COVID-19 TRANSMISSION AND STOCHASTIC MODELING – NIGERIA SITUATION REPORT

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ABSTRACT

This work is a product of efforts at finding statistical solutions to the menace of Covid-19 with many concerns for the random influence often disturbing many mathematical models. It aimed at studying the transmission of the disease and formulating a stochastic model with random perturbations for the pandemic, the model's basic reproduction number, the parameter sensitivity indices and making recommendations to control the Covid-19 based on the research findings. The disease infection flow transmission diagram was constructed identifying nine (9) population compartments. Set of non-linear differential stochastic equations (SDE) were derived from the deterministic differential equations (DDE) through the incorporation of white noise using parameters of perturbation. The model validity was confirmed through the establishment of the disease-free equilibrium point, endemic equilibrium point, existence of endemic global stability and disease-free global solution. The analytical study of the model was performed using R-programming language and MAPLE (version 18). The Stochastic basic reproduction number was estimated as R_o^S = 1.3202754. The parameters Υ (rate of symptomatic being transferred to isolation), ρ (proportion of tested exposed becomes infected), k (rate of transition of asymptomatic infected to isolation), and v (proportion that did not transit into asymptomatic) contributed to the stochastic model basic reproduction number with their respective sensitivity indices -0.4260 (42.60%); 0.0560 (5.60%); -0.0469 (4.69%); and - 0.00099 (0.99%). The rate of symptomatic infected population being transferred into isolation (Υ) has been identified as the most significant with percentage effect of 42.60%. This simply suggest that to manage the Covid-19 virus infection in Nigeria, transition of both asymptomatic and symptomatic to the isolation for treatment must be adequately handled.

1. INTRODUCTION

This work is a significant non-pharmaceutical research approach solution to the challenges of Covid-19 epidemic. It aimed at studying the transmission of the disease and formulating a stochastic model with random perturbations for the pandemic. Analyzing the behavior of infectious disease transmission dynamics in human and animals can be better understood using mathematical models (Tesfaye et al., 2021). The Covid-19 outbreak was declared a public health emergency of international concern on 30th January 2020 and a pandemic on March 11 same year by World Health Organization. Since the beginning of the ongoing global COVID-19 pandemic, there have been continuing many modeling efforts to study its transmission, control and find lasting solutions to address the generated public health nuisance it has created. Modeling is one of the most utilized mathematical strategies to mitigate effect of disease transmission in epidemiology study, and it has been found to be of significant application in epidemic studies like we have in covid-19 infection. Most of the statistical models used in describing spread of epidemic diseases employ traditional compartments like susceptible-exposed-infected-recovery (SEIR) structure as exposited in many research literatures of disease modeling. All these models are deterministic and do not consider uncertainty and some variations in the parameters as is obvious in the case of a growing epidemic. It has been shown that uncertainty is certain in the disease transmission rate of Covid-19. Consequent upon this realization, stochastic model has been proposed for Covid-19 epidemic transmission evaluation. Many of the modeling research works on Covid-19 studies have focused more on deterministic mathematical models, having fewer works to reference on the spatial stochastic simulations. Costa et al. (2021) posits that statistical modeling can provide useful insights concerning transmission patterns and detection of parameters to mitigate disease in the population.

With the growing efforts to combat the scourge of Covid-19 besides pharmaceutical medical approach, many research works have been undertaken through mathematical science modeling. Among such works are “A discrete stochastic model of the COVID-19 outbreak: Forecast and Control by Sha et al. (2020). Sha et al. (2020) employed the principle of SEIHR model and identified it appropriate for the study on the dynamic of this disease. The development of Covid-19 vaccines has since brought about a twist into the study of Covid-19 modeling generally. Hence, the formulated stochastic model can then be used to study the dynamics of Covid-19 distribution in Nigeria. Trottier and Philippe (2020) explained that stochastic models rely on among-individual chance variation in risks of exposure, disease, and other factors. They are used when chance fluctuations or known heterogeneities are important, as in small or isolated populations.

The solution of a stochastic model is a probability distribution for each of the random variables. Adak *et al*. (2021) in their study involving 228 days’ time series data of confirmed death cases of Spain for the time when the Covid-19 positive cases were only 6 with zero death. The study espoused four stage transmission flow of susceptible (S_t); latent (L_t); infectious (I_t) and recovered (R_t). The work concluded that the stochastic model better captured the observed uncertainty or variance in illness transmissibility. The comparism of the stochastic and deterministic models shown that the number of recovered cases increases in the stochastic cases compared to the deterministic cases (Alshammari *et al.,*2022)

2.0 MATERIALS AND METHODS

The model was developed with continuous vaccination and assumed presence of symptomatic and asymptomatic individuals in the population. The population is classified into nine (9) compartments by their Covid-19 health status of infection and assumptions around the rate of transforming from one status to another. Therefore,

Therefore,

$$N(t)=S_N(t)+S_V(t)+E(t)+T_e(t)+Q(t)+I_A(t)+I_S(t)+I_L(t)+R(t) \qquad 1$$

Where, (S_N) is non-vaccinated susceptible, (S_V) vaccinated susceptible, (E) exposed, (T_e) Covid19 test, (Q)quarantine, (I_A) asymptomatic, (I_S) symptomatic, (I_L) isolation and (R) recovered.

