have opined that using matrix exponentiation is quite difficult to compute (Crowford and Suchard[4]), instead a likelihood free approaches has been suggested in Owen et al[21] to overcome this difficulty.

To determine the actual population of the Susceptible, Infective and Removed, we have

$$\left.\begin{aligned} \frac{dS}{dt} &= \text{Population growth rate- new infections} \\ \frac{dI}{dt} &= \text{total number of new infections- death by natural cause-recovery} \\ \frac{dR}{dt} &= \text{number of recovery-deaths} \end{aligned}\right\} \quad (1)$$

$$\left.\begin{aligned} \frac{dS}{dt} &= N - \beta(N_T) - \mu S\,,\ S(0) = N_T - \lambda \quad \text{(i)} \\ \frac{dI}{dt} &= \beta(N_T) - \lambda I - \mu I,\ \ I(0) = \lambda \quad \text{(ii)} \\ \frac{dR}{dt} &= \lambda I - \mu R,\ \ R(0) = 0 \quad \text{(iii)} \end{aligned}\right\} \quad (2)$$

β is proportion of the disease transmission to the susceptible population(the number of contacts), λ is rate of infection per exposure, $N = S(t) - I(t) + R(t)$ is the total number of active population and μ is the removal rate.

2.1 Threshold Process

At the start of the disease outbreak, system (2) is reduced to

$$\frac{dS}{dt} = -\beta, \frac{dI}{dt} = \lambda, \frac{dR}{dt} = 0 \quad (3)$$

The implication of (-β) in (3) is an indication that the already exposed individuals who have been in contact with the virus should be isolated and observed for symptomatic exhibition and possible treatment. $R_0 S = 1$, confirms there is an epidemic, where R_0 is the disease reproductive number, that is, the ratio of

the transmission to the recovery rate. It can also denote the probable or expected number of infections in a susceptible population caused by the introduction of one infected individual(Eid et al[8]). Following the model presentation of [13], an epidemic gets to community transmission when $N > N_T$ and

$$I = E\ population - R = \sum_{\theta=0}^{t} v_{t,\theta} \quad (4)$$

(4) gives the infected individuals at each stage at time t. θ is the unit stage. We present a table of stages of infections up to the third level.

Fresh infection	No of patients at each stage of infection	No infected
v_3	$v_{3,0}$ $v_{3,1}$ $v_{3,2}$ $v_{3,3}$	I_3
	↗ ↗ ↗	
v_2	$v_{2,0}$ $v_{2,1}$ $v_{2,2}$	I_2
	↗ ↗	
v_1	$v_{1,0}$ $v_{1,1}$	I_1
	↗	
v_0	$v_{0,0}$	I_0

Table 1 : Pattern and stages of infections.

$v_{0,0} = v_0 + I_0$, the arrows shows the pattern followed by each infected individual. I_t is the number infected at time t and v_j is the individual threshold.

The Infective Pressure process is expressed as

$I(t) = \frac{\lambda}{n}\sum_{j=-m+1}^{[t]-m} I_j,\ 0 \le t \le n+m$, $I_t = \sum_{\theta=0}^{t} v_{t,\theta}$ is the total number of individuals who are ill at the beginning and $V_t = S_T \sum_{1}^{t} \lambda_\theta v_{t,\theta}$ is the total susceptible population.

The probability of an infection is proportional to the number infected on one side and the number not yet exposed to the virus on the other side. Therefore, the number of those who are removed from each group after time interval t are

$$R_\theta v_{t,\theta} = v_{t,\theta} - v_{t+1,\theta+1} \quad (5)$$

The number of persons still unaffected by the virus are;

$$S_T = N - \sum_{0}^{t} V_{t,\theta} = N - \sum_{0}^{t} v_t - R_t \quad (6)$$

If $S_n(t)\ and\ I_n(t)$ represent the numbers of susceptible and infective respectively at time t, the epidemic duration becomes

$$T_n = inf(t \ge 0 : I_n(t) = 0)$$

Introducing $Y = \{y(t): t \geq 0\}$, with infectious rate as φy and removal rate as γy, $\frac{\lambda}{\gamma} \leq 1$ will lead to extinction of the virus with probability 1. However, if $\frac{\lambda}{\gamma} > 1$ then Y becomes extinct from the population with probability $\left(\frac{\lambda}{\gamma}\right)^{-1}$ and explodes with probability $1 - \left(\frac{\lambda}{\gamma}\right)^{-1}$.

For these models to work, there are guiding principles.

2.2 **Assumptions**

i) All individuals/persons in the population are susceptible to the disease

ii) No immunity is conferred on a single critically exposed individual but only to those who are fully recovered

iii) The critically exposed(threshold density) of the population to the disease is either through the introduction of one or more infected persons (human to human contact) or through contacts to infected surfaces(infected objects and human contact).

iv) The number leaving susceptible group= number entering infected group and the number leaving infected class equals the number removed from the population.

