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Basic Reproduction Number and Sensitivity Index Estimates from a Modified Deterministic Model for Nigeria COVID-19 Transmission

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Abstract

Basic reproduction number and sensitivity index are necessary indices used in most epidemiological research to evaluate the adequacy of formulated model. In this research, a modified deterministic model (MDM) of Covid-19 outbreak in Nigeria is formulated. The R_0 is estimated alongside the SI to determine the acceptability of the formulated MDM. The analytic results showed that an R_0 of 0.0000295 is obtained which imply the spread of the virus is under control. The SI result showed that 14 parameters of the MDM were sensitive whereby 8 of the parameters SI are positive while the remaining 6 parameters [natural mortality rate (μ), Proportion of asymptomatic that did not transit to symptomatic (v), natural mortality rate plus Covid-19 death induced (μ_1), rate of vaccination (γ), rate of symptomatic being transferred to isolation (Υ), transition of undetected exposed to quarantine (ф)] SI are negative. The SI result clearly showed that the significant negative indices parameters are responsible for reducing the R_0 and enhanced the decline of the Covid-19 virus in Nigeria.

Keywords: Covid-19, Basic Reproduction Number, Sensitivity Index, Deterministic Model

INTRODUCTION

Covid-19 became a global concern from year 2020 and much research has been carried out and still being undertaking concerning its transmission and cure. The emergence of covid-19 dealt a severe and acute public health emergency due to the world, such that individual countries responded in an unpredictable manner influencing the trajectory of national epidemics. The outbreak of covid-19 has severely inflicted all human phases of live, from health to economy and social development activities. It is an outbreak that has brought a total standstill to human movements and activities in a manner that has never been experienced at least in the last two to three decades. By Marach 2020 Covid-19 had successfully transmitted round the countries and continents widely in such manner that large numbers were being recorded on daily basis.

In epidemiological studies, basic reproduction number, R_0 is a key epidemiological parameter or index as the expected number of infected individuals from an infectious person in a totally or partially susceptible population respectively or the average number of new infections generated by a single infected individual in a completely susceptible population (Shaw & Kennedy, 2021). In essence it implies that R_0 can represent a potential measure of the contagion of a contagious disease (Najafimehr *et al.*, 2020). According to Giesecke (2017), the potential of infection in a population depends on the R_0, and defined it as the average number of persons directly infected by an infectious case during his or her entire infectious period when he or she enters a totally susceptible population. Also, Delamater *et al.* (2019) stated that estimation of R_0 and R is largely reliant upon the estimation method, contact structure, and epidemiological parameters such as the infectious period and incubation period. In Lim *et al.* (2020) study, they reported that this metric can have value above one in a certain region or contact network, even if the estimated population-average is below one. More importantly, the presence of asymptomatic and undetected case of Covid-19 may bias the estimation of the R_0.

To understand the dynamics of the model over time with respect to the parameters, a sensitivity analysis ratio is required to be carried out on the data by a systematic varying of the model parameter's values. It is used to determine the parameters of high impact to be targeted by intervention strategies and at measuring the possible effect of relative change in a variable when a parameter change (Rodrigues *et al.* 2013). A highly sensitive parameter should be carefully estimated, because a small variation in that parameter will lead to large quantitative changes.

Sensitivity index is a very statistically significant ratio in model parameters' evaluation. According to Pianosi *et al.* (2016) sensitivity analysis defines the parameters and initial conditions (input) that influences the model's quantities of interest the most. Lim *et al.* (2020) reported that the presence of asymptomatic and undetected cases of Covid-19 may bias the estimation of R_0 since certain proportion of infected persons would be asymptomatic at the population level. Lim *et al.* (2020) further stated that when $R_0 < 1$, the disease dynamics are strongly affected by the initial conditions and there are still present new infection cases for some time. Hence, the number of infections attributed to an infected person in the early stage can be more than 1, even though R_0 is below 1. Also, when $R_0 > 1$, disease infection can die out since the transmission of an infectious disease is a branching process with a negative binomial probability distribution. Hence, a disease with $R_0 > 1$ can be eradicated if the population number is under the critical community size.