According to Leung (2019), every model is a simplification of reality and is never free of assumptions, A number of assumptions have been defined to guide the mathematical equations of this model. These are, the population is homogenous and constant in size *N*, *c*ontainment rate μ is introduced into the susceptible population, the vaccine is imperfect, it can fail (it helps to boost immunity to fight the SARS-COV-2 and the vaccinated individuals has a probability to get infected at rate β_v), SARS – COV - 2 can stay in the host body for at least 14 days (S. Pappas, 2020). Tesfay and Satana (2021) cited CDC claim that fever, cough or sneezing and shortness of breath are major symptoms of Covid-19 after which infection occurred 14 days. The Covid-19 test serves to detect the state of the exposed population and separates them into asymptomatic, symptomatic and undetected categories. The infected/infectious population with stimulated immunity fights off the virus and progresses to the recovered class R, those with symptoms and tested positive without symptoms get isolated for treatment. The disease is assumed fatal with probability of death (Hence, any death by person infected is assumed to have died from the disease). Quarantine is different from Isolation state, a state for separation of asymptomatic exposed individual from the population to manifest the disease before taken to isolation or be declared free of virus for susceptible compartment (Aromolaran et al.,2024). While Isolation is a government created center for treatment of asymptomatic and symptomatic infected individuals.

The Model Flow Diagram

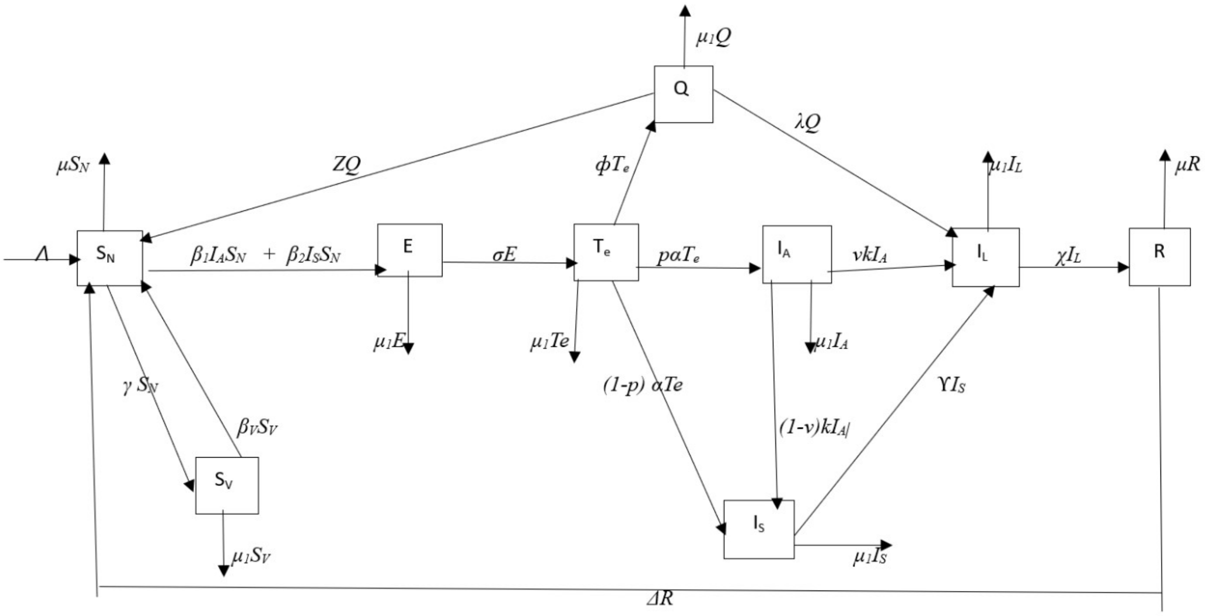

Figure 1: Proposed Schematic Model of Covid-19 Transmission by Nine Compartment Sub-Population Interactions

From the transmission flow diagram in figure 1 above, the transmission of the in-flow and out-flow rates of each compartment and parameters are as shown in the DDE (deterministic differential equations):

The proposed Covid-19 model

$$C_1 = \gamma + \mu, C_2 = \beta_v + \mu, C_3 = \sigma + \mu_1, C_4 = p\alpha + (1-p)\alpha + \Phi + \mu_1, C_5 = Z + \lambda + \mu_1$$
$$C_6 = k + \mu_1, C_7 = \Upsilon + \mu_1, C_8 = \chi + \mu_1, C_9 = \square + \mu.$$

$$\left.\begin{aligned}
\frac{dS_N}{dt} &= \Lambda - \beta_1 S_N I_A - \beta_2 S_N I_S + \beta_v S_v + \mathrm{V} R + ZQ - C_1 S_N \\
\frac{dS_V}{dt} &= \gamma S_N - C_2 S_v, \\
\frac{dE}{dt} &= \beta_1 S_N I_A + \beta_2 S_N I_S - C_3 E, \\
\frac{dT_e}{dt} &= \sigma E - C_4 T_e \\
\frac{dQ}{dt} &= \Phi T_e - C_5 Q, \\
\frac{dI_A}{dt} &= p\alpha T_e - C_6 I_A, \\
\frac{dI_S}{dt} &= (1-p)\alpha T_e + (1-v)kI_A - C_7 I_S, \\
\frac{dI_L}{dt} &= \lambda Q + vkI_A + \Upsilon I_S - C_8 I_L, \\
\frac{dR}{dt} &= \chi I_L - C_9 R.
\end{aligned}\right\}$$

Incorporating the randomness of stochastic factors βi and the Brownian motion $\beta_i(t)$ into the systems of deterministic model of equation 2 becomes stochastic differential equation (SDE) equation 3.