However, if the actual population density is less than or equal to the threshold value, then the addition of one or more infected persons will not lead to an epidemic. In addition, epidemic results when the actual density of the population is greater than or equal to the threshold value due to the introduction of one or more infected persons. Thus, epidemic continues as long as those exposed to the virus are greater than or equal to the threshold value. Epidemic comes to an end when all the susceptible persons have been removed and when the causative factors have reduced.

The covid-19 threshold occurs when

* an already infected person comes in contact with other persons

* respiratory droplets from an infected persons fall on surfaces and humans come in contact with these droplets(surfaces), that is human to surface to human infection.

* the virus gets into the eyes, nose or mouth of exposed persons.

This is where the analysis of covid-19 is different from other models of infectious diseases.

3. Simulation Technique

The essence of simulation is such that an entire process can be modeled to replicate the actual situation. We manually compute the estimated population of S(t), I(t) and R(t). If we let B_j *and* A_j denote the numbers of susceptible and infective respectively at time j where j can be seen as the next generation, the conditional probabilities

$$\Pr(A_{j+1} = a_{j+1}/B_0 = b_0, A_0 = a_0, .., A_j = a_j, B_j = b_j)$$
$$= \Pr(A_{j+1} = a_{j+1} / B_j = b_j, A_j = a_j)$$

$$= \binom{b_j}{a_{j+1}} (1 - q^{a_j})^{a_{j+1}} q^{a_j})^{b_j - a_{j+1}} \quad (7)$$

And $B_{j+1} = B_j - A_{j+1}$ (8)

By (8), a susceptible individual remains susceptible in the next consideration as long as the individual is not infected. An individual also remains infective until removed from population. These events are independent, hence the population is regarded as constant. There are several possibilities for the SIR model needed to obtain these parameters. In Ball et al[1], used the SIR model to describe how the threshold parameters to obtain exact values for a small population. Suppose we treat the rate of transmission as a continuous time Markov Process such that $\Pr(A(t)) = Pr\{A_1(t), A_2(t)\}, A(0) = 0, with\ t \geq 0$. $A_1(t)$ denotes new cases with mild symptoms and $A_2(t)$ new cases with complications(severe presentations). Let a, b ∈ be real integers, then

$$(i) Pr_{a,b}\begin{Bmatrix} A_1(t+dt) = a+1 \\ A_2(t+dt) = b \end{Bmatrix} \begin{matrix} | A_1(t) = a \\ | A_2(t) = b \end{matrix} = \lambda_{a,b}^{(1)} dt + 0(dt)$$

$$(ii) Pr_{a,b}\begin{Bmatrix} A_1(t+dt) = a \\ A_2(t+dt) = b+1 \end{Bmatrix} \begin{matrix} | A_1(t) = a \\ | A_2(t) = b \end{matrix} = \lambda_{a,b}^{(2)} dt + 0(dt)$$

$$(iii) Pr_{a,b}\begin{Bmatrix} A_1(t+dt) = a \\ A_2(t+dt) = b-1 \end{Bmatrix} \begin{matrix} | A_1(t) = a \\ | A_2(t) = b \end{matrix} = \mu_{a,b}^{(2)} dt + 0(dt)$$

$$(iv) Pr_{a,b}\begin{Bmatrix} A_1(t+dt) = a+1 \\ A_2(t+dt) = b-1 \end{Bmatrix} \begin{matrix} | A_1(t) = a \\ | A_2(t) = b \end{matrix} = \gamma_{a,b} dt + 0(dt)$$

$$Pr\begin{Bmatrix} A_1(t+dt) = a \\ A_2(t+dt) = b \end{Bmatrix} \begin{matrix} | A_1(t) = a \\ | A_2(t) = b \end{matrix} = 1 - \left(\lambda_{a,b}^{(1)} dt + \lambda_{a,b}^{(2)} \varphi + \mu_{a,b}^{(2)} + \gamma_{a,b}\right) + 0(dt) \quad (9)$$

Probabilities (i)-(iv) at time t signify new cases of infections{with mild symptoms, with severe infection, of transition from severe case to removed class and of transiting from severe infectious class to mild symptomatic group respectively}. λ is the rate at which the susceptible is becoming Infectious , μ is the rate of the infectious being removed through recovery or death and γ

To project the future trend of the pandemic, we can estimate the likely population of individuals that are infected in the population. To estimate infected count, there are several approaches

3.1 PARAMETER ESTIMATION USING TRANSITION PROBABILITY

We re-define $S_t + I_t + R_t = 1\ for\ all\ values\ of\ t$, if the initial values are $S_0, I_0\ and\ R_0$ with $\{S_k, I_k\ and\ R_k\}$ as their respective kth period value, R_0 here is the initial number of persons removed from the closed population. From (9)

$$I(t) = \lambda_{a,b}^{(1)} dt + \lambda_{a,b}^{(2)} dt + \gamma_{a,b} dt - \mu_{a,b}^{(2)} + 0(dt) \quad (10)$$

$$\lambda_{a,b} = \{(a,b): \lambda_{ab}^{(1)} + \lambda_{a,b}^{(2)} + \gamma_{a,b}\} \quad (11)$$