Several studies have calculated R_0 using mathematical or statistical methods in different populations for covid-19. Iyaniwura *et al.* (2022) in a study of nineteen African countries, estimated the R_0 of Covid-19 and it varies from 1.98 (Sudan) to 9.66 (Mauritius) with Nigeria having 3.86. Hilton & Kneeling (2020) opined that the estimate being highly dependent of the complexity of the mathematical model used. Hence, Ro values are dependent on the model structures and assumption. It is important to understand this metric called Ro in more detail to improve communication and understanding of how the public health practitioners can respond to the infectious disease outbreaks. In this research, the R_0 and SI of covid-19 from a modified deterministic model (MDM) are presented.

METHODS

The covid-19 transmission MDM with it's appropriate in-flow and out-flow parameters are constructed as follows in the system of deterministic differential equations below:

$$N_N(t) = S_N(t) + S_V(t) + E(t) + T_e(t) + Q(t) + I_A(t) + I_S(t) + I_L(t) + R(t) \tag{1}$$

$$\left.\begin{aligned}
\frac{dS_N}{dt} &= \Lambda - \beta_1 S_N I_A - \beta_2 S_N I_S + \beta_v S_v + \mathrm{V}R + ZQ - C_1 S_N \\
\frac{dS_V}{dt} &= \gamma S_N - C_2 S_v, \\
\frac{dE}{dt} &= \beta_1 S_N I_A + \beta_2 S_N I_S - C_3 E, \\
\frac{dT_e}{dt} &= \sigma E - C_4 T_e \\
\frac{dQ}{dt} &= \Phi T_e - C_5 Q, \\
\frac{dI_A}{dt} &= p\alpha T_e - C_6 I_A, \\
\frac{dI_S}{dt} &= (1-p)\alpha T_e + (1-v)kI_A - C_7 I_S, \\
\frac{dI_L}{dt} &= \lambda Q + vkI_A + \Upsilon I_S - C_8 I_L, \\
\frac{dR}{dt} &= \chi I_L - C_9 R.
\end{aligned}\right\} \tag{2}$$

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

Model Parameter Estimation and Basic Reproduction Number (Ro)

Initial values for estimating the parameters of the MDM are presented in Table 1. They are used to solve the set of non-linear differential equations in equation (2). The software used for the estimations are R version 4.2 and MAPLE version 20.

Table 1. Initial values for parameter estimation

Symbols & Parameter Description (unit: /day/week)		**Value**	**Unit**	**Reference**
Λ	Recruitment rate of the susceptible population	36400	per10^3 pp	Nigeria Birth Rate, 2022
M	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	1.727E-7	1/day	Anggriani *et al.* (2021)

	infected			
β_2	Prob. of transmission from symptomatic infected	7.474E-8	1/day	Anggriani *et al.* (2021)
β_v	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	Peter *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	Ohajunwa *et al.* (2020)
Υ	Rate of symptomatic being transferred to Isolation	0.1900	1/day	Ohajunwa *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

Basic Reproduction Number, R_0

In this research, the next generation method was used in estimating R_0 and the R_0 for the MDM is obtained as follows:

$$R_0 = \rho\left(FV^{-1}\right) = \frac{\alpha\sigma\Lambda C_2\left[\left[k\rho(1-v)+C_6(1-\rho)\right]\beta_2 + k\rho\beta_1 C_7\right]}{\left(C_1C_2-\gamma\beta_v\right)C_6C_4C_3C_7} \tag{3}$$

$$F = \begin{bmatrix} 0 & 0 & 0 & \frac{\beta_1\Lambda C_2}{C_1C_2-\gamma\beta_v} & \frac{\beta_2\gamma\Lambda}{C_1C_2-\gamma\beta_v} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \text{and} V = \begin{bmatrix} C_3 & 0 & 0 & \frac{\beta_1\Lambda C_2}{C_1C_2-\gamma\beta_v} & \frac{\beta_2\gamma\Lambda}{C_1C_2-\gamma\beta_v} & 0 \\ -\sigma & C_4 & 0 & 0 & 0 & 0 \\ 0 & -\Phi & C_5 & 0 & 0 & 0 \\ 0 & -\rho\alpha & 0 & 0 & 0 & 0 \\ 0 & -(1-\rho)\alpha & 0 & -(1-v)k & C_7 & 0 \\ 0 & 0 & -\lambda & -vk & -\Upsilon & C_7 \end{bmatrix} \tag{4}$$

where, F and V are the Jacobian matrices of newly infected matrices (f) and existing matrices (v) that are evaluated from the disease-free equilibrium point (P_0), and ϱ is the spectral radius of the dominant eigenvalue of the matrix FV^{-1}.