$$\left.\begin{aligned}
dS_N(t) &= \{\Lambda - \beta_1 S_N(t) I_A(t) - \beta_2 S_N(t) I_S(t) + \beta v S_V(t) + \Delta R(t) + ZQ(t) - C_1 S_N(t)\}dt + \\
&\qquad + \phi_1 S_H(t) dB_1(t), \\
dS_V(t) &= \{\gamma S_N(t) - S_V(t) C_2\}\, dt + \phi_2 S_V(t) dB_2(t), \\
dE(t) &= \{\beta_1 I_A(t) S_N(t) + \beta_2 I_S(t) S_N(t) - E(t) C_3\}dt + \phi_3 E(t) dB_3(t), \\
dTe(t) &= \{\sigma E(t) - Te(t) C_4\}dt + \phi_4 Te(t) dB_4(t) \\
dQ(t) &= \{\phi T_e(t) - Q(t) C_5\}dt + \phi_5 Q(t) dB_5(t), \\
dI_A(t) &= \{p\alpha Te(t) - I_A(t) C_6\}dt + \phi_6 I_A(t) dB_6(t), \\
dI_S(t) &= \{(1-p)\alpha Te(t) + (1-v)kI_A(t) - I_S(t) C_7\}dt + \phi_7 I_S(t) dB_7(t), \\
dI_L(t) &= \{\lambda Q(t) + kI_A(t) + \Upsilon I_S(t) - I_L(t) C_8\}dt + \phi_8 I_L(t) dB_8(t), \\
dR(t) &= \{\chi I_L(t) - R(t) C_9\}dt + \phi_9 R(t) dB_9(t),
\end{aligned}\right\} \quad 3$$

where $\phi_1, \phi_2, \phi_3, \phi_4, \phi_5, \phi_6, \phi_7, \phi_8, \phi_9 \geq 0$ (intensities of Brownian motions)
and $B_1, B_2, B_3, B_4, B_5, B_6, B_7, B_8, B_9$ are independent standard Brownian motions.

2.1 Mathematical Theories of Compliance

Analyses and estimations of the formulated model are expected to begin with assertion of certain mathematical theorems to substantiate the model 3 validity. Theorems of significant points point of disease-free equilibrium, point of endemic equilibrium, and global stability of the disease-free equilibrium.

Point of Disease-Free Equilibrium

The infection disappears at disease free-equilibrium point.

If E_o represents disease-free equilibrium $(i.e.\ E = T_e = Q = I_A = I_S = I_L = 0)$.

$$\frac{dS_N}{dt} = \frac{dS_v}{dt} = \frac{dE}{dt} = \frac{dT_e}{dt} = \frac{dQ}{dt} = \frac{dI_A}{dt} = \frac{dI_S}{dt} = \frac{dI_L}{dt} = \frac{dR}{dt} = 0 \qquad 4$$

Hence, from (3) above, we have

$$\Lambda + \beta_v S_v - C_1 S_N = 0. \tag{5}$$

$$\gamma S_N - C_2 S_v = 0. \tag{6}$$

From (6),

$$S_v = \frac{\gamma S_N}{C_2}. \tag{7}$$

Substituting (7) into (5), we have

$$S_N = \frac{\Lambda C_2}{C_1 C_2 - \gamma \beta_v} \tag{8}$$

Putting (8) into (7), we have

$$S_v = \frac{\gamma \Lambda}{C_1 C_2 - \gamma \beta_v} \tag{9}$$

Therefore, the disease-free equilibrium E_0 is given by

$$E_0 = (S_N, S_v, E, T_e, Q, I_A, I_S, I_L, R)$$

$$E_0 = \left[\frac{\Lambda C_2}{(C_1 C_2 - \gamma \beta_V)}, \frac{\gamma \Lambda}{(C_1 C_2 - \gamma \beta_V)}, 0, 0, 0, 0, 0, 0, 0 \right] \tag{10}$$

Point of Endemic Equilibrium

The point where the disease is prevalent is known as the endemic equilibrium point.

(i.e. $E \nvDash Te \nvDash Q \nvDash IA \nvDash IS \nvDash IL \nvDash 0$).

Letting the rates of change of the model (3) to zero gives

$$\Lambda - \beta_1 S_N I_A - \beta_2 S_N I_S + \beta_v S_v + \square R + \sigma Q - C_1 S_N = 0 \tag{11}$$

$$\gamma S_N - C_2 S_V = 0, \tag{12}$$

$$\beta_1 S_N I_A + \beta_2 S_N I_S - C_3 E = 0 \tag{13}$$

$$\sigma E - C_4 T_e = 0, \tag{14}$$

$$\Phi T_e - C_5 Q = 0, \tag{15}$$

$$p \alpha T_e - C_6 I_A = 0, \tag{16}$$

$$(1-p)\alpha T_e + (1-v)kI_A - C_7 I_S = 0, \tag{17}$$

$$\lambda Q + vkI_A + \Upsilon I_S - C_8 I_L = 0 \tag{18}$$

$$\chi I_L - C_9 R = 0 \tag{19}$$

To solve the equations 11 – 19. when $R_0 > 1$, see Aromolaran et al., 2024.

Expectedly from the solution, the COVID-19 model (3.0) has a positive and unique endemic equilibrium point.

Global Stability of the Disease-free Equilibrium

The overall stability of the disease-free equilibrium is being examined to find out whether the eradication of COVID-19 depends on the beginning sizes of the sub-populations when *R*o < 1. Hence, linear Lyapunov function is used to prove the global stability of the disease-free equilibrium.

Theorem Asymptotically stable on a global scale is t*he disease-free equilibrium* (10) *of the model* (2). *Except when Ro is greater than 1 (R*$_0$ > 1).

Proof. By linear Lyapunov function defined by

$$L = AE + BT_e + CQ + DI_A + UI_S + WI_L \tag{20}$$

Differentiating (20), leads to

$$L' = AE' + BT_e' + CQ' + DI_A' + UI_S' + WI_L' \tag{21}$$

Substituting the right-hand side of equation (2) into (21) gives

$$\begin{aligned} L' &= A\left[\beta_1 S_N I_S - C_3 E\right] + B\left[\sigma E - \left(p\alpha + (1-p)\alpha + \Phi + \mu_1\right)T_e\right] + C\left[\Phi T_e - C_5 Q\right] + D\left[p\alpha T_e - C_6 I_A\right] \\ &+ U\left[(1-p)\alpha T_e + (1-v)kI_A - C_7 I_S\right] + W\left[\lambda Q + vkI_A + \Upsilon I_S - C_8 I_L\right] \end{aligned} \tag{22}$$

From 22, we try to find the coefficients.