The transition probability of infection given the susceptible class is given as

$Pr(I/S) = q(I/S)\alpha(S,I)$, $\forall S \neq$ I and $Pr(S/S) = 1 - \int_0^\infty (\mathrm{I/S})\alpha(\mathrm{S,I})\mathrm{dI}$

We assume that $Pr_{a_0,b_0} = 0 \; \forall \; a < a_0$ and $f_{ab}(s), s \in \mathbb{C}$ is the Laplace transform of Pr_{a_0,b_0}

$$f_{ab}(s) = \mathcal{L}\{Pr_{a_0,b_0}(t)\}(s) = \int_0^\infty e^{-st} Pr_{a_0,b_0}(t)dt \qquad (12)$$

Using (12), the simulated number of infected is obtained. This includes the recovered, the dead and those still with the virus. Note that at this stage, the population is still susceptible.

Again, from (9), we have

$$sf_{ab}(s) - Pr_{a_0,b_0}(0) = \lambda^{(1)}_{a-1.b} f_{a-1,b}(s) + \lambda^{(2)}_{a,b-1} f_{a,b-1}(s) + \mu^{(2)}_{a,b+1} f_{a,b+1}(s) + \gamma_{a-1,b+1} f_{a-1,b+1}(s) - \left(\lambda^{(1)}_{a,b} + \lambda^{(2)}_{a,b} + \mu^{(2)}_{a,b} + \gamma_{a.b}\right) f_{a,b}(s), a, b \in \mathbb{N}^2 \qquad (13)$$

$f_{ab}(s)$is the unique solution of (13) and this is as a result of the uniqueness $Pr_{a,b}(t)$

To show uniqueness of $Pr_{a,b}(t)$,

Let θ b the rate of growth per unit period, we can construct the sequence $\{\theta^{(0)}_{a,b}(s)\}_{b=0}^{\infty}$

$$\left(s + \lambda^{(1)}_{a,0} + \lambda^{(2)}_{a,0}\right)\theta^{(0)}_{a,0}(s) - \mu^{(2)}_{a,0}\theta^{(0)}_{a.1}(s) = 1 \;\; and$$

$$\left(s + \lambda^{(1)}_{a,b-1} + \lambda^{(2)}_{a,b-1} + \mu^{(2)}_{a,b-1} + \gamma_{a,b-1}\right)\theta^{(0)}_{a,b-1}(s) - \lambda^{(2)}_{a,b-2}\theta^{(0)}_{a,b-2}(s) - \mu^{(2)}_{a,b}\theta^{(0)}_{a,b}(s) = 0, b \geq 2 \qquad (14)$$

If we compare the sequences in (13) and (14), we deduce that

$$\mathcal{L}^{-1}\left[\theta^{(0)}_{a,b}(s)\right] = \mathrm{Pr}_{a_0,0}(t) \qquad (15)$$

Since Pr(t) is a probability distribution, $\sum_{a,b\in\mathbb{N}x\mathbb{N}} \mathrm{Pr}_{a_0,b}(t) = 1$.

However, taking the Laplace transform of (14) yields

$$f_{ab}(s)\sum_{a,b\in\mathbb{N}x\mathbb{N}} \theta^{(0)}_{a,b}(s) = \frac{1}{s} \qquad (16)$$

Therefore, $\lim_{b\to\infty} \theta^{(0)}_{a_0,b}(s) = 0 \; for \; all \; s > 0$

To continue, we state the necessary and sufficient conditions of $Pr_{a,b}(t)$ as Lemmas 1 and 2;

Lemma 1

The sequence $\theta^{(0)}_{a,0}$ converges for $s > 0$

Proof:

$$\theta^{(0)}_{a,b}(s) = \prod_{i=1}^{b} A_{1(a,i)} \frac{A_1(a,b+1)}{A_2(a,b+1)} + \frac{A_1(a,b+2)}{A_2(a,b+2)} + \frac{A_1(a,b+3)}{A_2(a,b+3)} + \frac{A_1(a,b+4)}{A_2(a,b+4)} + \cdots \qquad (17)$$

Where $A_2(a,b)$ is the denominator of the b[th] convergent of $\{\theta^{(0)}_{a,0}(s)\}$

From (14),

$$\left(s + \lambda^{(1)}_{a,b} + \lambda^{(2)}_{a,b} + \mu^{(2)}_{a,b} + \gamma_{a,b}\right) f_{a,b}(s) - \lambda^{(2)}_{a,b-1} f_{a,b-1}(s) - \mu^{(2)}_{a,b+1} f_{a,b+1}(s) = \lambda^{(1)}_{a-1,b} f_{a-1,b}(s) + \gamma_{a-1,b+1} f_{a-1,b+1}(s), b \in \mathbb{N} \qquad (18)$$

