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Sensitivity Analysis of the Basic Reproduction Number for Two Strains Covid-19 Model with Vaccination and Awareness Program

Anate A.O.[1], Adamu M. M.[2], Adamu M.S.[3], Kwami A. M.[4]
[1]Yusuf Maitama Sule Federal University of Education, Kano, Nigeria
[2,3,4]Abubakar Tafawa Balewa University, Bauchi, Nigeria
anateao2015@gmail.com

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Abstract

Sensitivity analysis of the basic reproduction number is an essential mathematical tool for identifying the parameters that most strongly influence disease transmission in epidemiological models. This study analyzes the sensitivity of the basic reproduction number in a COVID-19 transmission model comprising seven mutually exclusive compartments and incorporating vaccination and awareness interventions. The basic reproduction number, R_0, was derived using the next-generation matrix method, after which local sensitivity analysis was conducted using data obtained from the Nigeria Centre for Disease Control and other sources. The analysis produced two values of R_0 whose magnitudes depend on the model parameters, particularly those associated with vaccination and public awareness. The findings indicate that recruitment and infection rates exert strong positive effects on disease transmission, whereas vaccination and natural recovery rates have negative effects on disease progression. These results demonstrate that reducing infection-related parameters while strengthening vaccination and recovery

mechanisms is critical for controlling COVID-19 transmission. The study contributes to epidemiological modeling by identifying the parameters that should be prioritized in disease-control strategies. Accordingly, policymakers should implement coordinated interventions, including quarantine, lockdown measures, vaccination programs, and effective public awareness campaigns, to reduce transmission and limit disease growth.

Keywords: Awareness Campaigns; Basic Reproduction Number; COVID-19; Sensitivity Analysis; Vaccination

INTRODUCTION

Mathematical modeling has become an important tool in analyzing the spread and control of infectious diseases. About 250 years ago, Bernoulli presented some works on human epidemiology with the help of mathematical models. Toward the beginning of the second quarter of the 20th century, Kermack and McKendrick established the classical SIR model on epidemiology. Later on, many mathematical models have been proposed to study the transmission dynamics and control of infectious diseases [1]. Mathematical analysis and modeling has been employed to study infectious diseases epidemiology in order to reveal the most promising and realistic strategies that influence the transmission and control of these diseases [2].

The latest epidemic that ravaged the world known as Covid-19 is a viral disease caused by the Severe Acute Respiratory Syndrome Corona virus 2 (SARS-COV-2 virus). It was first detected in the Wuhan province of China in December of 2019 [3]. The disease (appropriately coined COVID-19, to indicate that it is a member of the coronavirus family of viruses identified in the year 2019) started as an outbreak of pneumonia of unknown cause. It rapidly became a devastating pandemic, spreading to over 210 countries across the globe, and inflicting severe public health and socio-economic burden globally [4, 5]. Much attention is paid to models that support the assessment of the effectiveness of intervention measures [6].

Sensitivity analysis of a model is a systematic way of checking how changes in model parameters affect the outputs of the model. It helps us to understand those parameters that the model is most sensitive to. This will help to prioritize data collection,

improves model calibration and supports policy decisions to know which parameter to emphasize on.

There are various types sensitivity analysis viz: Local sensitivity analysis, Global sensitivity analysis and Forward-Backward Sensitivity analysis.

Many scholars have carried out works on sensitivity analysis of infectious disease model. Powell et. al work gave the usefulness of sensitivity analysis in infectious disease modeling. Their analysis shows that contact rate of infected persons and vaccination policy are the major ingredients that drive infectious disease dynamics [7].

In this work we shall compute the basic reproduction number of our model and apply the local sensitivity analysis on it. This will enable us to check how changes in any of the model parameters affect the basic reproduction number and which parameter is most sensitive.

METHODOLOGY

Our proposed model consists of seven mutually exclusive compartments with the following differential equations. Table 1 gives the model State variables while table 2 gives the model parameters and their descriptions as used in this work.

The following are the differential equations of the model:

$$\frac{dS_u}{dt} = \Lambda - (\alpha_1 I_1 + \alpha_2 I_2 + \theta + \mu)S_u, \quad (1)$$

$$\frac{dS_a}{dt} = \theta S_u + \gamma R - \left(\frac{\alpha_1 I_1}{1+\theta I_1} + \frac{\alpha_2 I_2}{1+\theta I_2} + \omega + \mu\right) S_a, \quad (2)$$

$$\frac{dV}{dt} = \omega S_a - (\tau + \mu)V, \quad (3)$$

$$\frac{dI_1}{dt} = \frac{\alpha_1 I_1}{1+\theta I_1} S_a + \alpha_1 I_1 S_u - (\delta_1 + \beta_1 + d_1 + \mu)I_1, \quad (4)$$