$$\left.\begin{aligned} &-AC_3 + B\sigma = 0 \\ &-BC_4 + C\Phi + Dp\alpha + U(1-p)\alpha = 0 \\ &-CC_5 + W\lambda = 0 \\ &A\beta_1 S_N - DC_6 + U(1-v)k + Wvk = 0 \\ &A\beta_2 S_N - UC_7 + W\Upsilon = 0 \end{aligned}\right\} \tag{23}$$

Then, solving 23, the coefficients are obtained as follows:

$$\left.\begin{aligned}
&U=1\\
&A=\frac{\sigma([(1-p)C_6\Upsilon+[(1-v)\Upsilon+C_7v]kp]\alpha C_5+C_6C_7\Phi\lambda)}{(S_Np\sigma\alpha(kv\beta_2-\Upsilon\beta_1)+C_6\Upsilon C_4C_3)C_5+C_6\Phi\lambda\sigma\beta_2S_N}\\
&B=\frac{C_3([(1-p)C_6\Upsilon+[(1-v)\Upsilon+C_7v]kp]\alpha C_5+C_6C_7\Phi\lambda)}{(S_Np\sigma\alpha(kv\beta_2-\Upsilon\beta_1)+C_6\Upsilon C_4C_3)C_5+C_6\Phi\lambda\sigma\beta_2S_N}\\
&C=\frac{\lambda(C_4C_5C_6C_7-\alpha\sigma S_N[C_6[(1-p)+(1-v)kp]\beta_2+C_7\beta_1p]])}{S_N\sigma(C_5p\alpha(kv\beta_2-\Upsilon\beta_1)+C_6\beta_2\Phi\lambda)+C_6\Upsilon C_5C_4C_3}\\
&D=\frac{C_5[\alpha\sigma S_N(1-p)(\Upsilon\beta_1-kv\beta_2)+C_4C_3k((1-v)\Upsilon+C_7v)]+(\beta_2k(1-v)+C_7\beta_1)\sigma\lambda\Phi S_N}{(S_Np\sigma\alpha(kv\beta_2-\Upsilon\beta_1)+C_6\Upsilon C_4C_3)C_5+C_6\Phi\lambda\sigma\beta_2S_N}\\
&W=\frac{C_5(C_4C_5C_6C_7-\alpha\sigma S_N[C_6[(1-p)+(1-v)kp]\beta_2+C_7\beta_1p]])}{S_N\sigma(C_5p\alpha(kv\beta_2-\Upsilon\beta_1)+C_6\beta_2\Phi\lambda)+C_6\Upsilon C_5C_4C_3}
\end{aligned}\right\rbrace 24$$

Substituting 24 into 22 leads to

$$\left.\begin{aligned}
L'=&\left(\frac{\sigma([(1-p)C_6\Upsilon+[(1-v)\Upsilon+C_7v]kp]\alpha C_5+C_6C_7\Phi\lambda)}{(S_Np\sigma\alpha(kv\beta_2-\Upsilon\beta_1)+C_6\Upsilon C_4C_3)C_5+C_6\Phi\lambda\sigma\beta_2S_N}\right)[\beta_1S_NI_A+\beta_2S_NI_S-C_3E]\\
&+\left(\frac{C_3([(1-p)C_6\Upsilon+[(1-v)\Upsilon+C_7v]kp]\alpha C_5+C_6C_7\Phi\lambda)}{(S_Np\sigma\alpha(kv\beta_2-\Upsilon\beta_1)+C_6\Upsilon C_4C_3)C_5+C_6\Phi\lambda\sigma\beta_2S_N}\right)[\sigma E-(p\alpha+(1-p)\alpha+\Phi+\mu_1)T_e]\\
&+\left(\frac{\lambda(C_3C_4C_6C_7-\alpha\sigma S_N[[C_6(1-p)+(1-v)kp]\beta_2+C_7\beta_1p]])}{S_N\sigma(C_5p\alpha(kv\beta_2-\Upsilon\beta_1)+C_6\beta_2\Phi\lambda)+C_6\Upsilon C_5C_4C_3}\right)[\Phi T_e-C_5Q]+\\
&\left(\frac{C_5[\alpha\sigma S_N(1-p)(\Upsilon\beta_1-kv\beta_2)+C_4C_3k((1-v)\Upsilon+C_7v)+(\beta_2k(1-v)+C_7\beta_1)\sigma\lambda\Phi S_N]}{(S_Np\sigma\alpha(kv\beta_2-\Upsilon\beta_1)+C_6\Upsilon C_4C_3)C_5+C_6\Phi\lambda\sigma\beta_2S_N}\right)\\
&\times[p\alpha T_e-C_6I_A]+1\times[(1-p)\alpha T_e+(1-v)kI_A-C_7I_S]\\
&\left(\frac{C_5(C_3C_4C_6C_7-\alpha\sigma S_N[[C_6(1-p)+(1-v)kp]\beta_2+C_7\beta_1p]])}{S_N\sigma(C_5p\sigma(kv\beta_2-\Upsilon\beta_1)+C_6\beta_2\Phi\lambda)+C_6\Upsilon C_5C_4C_3}\right)[\lambda Q+vkI_A+\Upsilon I_S-C_8I_L]
\end{aligned}\right\rbrace 25$$

Simplifying (25) further gives

$$\left.L'=\frac{[[C_6\beta_2(1-p)+(1-v)kp\beta_2+C_7\beta_1p]\sigma\alpha S_N-C_3C_4C_6C_7]C_5C_8I_L}{\sigma S_N(C_5p(kv\beta_2-\tau\beta_1)\alpha+C_6\beta_2\Phi\lambda)+C_6\tau C_5C_4C_3}\right\rbrace \qquad 26$$