The value from (18) is sufficiently large if we consider

$\sum_{a}^{\infty}\sum_{b=d+1}^{\infty} Pr_{a_0,b_0}(t)\ as\ small,\ \ 0 \le b \le d$

Lemma 2

$f_{a_0,b}(s) = \theta_{a_0,b}^{(b_0)}(s)$ such that

$$\theta_{a,b}^{(j)}(s) = \begin{Bmatrix} \frac{(-1)^{j-b+1}A_{2(a,b)}}{\mu_{a,j+1}^{(2)}\prod_{k=1}^{j+1}A_{1(a,k)}}\theta_{a,j}^{(0)}(s), & if\ \ b \le j \\ \frac{-A_{2(a,j)}}{\mu_{a,j+1}^{(2)}\prod_{k=1}^{j+1}A_{1(a,k)}}\theta_{a,b}^{(0)}(s), & if\ b \ge j \end{Bmatrix} \quad (19)$$

Proof:

From (19), we have

$$f_{a,b}(s) \approx \sum_{j=0}^{d}\left[\lambda_{a-1}^{(1)}f_{a-1,j}(s) + \gamma_{a-1,j+1}f_{a-1,j+1}(s)\right]\theta_{a,b}^{(j)}(s) \quad (20)$$

Continuing,

Let $\theta_{a,b}^{(j)}(s)$ be defined as in (15) and (17), we have

$$Pr_{a_0,b_0}(t) = \begin{Bmatrix} 0, & if\ a < a_o \\ \mathcal{L}^{-1}[f_{a,b}(s)](t). & if\ \ a \ge a_0 \end{Bmatrix} \blacksquare \quad (21)$$

From system (2(ii))

$$\frac{dI(t)}{dt} = I(t)Q \quad (22)$$

where Q is the matrix generator, comparing (22) to a forward Kolmogorov differential equation, we have the following matrix transformation

$$\begin{bmatrix} \frac{dP_{a,0}(t)}{dt} \\ \frac{dP_{a,1}(t)}{dt} \\ \frac{dP_{a,2}(t)}{dt} \\ \cdot \\ \cdot \\ \frac{dP_{a,T}(t)}{dt} \end{bmatrix} = [P_{a,0} \quad P_{a,1} \quad P_{a,2} \quad .. \quad P_{a,T}] \begin{bmatrix} -\lambda_0 & \lambda_1 & 0 & 0 & .. \\ \gamma_1 & -(\lambda_1+\gamma_1) & \lambda_1 & 0 & .. \\ 0 & \gamma_2 & -(\lambda_1+\gamma_1) & \varphi_1 & .. \\ 0 & 0 & \gamma_3 & -(\lambda_1+\gamma_1) & .. \\ . & . & . & , & \\ . & . & . & , & \end{bmatrix} \quad (23)$$

For a,b ≥ 1

(i)one or more individuals are infective

$$P_{a,b}(t+\delta t) = P_{a,b}(t)(1-\lambda\delta t)(1-\mu\delta t) + P_{a+1,b}(t)(1-\lambda\delta t)\mu\delta t + P_{a,b+1}(t)\lambda\delta t(1-\mu\delta t) \quad (24)$$

Simplifying,

$$P_{a,b}(t+\delta t) = P_{a,b}(t) - (\lambda+\mu)P_{a,b}(t)\delta t + \lambda\mu P_{a,b}(t)(\delta t)^2 + \mu P_{a+1,b}(t)\delta t - \lambda\mu P_{a+1,b}(t)(\delta t)^2 + \lambda P_{a,b+1}(t)\delta t - \lambda\mu P_{a,b+1}(t)(\delta t)^2$$

Ignoring the terms of $(\delta t)^2$, we have,

$$P_{a,b}(t+\delta t) = P_{a,b}(t) - (\lambda+\mu)P_{a,b}(t)\delta t + \mu P_{a+1,b}(t)\delta t + \lambda P_{a,b+1}(t)\delta t$$

$$\frac{P_{a,b}(t+\delta t)-P_{a,b}(t)}{\delta t} = -(\lambda+\mu)P_{a,b}(t) + \mu P_{a+1,b}(t) + \lambda P_{a,b+1}(t) \quad (25)$$

As $\delta t \to 0$, Eq (25) becomes

$$\lim_{\delta t\to 0}\left\{\frac{P_{a,b}(t+\delta t)-P_{a,b}(t)}{\delta t}\right\} = \frac{d}{dt}\{P_{a,b}\} = -(\lambda+\mu)P_{a,b}(t) + \mu P_{a+1,b}(t) + \lambda P_{a,b+1}(t). \quad (26)$$