Sensitivity Analysis (SI)

The normalized forward SI of R_0 for each parameter in the MDM that depended on parameter ϱ is estimated by (Rodrigues, 2013):

$$SI = \frac{\partial R_o}{\partial \rho} \times \frac{\rho}{R_o} \tag{5}$$

It highlights the parameters that should be attended to in the disease management strategy.

RESULTS AND DISCUSSION

After applying the initial values in estimating the model parameters, the MDM parameters estimates obtained are presented in Table 2.

Table 2. MDM Parameters and R_0 Estimates

Parameters	Estimates
$\boldsymbol{\Lambda}$	3.644E+01
$\boldsymbol{\Upsilon}$	1.1020
$\boldsymbol{\beta_v}$	1.791-02
$\boldsymbol{Z}$	4.465E-01
$\boldsymbol{\beta_1}$	7.884E-03
$\boldsymbol{\beta_2}$	5.100E-04
$\boldsymbol{\gamma}$	1.790E-01
$\boldsymbol{\Sigma}$	1.1150
$\boldsymbol{\mu}$	3.4662
$\boldsymbol{P}$	6.68E-02
$\boldsymbol{A}$	7.200E-02
$\boldsymbol{\Phi}$	5.250E-02
$\boldsymbol{\lambda}$	7.100E-01
$\boldsymbol{\mu_1}$	1.4300
$\boldsymbol{k}$	0.2100
$\boldsymbol{v}$	0.3000
$\boldsymbol{X}$	3.900E-02
$\boldsymbol{\Delta}$	0.1460
$\mathbf{R_0}$	**0.0000295**

The SI values are presented in Table 3 for the MDM parameters R_0. It can be observed that the parameters Λ, β_1, β_2, β_V, a, σ, k, and ϱ have positive impact on the basic reproduction number while v, ɸ, γ, ϒ, μ, and μ_1 have negative impact on covid-19 pandemic in Nigeria. This imply an increase in the positive parameters there will be increase in the spread of covid-19 in Nigeria but an increase in the negative parameters leads to a steady decline of covid-19 spread in Nigeria.

Table 3. Sensitivity Indices on Significant Parameters

Parameter	Value
Λ	1
β_1	0.269
β_2	0.731
β_v	0.00025
a	0.964
σ	0.562
k	0.236
ϱ	0.051
Φ	-0.257
γ	-0.13
Υ	-0.103
μ	-1
μ_1	-1
v	-0.0051

CONCLUSION

The model basic reproduction number, which is a milestone in every epidemic for the deterministic models was estimated using next generation matrix approach, the basic reproduction number obtained is sufficient to agree that the disease will die out over time as the value does not exceed the standard ratio. It can be established that the disease-free equilibrium is locally asymptomatically stable almost surely since $R_0 < 1$ (0.0000295). The results from the SI in Table 3 clearly showed that recruitment rate (Λ), probability of transmission from asymptomatic infected (β_1), Probability of Transmission from symptomatic infected (β_2), Probability of vaccinated get back to susceptible (β_v), probability of tested exposed becomes infected (a), Rate at which exposed population get tested (σ), natural mortality rate (μ) and proportion of tested exposed becomes infected (ϱ), rate of transition of asymptomatic infected to isolation (k), proportion of asymptomatic that did not transit to symptomatic (v), natural mortality rate plus covid-19 death induced (μ_1), rate of transition from quarantine to isolation (λ), Rate of symptomatic being transferred to Isolation (ϒ), transition of undetected exposed to quarantine (ɸ), rate of transition from quarantine to susceptible (Z), and rate of vaccination (γ) are found to have significant effect on the covid-19 transmission.

The parameters Λ, β_1, β_2, β_V, a, σ, k, and ϱ are identified as promoters of the Covid-19 epidemic infection in Nigeria. However, v, ф, γ, ϒ, μ, and μ_1 are the identified parameters that helped in reducing covid-19 virus spread and transmission in Nigeria. These conclusions are based on the SI values obtained in Table 3.

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