But at disease free equilibrium. Then, equation (26) becomes

$$L' = \left.\frac{\left[R_0 C_3 C_4 C_6 C_7 - C_3 C_4 C_6 C_7\right]\left(C_1 C_2 - \gamma\beta_v\right) C_5 C_8 I_L}{\sigma\Lambda C_2\left(C_5 p\left(kv\beta_2 - \tau\beta_1\right)\alpha + C_6\beta_2\Phi\lambda\right) + C_6\tau C_5 C_4 C_3\left(C_1 C_2 - \gamma\beta_v\right)'}\right\} \qquad 27$$

$$L' = \left.\frac{\left[R_0 - 1\right]\left(C_1 C_2 - \gamma\beta_v\right) C_3 C_4 C_5 C_6 C_7 C_8 I_L}{\sigma\Lambda C_2\left(C_5 p\left(kv\beta_2 - \tau\beta_1\right)\alpha + C_6\beta_2\Phi\lambda\right) + C_6\tau C_5 C_4 C_3\left(C_1 C_2 - \gamma\beta_v\right)'}\right\} \qquad 28$$

Therefore, $L' < 0$ if $R_0 < 1$ and $L' = 0$ if $I_L = 0$. Thus, L is a Lyapunov function in Ω. Also, the largest invariant set in $(S_N, S_V, E, T_e, Q, I_A, I_S, I_L, R) \in \Omega$: $L' = 0$ is the singleton E_0. According to LaSalle's Invariance Principle (LaSalle, 1976), every solution with initial values in Ω moves to E_0 as t tends to infinity.

The implication of this theorem is that the elimination of COVID-19 is possible regardless of the initial sizes of the subpopulations of the model whenever the associated reproduction number is less than unity.

3.0 RESULTS

3.1 Model Parameter Estimation

Some of the model parameters were obtained from published works, while others were estimated. These estimates were then used to solve the set of non-linear differential equations 3 using R version 4.2 and Maple version 20.

Table 1: Initial values of Parameter Estimation from Proposed Model Analysis (unit: /day/week)

Symbols & Parameter Description		Value	Unit	Reference
Λ	Recruitment rate of the susceptible population	36400	per10^3 pp	Nigeria Birth Rate 2022
μ	Natural mortality rate	10.994	per10^3 pp	Nigeria Death Rate 2022
μ_1	Natural mortality rate plus Covid-19 death induced	1.124	1/day	Estimated
β_1	Prob. of transmission from asymptomatic infected	1.727E-7	1/day	Anggriani *et al* (2021)
β_2	Prob. of transmission from symptomatic infected	7.474E-8	1/day	Anggriani *et al* (2021)
Bv	Probability of vaccinated get back to susceptible	0.0005	1/day	Tesfaye &Satang (2021)
γ	Rate of vaccination	0.5000	1/day	Estimated
Z	Rate of transition from Quarantine to Susceptible	0.0680	1/day	O. J. Peters *et al* (2021)
σ	Rate at which Exposed population gets tested	0.7000	1/day	NCDC (ncdc.gov.ng)

ϕ	Transition of undetected Exposed to Quarantine	0.1818	1/day	Evensen *et al* (2020)
ρ	Proportion of tested Exposed becomes Infected	0.2000	1/day	Anggriani *et al* (2021)
A	Prob. of tested Exposed people becomes Infected	0.0714	1/day	Estimated
Λ	Rate of transition from Quarantine to Isolation	0.1430	1/day	Estimated
K	Rate of transition of asymptomatic infected to Isolation	0.1900	1/day	Belkhiria &Nascimento, Ohajunwa *et al* (2020)
Υ	Rate of symptomatic being transferred to Isolation	0.1900	1/day	Lyra et al (2020)
χ	Rate of Isolated individuals become Recovered	0.7310	1/day	Nino-Torres *et al* (2022)
Δ	Rate of Recovered individual transits to Susceptible	0.1500	1/day	Tilahun &Alemneh (2021)
V	Proportion that did not transit into symptomatic	0.9000	1/day	Assumed

4.1 Stochastic Basic Reproduction Number (R_0^S) of the model

Using the method for the epidemic models with random perturbations (RIOS – Gutierrez et al, 2021), the basic reproduction number R_0 is referred as;

$$R_0 = \int_0^{\infty} b(a)F(a)da$$

The $b\ (a)$ defines the average number of new infected individuals (in an assumed completely susceptible population) by an infected individual between $t = 0\ and\ t = a$.

While, $F\ (a)$ is probability that a new infected individual will infect others during the same time interval 0 and a. It is called survival function.

In this work, infectivity rate when the population is completely susceptible can be defined by

$$\hat{\beta}_{1a} = \frac{\beta_1}{N} + \frac{\Omega_1}{N} B_1(t)$$

If the first infected individual is asymptomatic or symptomatic, we have,

$$\hat{\beta}_{1b} = \frac{\beta_1}{N} + \frac{\Omega_2}{N} B_2(t)$$

When the infected individual infects a completely susceptible population with N individuals, the expected number of asymptomatic individuals who were infected S_y asymptomatic individual is obtainable by; $b_1(a) = N\hat{\beta}_{1a}\left(p\right)\left\{\beta_1 + \Omega_2 T_e(B_2(+\infty)), p\right\}$

The expected number of symptomatic individuals infected by a symptomatic individual is:

$$b_2(a) = N\hat{\beta}_{1a}\left(1-p\right) = \left\{\beta_1 + \Omega_2 T_e(B_2(+\infty))\right\}(1-p)$$

And the expected number of asymptomatic individuals infected by an asymptomatic individual and have not recovered from the illness. This is, turned symptomatic is.

$$b_3(a) = N\hat{\beta}_{1a}\left(\theta\right)p = \left\{\beta_1 + \Omega_2 T_e(B_1(+\infty))\right\}\theta p,$$

The expected number of symptomatic individuals that will be infected by the asymptomatic will be $b_4(a) = N\hat{\beta}_{1a}\left(1-p\right) = \left\{\beta_1 + \Omega_1 T_e(B_1(+\infty))\right\}\left(1-p\right),$