(ii) a case of no new infective person

$$P_{0,0}(t+\delta t) = P_{0,0}(1-\lambda\delta t)(1-\mu\delta t) + P_{a,b}(t)(1-\lambda\delta t)\mu\delta t \quad (27)$$

$$= P_{0,0}(t) - \lambda P_{0,0}(t)\delta t + \mu P_{a,b}(t)\delta t - \lambda\mu P_{a,b}(t)(\delta t)^2 \quad (28)$$

Just as in Eq.(28),

$$\lim_{\delta t\to 0}\left\{\frac{P_{0,0}(t+\delta t)-P_{0,0}(t)}{\delta t}\right\} = \frac{d}{dt}\{P_{0,0}\} = -\lambda P_{0,0}(t)\delta t + \mu P_{a,b}(t)\delta t \quad (29)$$

3.2 State space Analysis

The Bayesian inference for Covid-19 is an approach that draws inferences on the probability when observed data are used instead of parameters as in section 3.1 above. That is using the observed data to make inferences on the rates of infections and removal(recovery and deaths). Let D=observed data and all the model parameters be denoted as $\{\theta, a\ vector\}$, then the joint probability of any parameter estimation given the observed data is $\Pr(D,\theta) = \Pr(\theta)\, L(D/\theta)$. $\Pr(\theta)$ is the prior distribution(previous record) of θ and $L(D/\theta)$is the likelihood function. The advantage of this process is that the Bayesian theorem is used to derive the future data(posterior distribution) of the observed data. That is,

$$Pr(\theta/D) = \frac{Pr(\theta)L(D/\theta)}{\int_0^\infty \Pr(q)L(D/q)dq} \quad (*)$$

Eq.(*) is very useful, it determines the focus of the distribution used in drawing inference on the future trend of the disease. Suppose we let θ_t be time indexed latent state and $\emptyset$ be the model parameter for all time t = (1,2,…,T)

$\theta_t = (\theta S_t, \theta I_t, \theta R_t)$ denotes the unobservable Susceptible, infectious and removed population. The likelihood that an unobserved proportion of the population may experience increase or decrease in the number infected depends more on the time interval in the susceptible state before becoming infected, and this can be obtained considering the state variables;

$$\emptyset = \{\theta_0, \beta, \varphi, a+b, \mu\}$$

$$E[min(T_I/T_s)] = \int_0^\infty e^{-(\beta+\delta)y}dy \quad (30)$$

expected rate of the susceptible becoming infected $= \lambda_{n-1}P_{n-1} + \mu_{n+1}P_{n+1}$

The susceptible class remaining susceptible is the mean length of time the active cases exist given that the individuals remains susceptible.

$(expected\ rate\ of\ removed\ from\ infected) = (\lambda_n + \mu_n)P_n$ (31)

and infective class in a steady state are the individuals entering the infected class times the rate of infection times the duration of infectiveness, that is,

$\lambda_{n-1}P_{n-1} + \mu_{n+1}P_{n+1} = (\lambda_n + \mu_n)P_n$ (32)

When n=0, we have $\lambda_0 P_0 = \mu_1 P_1,\ i.e$

$P_1 = \left(\frac{\lambda_0}{\mu_1}\right) P_0$

For n=1, $\lambda_0 P_0 + \mu_2 P_2 = (\lambda_1 + \mu_1)P_1$, substituting for P_1, we obtain

$P_2 = \left(\frac{\lambda_1 \lambda_0}{\mu_2 \mu_1}\right) P_0$,

continuing in this order, we have for

$P_n = \left(\frac{\lambda_{n-1}\lambda_{n-2}\cdots\lambda_0}{\mu_n \mu_{n-1}\cdots\mu_0}\right) P_0$

where

$\sum_{n=0}^{\infty} P_n = 1$

3.3 EXAMPLE

Suppose the susceptible population involves 3kinds of exposure index coming into a locality. The first kind appearing in a place of at least 1 to 3individuals being in close proximity such that one individual has a direct contact with the index. The second kind deposited droplets where 4 to 6 individuals have access with 2 positive contacts while the third index exposes more than 6 individuals with 3 positive contacts. If in one hour, 10 individuals have been to each of these 3 separate locations and probably 12 persons from the three sets exposed. Then the steady state probability for the various exposed categories(3 contact group) can be obtained thus;

$$\lambda_n = \lambda = 10 \Longrightarrow \mu_n = \left\{ \begin{array}{c} \frac{60}{12} = 5\ persons\ per\ hour, for\ atleast\ 0\ to 3\ positive\ contacts \\ 2 \times 5 = 10\ persons\ per\ hour, for\ 4\ to\ 6 persons\ having\ contacts \\ 3 \times 5 = 15 persons\ per\ hour, for\ 7\ to 9 \end{array} \right\}$$

Moreover,

$$P_1 = \frac{10}{5}P_0 = 2P_0,\ P_2 = \left(\frac{10}{5}\right)^2 P_0 = 4P_0, \cdots P_6 = \left(\frac{10}{5}\right)^3 \left(\frac{10}{10}\right)^3 P_0 = 8P_0,$$

$$P_{n\geq 7} = \left(\frac{10}{5}\right)^3 \left(\frac{10}{10}\right)^3 \left(\frac{10}{15}\right)^{n-6} P_0 = 8\left(\frac{2}{3}\right)^{n-6} P_2 \quad (33)$$

4 DATA REPRESENTATION AND ANALYSIS

Using Nigeria Centre for Disease Control(NCDC) data for June 1, 2020, as reported night of 31st May, 2020. We classify the report into the six geographical zones of the country and take a closer look at the

total confirmed cases. Where the 36states of the federation and the geopolitical zones have been abbreviated as

Abia(ABIA), Anambra(ANB), Ebonyi(EBY), Enugu(ENU), Imo(IMO),Ekiti(EKT), Lagos(LAG), Ondo(OND), Ogun(OGN), Osun(OSN), Oyo(OYO),Edo(EDO), Delta(DEL), Rivers(RIV), Bayelsa(BAY), Akwa Ibom(A/IB), Cross River(C/R), Borno(BOR), Bauchi(BAU), Gombe(GOM), Yobe(YOB), Adamawa(ADAM), Taraba(TARA),Kano(KAN),Katsina(KATS), Kaduna(KAD), Jigawa(JIGA), Sokoto(SOK), Zamfara(ZAM), Kebbi(KEBB), Niger(NIGR), Federal Capital Territory(FCT), Nasarawa(NAS), Benue(BNU), Kwara(KWA), Kogo(KOG), Platue(PLT) for the 36states and FCT and Southwest(SW), Southeast(SE), South south(SS), Northeast(NE),Northwest(NW), North central(NC) for geopolitical zones.

SW	CUM	SE	CUM	NC	CUM	SS	CUM	NW	CUM	NE	CUM
EKT	20	EBY	40	NIGR	33	EDO	325	KAN	986	BOR	288
LAG	5135	IMO	39	FCT	674	RIV	239	KATS	371	BAU	240
OGN	280	ENU	18	NAS	80	DEL	88	KAD	288	GOM	161
OND	28	ABIA	15	BNU	9	A/Ib	45	JIGA	270	YOB	52
OSN	45	ANB	11	KWA	111	BAY	21	SOK	116	ADAM	42
OYO	302			KOG	2	C/R	0	ZAMF	76	TARA	18
				PLT	105			KEBB	33		
Total	5810		123		1014		718		2064		801

Figure 2: infective population by zones for the country as at end 31/5/2020

Below is the chart representing covid-19 active cases in the six geopolitical zones. The different colours in each bar of the zones represent the cases of the component states.