Let $T_e(B_1(+\infty) = \lim\limits_{i\to\infty} B_i(t) = 1, 2, \ldots$

Then, we have $\beta_1\left(a\right)+\beta_2\left(a\right)+\beta_3\left(a\right)+\beta_4\left(a\right)$, $\Rightarrow N\hat{\beta}_{1b}p + N\hat{\beta}_{1b}(1-p) + N\hat{\beta}_{1a}\theta p + N\hat{\beta}_{1a}\left(1-p\right)$

Hence, the number of infected individuals by an infectious individual for $a \Rightarrow +\infty$ is;

$$(\beta_1+\Omega_2 B_2(a))p+(\beta_1+\Omega_2 B_2(a))(1-p)+(\beta_1+\Omega_2 B_2(a))p\theta+(\beta_1+\Omega_2 B_1(a))(1-p)$$

And the survival function will be

$$F_1\left(a\right) = e^{\Upsilon a} \text{ and } F_2\left(a\right) = e^{\theta a} \text{ e}$$

For when;

1). A symptomatic infected by a symptomatic individual remain symptomatic on $\left[0,\ a\right]$.

2). An asymptomatic infected by a symptomatic individual remain asymptomatic on $\left[0,\ a\right]$.

3). An asymptomatic infected by an asymptomatic remains infectious on $\left[0,\ a\right]$.

4). A symptomatic infected by an asymptomatic remains symptomatic on $\left[0,\ a\right]$.

Then, the following set of equations will define the basic reproduction number $\left(R_0\right)$;

$$R_0^{\text{cov}} = \int_0^\infty b\left(a\right) f\left(a\right) da$$

Let v – proportion of asymptomatic that recovered and $\left(1 - v\right)$ – proportion of asymptomatic that become symptomatic.

$$R_0^{\text{cov}} = \int_0^\infty b(a)f(a)da = \int_0^\infty \beta_1(1-p)F_1(a)da + \int_0^\infty \beta_1 pF_2(a)da + \int_0^\infty \beta_1 p(1-V)F_1(a)da + \int_0^\infty \beta_1(1-p)F_1(a)da$$

Substituting $b\left(a\right)$, b_e, and $F\left(a\right)$ for $F_e\left(a\right)$ respectively. Hence, for the stochastic differential equation 3.13, this gives. $\int_0^\infty b(a)f(a)da = \int_0^\infty b_e(a)F_e(a)da$

We then have,

$$\int_0^\infty b_e(a)F_e(a)da = 2\left(\frac{\beta_1(1-p)}{\Upsilon}+\frac{\beta_1 p}{\theta}+\frac{\beta_1 p(1-v)}{\Upsilon}\right)+\int_0^\infty \Omega_2 B_2(a)\left((1-p)e^{-\Upsilon a}+pe^{-\theta a}\right)da$$

$$+\int_0^\infty \Omega_1\left(p(1-v)+(1-p)\right)B_1(a)e^{-\Upsilon a}da \sim \mathrm{N}\left(0,\frac{\Omega_1^2\left((I-v)^2(I-p)+p\right)^2}{2\Upsilon^3}\right)$$

Using integration by parts rule (Chung and Williams, 2014) we have that.

$$\lim_{l\to+\infty} B_2(l)\left(\theta pe^{-\Upsilon l}+\Upsilon pe^{-\theta l}\right)=B_2(0)\left((I-p)\theta+p\Upsilon\right)-l_1-l_2+l_3$$

Where; $l_1=\int_0^\infty \theta(I-p)\Upsilon B_2(a)e^{-\Upsilon a}da$

$$l_2=\int_0^\infty \Upsilon p\theta B_2(a)e^{-\theta a}da$$

$$l_3=\int_0^\infty (\theta(I-p)e^{-\Upsilon a}+\Upsilon pe^{-\theta a})dB_2(a)$$

Computing the $\lim_{l\to+\infty} B_2(l)\left(\theta(1-p)e^{-\Upsilon l}+\Upsilon pe^{-\theta l}\right)=0$ a.s. in addition $\beta_2(0)=0$ using Klebaner (2012), we have;

$$R_2=\int_0^\infty \Omega_2 B_2(a)\left((1-p)e^{-\Upsilon a}+pe^{-\theta a}\right)da=\int_0^\infty \Omega_2\left(\theta(I-p)e^{-\Upsilon a}+\Upsilon pe^{-\theta a}\right)dB_2(a)\sim \mathrm{N}\left(0,\frac{\Omega_2^2p^2+2\Omega_2^2p(1-p)}{2\theta^3+(\Upsilon+\theta)\Upsilon\theta}\right)$$

Since it is assumed $\{B_1(t)\}_{t\geq 0}$ and $\{B_2(t)\}_{t\geq 0}$ are two Browman Independent motions.

Consequently,

$$R_0^{\mathrm{cov}}=\int_0^\infty b_e(a)F_e(a)da=R_0^{\mathrm{cov}}+R_2+R_1\sim \mathrm{N}\left(R_0^{\mathrm{cov}},\mathrm{Var}(R_1)+\mathrm{Var}(R_2)\right)$$

The above is the distribution of the basic reproduction number for the proposed stochastic model.

$$R[0]:=\mathrm{int}\left(\left(1-p\right)e^{-\Upsilon a}+pe^{-\theta a},a=0\ldots\infty\right)+\mathrm{int}\left(p\left(1-v\right)+\left(1+p\right)e^{-\Upsilon a},a=0..0.000000125\right)$$

$V := 0.0390$, $\Upsilon = 1.1020$, $\alpha = 0.07376$, and $k = 0.2100$

$$R[0] := int(\,(1-\rho)\cdot\exp(-Y\cdot a)+\rho\cdot\exp(-V\cdot a),\ a=0..1)+int(\rho\cdot(1-k)+(1+\rho)\cdot\exp(-Y\cdot a), a=0..1)$$

$$R_o^S = 1.653939264*\rho + 1.211967320$$

With $\rho = 0.0670$ $R_o^S = 1.32278$

Table 2: Final Parameter Estimates

Parameters	Estimates
Λ	3.644E+01
Υ	1.1020
β_v	1.791-02
Z	4.465E-01
β_1	7.884E-03
β_2	5.100E-04
γ	1.790E-01
σ	1.1150
μ	3.4662
P	6.68E-02
A	7.200E-02
Φ	5.250E-02
Λ	7.100E-01
μ_1	1.4300
k	0.2100
V	0.3000
X	3.900E-02
Δ	0.1460

Remark: Result from R – programming language was used to generate the Initial values for Maple to run the Solutions for the Model Differential Equations.