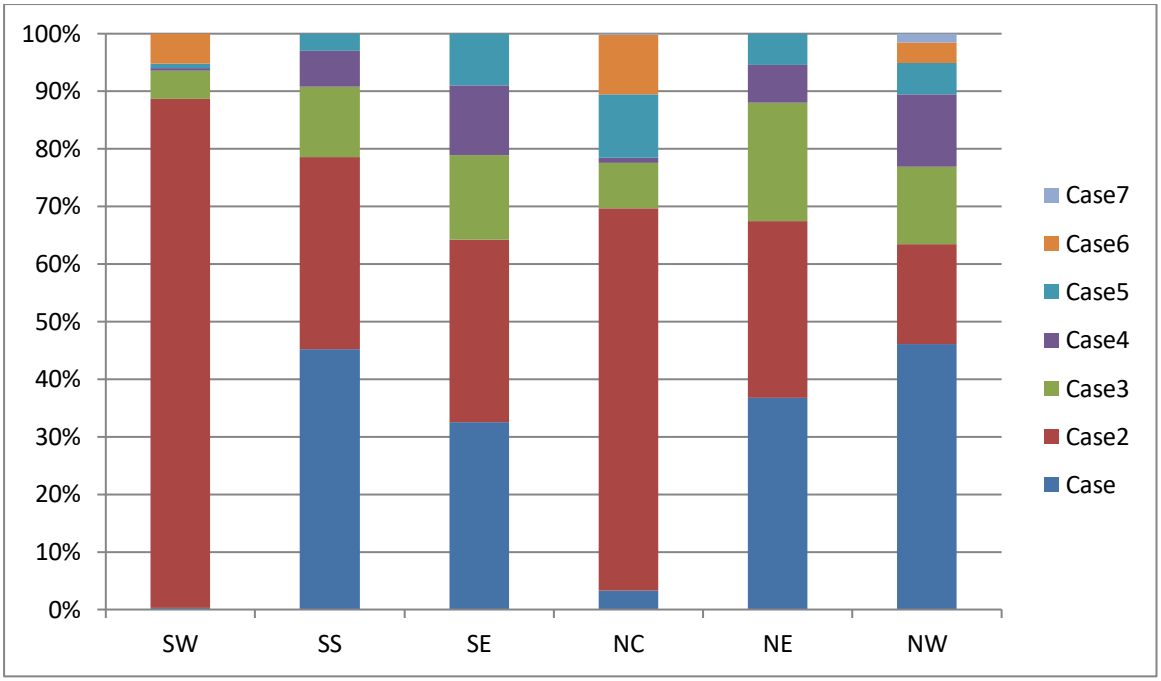

Figure3: A chart of active cases in the six geographical zones

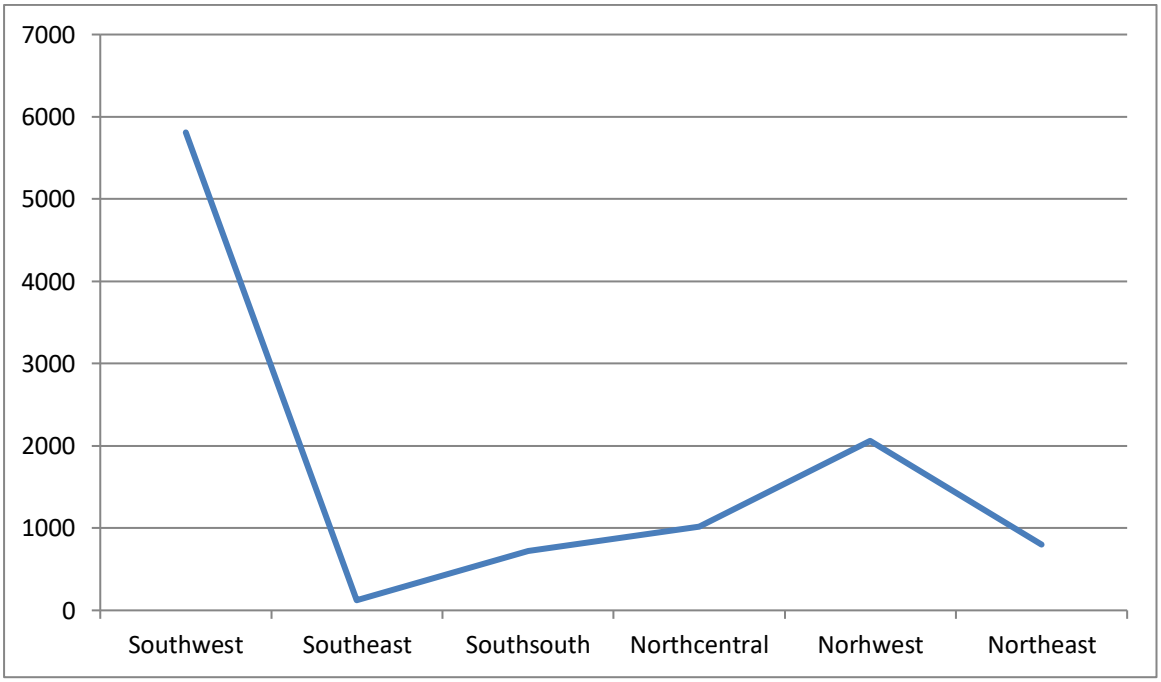

Figure4: Graph of the zones as at 31st May, 2020.

Cumulative confirmed cases so far is 10578 with daily new case for the country as 416. Total removed is 3421 with 3122persons fully recovered and 299 individuals dead. Demographic data revealed that out of

the 10578 confirmed cases, 7133 were males and 3445 females which is 67% and 33% respectively. From this report also, the most susceptible to the virus are those between the age range of 31-40 having about 24% confirmed cases . This is the most active population group most of whom could not stay locked down for long. By June 30 according to NCDC data, the total confirmed cases had risen to 25,694 with 590 deaths. This is more than double the number at the beginning of the month.

SW	CUM	SE	CUM	NC	CUM	SS	CUM	NW	CUM	NE	CUM
EKT	141	EBY	796	NIGR	223	EDO	2300	kAN	1597	BOR	613
LAG	15186	IMO	469	FCT	3933	RIV	1806	KATS	745	BAU	560
OGN	1397	ENU	821	NAS	239	DEL	1510	KAD	1457	GOM	607
OND	1192	ABIA	551	BNU	346	A/Ib	221	JIGA	322	YOB	67
OSN	553	ANB	135	KWA	753	BAY	339	SOK	154	ADAM	164
OYO	2768			KOG	5	C/R	45	ZAM	77	TARA	54
				PLT	105			KEBB	33		

Figure 5: infective population for the 36states and FCT as at the end 31/7/2020.

As at 1st September, 2020, the total confirmed cases are now 54,247 with 1,023 deaths and 42,010 persons discharged. From the total confirmed cases, 34,522 were male and 19,725 female(36%). Next, we present a graph of the cumulative infective and removed class from May 31, June 30, July 31 and September 30.