4.2 Simulation of Stochastic Basic Reproduction Number (R_o^S) and Model Parameters

The stochastic basic reproduction number (R_o^S) is 1.32278, being greater than 1 is an indication of continuing tendency of the infection to spread. By this, increasing the value of any of the parameters will consequentially increase the value of basic reproduction number (R_o^S).

A: Proportion of tested Exposed People become Infected (ρ) on R0
Ro = 1.3228, ρ = 0.0010, 0.0670, 1.0000

B: Rate of Infected Symptomatic being transferred to Isolation
(ϒ) on Ro Ro = 1.3228, ϒ = 0.0010, 1.1020, 1.0000

C:Rate of asymptomatic Infected become infected symptomatic (k)
on Ro. Ro = 1.3228, k = 0.0010, 0.2100, 1.0000

D: Proportion of asymptomatic that became symptomatic (V)
on Ro. Ro = 1.3228, V = 0.0010, 0.3000, 1.0000

Figure 2: Plots of Parameter variation effect on the SDE Basic Reproduction Number

Figure 2: (A, B, C & D) shows the effect of the parameters (ρ, ϒ, k and v) representing the proportion of tested exposed people becomes infected, rate of infected symptomatic being transferred to isolation, rate of asymptomatic infected become infected symptomatic and the proportion of asymptomatic become symptomatic.

4.3 Sensitivity Analysis of Basic Reproduction Number (Ro) for the Stochastic Model

This determines the parameters of high impact to be targeted by intervention strategies and that makes possible effect of relative change in a model (Rodrigues *et al*. 2013). Sensitivity analysis defines the parameters that influence the model's quantities of interest the most. The normalized forward sensitivity index of basic reproduction number Ro that depended differentiable on parameter p is given by (Rodrigues et al. 2013).

$$Y_p^{Ro} = \frac{\partial R_o}{\partial p} \times \frac{p}{R_o}$$

Table 3: Sensitivity Indices for Basic Reproduction Number (Stochastic model)

Parameter	Sensitivity value	% Effect on R_0
Υ	-0.4260	42.60%
ρ	0.0560	5.60%
k	-0.0469	4.69%
v	-0.00099	0.99%

The Table 3 above shows the stochastic model basic reproduction number parameters sensitivity indices which are Υ = -0.4260 (42.60%), ρ = 0.0560 (5.60%), k = -0.0469 (4.69%) and v = - 0.00099 (0.99%). From the data, the "Υ “is the most sensitive among the parameters of the stochastic model that determines its basic reproduction number. While other parameters level of sensitivity follows in the arranged order ρ , k and v. These four parameters that influence the stochastic basic reproduction number Ro are Υ (rate of infected symptomatic being transferred to isolation), ρ (proportion of tested exposed people becomes infected), k (rate of symptomatic infected become infected symptomatic) and v (the proportion of asymptomatic become symptomatic). The rate of symptomatic infected population being transferred into isolation (Υ) has been identified as the most significant with percentage effect of 42.60%. This simply suggest that to manage the Covid-19 virus in Nigeria infection, transition of both asymptomatic and symptomatic to the isolation for treatment must be adequately handled. Hence, the need for effective quarantine and isolation centres to care for the disease population.

4 DISCUSSION

This work has successfully formulated a stochastic model that accounts for the dynamic randomness of Covid-19 reported cases in Nigeria with basic reproduction number R_o^S = 1.32278. The dynamic properties of the root of the system before disease occurrence and checking of at least one repeating solution greater than zero of the formulated stochastic Covid-19 epidemic model with time delay. The systems of equations 2 and 3 derived were found to offer valid results for the dynamical behaviours of the stationary distribution are achieved, with the disease-free equilibrium lies at point $\left[\frac{\Lambda C_2}{(C_1C_2-\gamma\beta_V)},\frac{\gamma\Lambda}{(C_1C_2-\gamma\beta_V)},0,0,0,0,0,0,0\right]$ has been established.

The global stability of the endemic equilibrium and the disease equilibrium were found to exist. In line with Lim et al (2020), when R_0 is above 1, it is possible that the disease will die out since the transmission of an infectious disease is a branching process with a negative binomial probability distribution. Hence, in a situation where the basic reproduction number $R_0 > 1$, the disease can be eradicated if the population number is under the critical community size.

The rate of the tested exposed becoming infected through early movement restriction should be instituted and creation of both quarantine and isolation centres to manage the asymptomatic and the symptomatic infected populations.

The findings of Covid-19 test being an important stage of the model is quite in agreement with Alshammari et al. (2022) which reported that increasing the test of people and identifications of the symptomatic and asymptomatic individuals by quarantine and educating them about the disease best minimize the future infected cases in the population.

5. CONCLUSION

From the findings these conclusions were drawn.

1. The stochastic basic reproduction number (R_o^S) is 1.32278, being greater than 1 is an indication of continuing tendency of the infection to spread. By this, increasing the value of any of the parameters exposed tested get infected (ρ), symptomatic that did not transit to symptomatic (v), the rates of asymptomatic to isolation (k), and rate of symptomatic being transferred to isolation (Υ) will consequentially increase the value of basic reproduction number (R_o^S).
2. The effect of these parameters needed to be controlled and can be mitigated by introducing some social distancing, wearing of nose/mouth guide in a crowded environment to curtail the transmission rates from (asymptomatic, symptomatic, undetected but exposed) population, provision of Covid-19 vaccine/free testing and creation of effective government quarantine center for isolation treatment for asymptomatic/symptomatic population members.

References

Adak, D., Majumder, A. & Bairagi, N. (2021). Mathematical perspective of Covid-19 pandemic: Disease Extinction Criteria in Deterministic and Stochastic Models. *Chaos, Solitons and Fractals.* https://Doi.org/10.1016/j.chaos.2020.110381

Alshammari, F. S., Akyildiz, F. T., Khan, M.A., Din, A., Sunthrayuth, P. A. (2022). Stochastic Mathematical Model for Understanding the COVID-19 Infection Using Real Data. Symmetry 14, 2521. https://doi.org/ 10.3390/sym14122521

Anggriani, N., Ndii, M., Amelia, R. & Suryaningrat, W. (2021). A Mathematical COVID-19 model considering Asymptomatic and Symptomatic classes with waning immunity, *Alexandria Engineering Journal*. https://doi.org/10.1016/j.aej.2021.04.104

Aromolaran, A. D., Okeke, E. N., Lasisi, K. E. & David, I. J. (2024). Modified Deterministic Modeling of Covid-19 in Nigeria: A Case of a Closed System.

Journal of Biometrical Letters, vol. 61. No.1. 63-84. DOI: 10:2478/bile-2024-0005

Aychew Wondyfraw Tesfaye & Tesfaye Sama Satana (2021). Stochastic Model of the Transmission Dynamics of Covid-19 Pandemic. Journal of Advances in Difference Equation, https://doi.org/10.1186/s13662-021-03597-1

Chung, K. L., & Williams, R. J. (1990). *Introduction to stochastic integration* (Vol. 2). Boston: Birkhäuser.

Costa, Anderson Luiz Pena, Pires, Marcelo Amanajas, Resque, Rafael Lima & Sheylla Susan Moreira da Silva de Almeida (2021). Mathematical Modeling of the Infectious Diseases: Key Concepts and Applications. Journal of Infectious Diseases Epidemiology, 7:209 7(5), DOI:10.23937/2474-3658/1510209 ISSN: 2474-3658

Covid-19 Vaccination in Nigeria. https://en.wikipedia.org/w/index.php?title=COVID-19_vaccination_in_Nigeria&oldid=1116696626 Retrieved 10th April 2023 from

Evensen, G., Amezcua, J., Bocquet, M., Alberto Carrassi, Alban Farchi, Alison Fowler, Peter L. Houtekamer, Christopher K. Jones, Rafael J. de Moraes, Manuel Pulido, Christian Sampson & Femke C. Vossepoel (2020). An International Assessment of the Covid-19 Pandemic using Ensemble Data Assimilation. MedRxiv preprint Doi: https://doi.org/10.1101/2020.06.11.20128777

Klebaner, Fima C. (2012). Introduction to Stochastic Calculus with Applications. 3rd Edition Pg. 452. https://doi.org//10.1142/p821

LaSalle, J.P. (1976). The Stability of Dynamical System. Society for Industrial and Applied Mathematics. Philadelphia, Pennsylvania.

Leung, N. N. (2019). Model of Infectious disease transmission to explore the effects of immune boosting (Doctoral dissertation, University of Melbourne, Parkville, Victoria, Australia).

Lyra W, do Nascimento J-D, Jr., Belkhiria J, de Almeida L, Chrispim PPM, de Andrade I (2020). COVID-19 pandemics modeling with modified determinist SEIR, social distancing, and age stratification. The effect of vertical confinement and release in Brazil. PLoS ONE 15(9): e0237627. https://doi.org/10.1371/journal.pone.0237627

Niño-Torres, D., Ríos-Gutiérrez, A., Arunachalam, V., Ohajunwa, C., & Seshaiyer, P. (2022). Stochastic modeling, analysis, and simulation of the COVID-19 pandemic with explicit behavioral changes in Bogotá: A case study. *Infectious Disease Modelling*, *7*(1), 199-211.

Pappas, S. (2020). Can People Spread Coronavirus after they Recover? https://www.livescience.com/coronavirus-spread-after-recovery.html

Peter, O. J., Shaikh, A. S., Ibrahim, M. O., Nisar, K. S., Baleanu, D., Khan, I., & Abioye, A. I.(2021). Analysis and dynamics of fractional order mathematical model of COVID-19 in Nigeria using atangana-baleanu operator. *Journal of Computers, Materials & Continua*, 66 (2). https://DOI:32604/cmc.2020.012314

Ríos-Gutiérrez, A., Torres, S., & Arunachalam, V. (2021). Studies on the basic reproduction number in stochastic epidemic models with random perturbations. *Advances in difference equations*, *2021*(1), 288.

Rodrigues, H. S. M. Teresa T. Monteiro, M. T. T. and Torres, D. F. M. (2013). Sensitivity Analysis in a Dengue Epidemiological Model, Conference Papers in Mathematics, vol. 2013, Article ID 721406, http://dx.doi.org/10.1155/2013/721406

Sha He, Sanyi Tang & Libin Rong. (2020) A discrete Stochastic model of the Covid-19 Outbreak: Forecast and Control. Journal of Mathematical Biosciences and Engineering, 17(4): 2792-2804. Doi: 10:3934/mbe.2020153

Tilahun, G. T. & Alemneh, H. T. (2021). Mathematical modeling and optimal control analysis of COVID-19 in Ethiopia. Journal of Interdisciplinary Mathematics, 24(8), https://doi.org/10.1080/09720502.2021.1874086

Trottier, H., & Phillipe, P. (2002). Deterministik Modeling of Infectious Diseases: Applications to Measles and Other Similar Infections. *The Internet Journal of Infectious Diseases (Online)*, *2*(1).

WHO (2020). Corona Virus Disease (COVID-19)

Outbreak Situation. World Health Organization.

https://www.who.int/emergencies/diseases/novel-coronavirus-2019