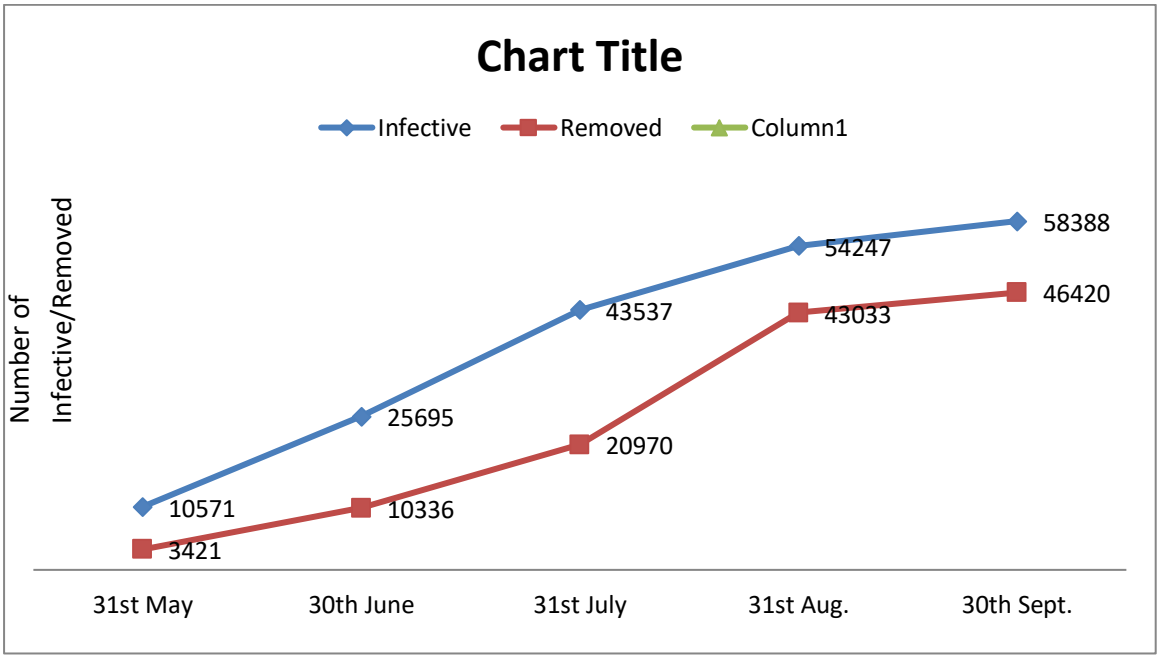

Figure 6:Graph of infective and remove classes from May to September.

From Figure 6, the rate of removal to infection for the 5months considered are;
0.32, 0.40, 0.48, 0.79, 0.80. These values are all less than one for each month, although on the increase. This is a positive sign than more persons will recover.

4.1 The range of possibilities for characterizing the data

From the ongoing report, the rate of transmission/infection is 0.11 per exposed population. Consequently, from the records of NCDC as at the end of February 2021, 1544008 individuals have been tested. From this number, 158042 persons were confirmed positive and at the time of compiling this report, 137025 individuals have recovered while 19063 cases are still active. However, 1,954 persons died due to this disease(February, 2021).

A projection can be made into the future from the graphs displayed in the Figures above. The disease will not be exterminated immediately. Transmission rate of 0.1 on the average have been observed. With this value, covid-19 cannot easily be extinct from the population. The surge in the number of cases till date is still on the increase as some states are experiencing second wave of the epidemic. A change in lifestyle that involves adherence and strict compliance to health protocol. We present some of these health protocol as stipulated by World Health Organization (WHO)

4.2 Health Protocol for Covid-19

Some health tips from WHO

i) Maintain physical and social distances from other people
ii) Protect yourself and others by wearing of face mask
iii) Avoid large gatherings make do with small public gathering
iv) Myth Busters: believe that covid-19 is real
v) Engage in regular hand washing with soap and running water. Clean your surroundings and disinfect places that are regularly touched.
vi) Getting vaccinated. These are but a few.

5. CONCLUSION

Covid-19 is the deadliest communicable disease the world has seen so far. It has touched lives negatively in different magnitudes across the geopolitical zones. In this work, a simulation model has been dealt with. Different approaches have been used in characterizing the likely situation resulting in infection of one or more individuals in a completely susceptible population. Epidemic prediction is enhanced from these estimates. Selected updates of the covid-19 records have been used to identify the pattern and trend of the disease . The focus of this work is on adopting some mathematical processes for analyzing the rates and pattern of covid-19 infection as discussed in section 3 and then the presentation of the data in tables, charts and graphs as it affects the 6geopolitical zones of the country using data randomly collected from the daily report of NCDC, The results clearly show an upsurge in covid-19 cases in southwest and North central. The cases also show that there is need to extend the partial lockdown of certain areas of the country. The study has also suggested ways of preventing human to human contacts.

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