$$\frac{dI_2}{dt} = \tau V + \frac{\alpha_2 I_2}{1+\theta I_1} S_a + \alpha_2 I_2 S_u - (\delta_2 + \beta_2 + d_2 + \mu)I_2, \quad (5)$$

$$\frac{dH}{dt} = \delta_1 I_1 + \delta_2 I_2 - (\phi + d_3 + \mu)H, \quad (6)$$

$$\frac{dR}{dt} = \beta_1 I_1 + \beta_2 I_2 + \phi H - (\gamma + \mu)R \quad (7)$$

with the initial conditions,

$$S_u(0) = \Lambda + S_{u,0}, Sa(0) = S_{a(0)}, V(0) = V_0, I_1(0) = I_{1,0}, I_2(0) = I_{2,0},$$

$$H(0) = H_0, R(0) = R_0 \quad (8)$$

Table 1: State Variables and Description

State Variables	Description
S_u	Susceptible unaware population
S_a	Susceptible aware population
V	Vaccinated population
I_1	Population infected by first strain
I_2	Population infected by second strain
H	Hospitalised Population
R	Recovered population

Table 2: Model parameters and their descriptions

Parameter	Description
Λ	Recruitment rate into S_u
Θ	Awareness parameter
α_1	Infection rate of strain 1
α_2	Infection rate of strain 2
Ω	Vaccination rate of S_a
β_1	Natural recovery rate against I_1
β_2	Natural recovery rate against I_2
τ	Loss of immunity rate of vaccinated
δ_1	Rate at which I_1 get hospitalized
δ_2	Rate at which I_2 get hospitalized
γ	Rate at which recovered population move to S_a
$\emptyset$	Recovery rate of hospitalised population
ω	Vaccination rate
μ	Natural death rate
d_1	Death due to first strain
d_2	Death due to second strain
d_3	Death due to first or second strain

Basic Reproduction Number

The basic reproduction number R_0 is a measure of the transmissibility of a viral disease. It is defined as the expected number of secondary cases produced, in a completely susceptible population by a typical infected individual [8].

There are various methods of computing basic reproduction number R_0 as described in [9, 10]. They include the New Generation Matrix NGM method, Jacobian/eigen vales method, survival function (Probabilistic) method.

We shall however use the Next Generation Matrix *NGM* method for the computation where R_0 is defined as the dominant eigen value of the matrix $K - \lambda I = 0$, where $K = FV^{-1}$

Matrix F and V are derived from the infection equations (3) and (4)

New Infection for I_1 from (4) is

$$F_1 = \frac{\alpha_1 I_1}{1+\theta I_1} S_a + \alpha_1 I_1 S_u \tag{9}$$

While the new Infection for I_2 from (5)

$$F_2 = \frac{\alpha_2 I_2}{1+\theta I_2} S_a + \alpha_2 I_2 S_u \tag{10}$$

The transition rates for I_1 and I_2 are respectively

$$V_1 = (\delta_1 + \beta_1 + d_1 + \mu) I_1 \tag{11}$$

$$V_2 = (\delta_2 + \beta_2 + d_2 + \mu) I_2 \tag{12}$$

The Jacobian matrices $J(F)$ of the new infection F and transition rate are derived using

$$J(F) = \begin{pmatrix} \frac{\partial F_1}{\partial I_1} & \frac{\partial F_1}{\partial I_2} \\ \frac{\partial F_2}{\partial I_1} & \frac{\partial F_2}{\partial I_2} \end{pmatrix} \text{ and } J(V) = \begin{pmatrix} \frac{\partial V_1}{\partial I_1} & \frac{\partial V_1}{\partial I_2} \\ \frac{\partial V_2}{\partial I_1} & \frac{\partial V_2}{\partial I_2} \end{pmatrix} \tag{13}$$

Applying (13) in (9)-(13), we have

$$J(F) = \begin{pmatrix} \frac{(1+\theta I_1)\alpha_1 S_a - \alpha_1 \theta I_1 S_a}{(1+\theta I_1)^2} + \alpha_1 S_u & 0 \\ 0 & \frac{(1+\theta I_2)\alpha_2 S_a - \alpha_2 \theta I_2 S_a}{(1+\theta I_2)^2} + \alpha_2 S_u \end{pmatrix}$$

At disease free i.e. $I_1 = I_2 = 0$, we have $J(F^0) = F$ as

$$F = \begin{pmatrix} \alpha_1 S_a + \alpha_1 S_u & 0 \\ 0 & \alpha_2 S_a + \alpha_2 S_u \end{pmatrix}$$

and

$$V = \begin{pmatrix} \delta_1 + \beta_1 + d_1 + \mu & 0 \\ 0 & \delta_2 + \beta_2 + d_2 + \mu \end{pmatrix}$$

Thus we have $K = F\boldsymbol{V}^{-1} = \begin{pmatrix} \frac{\alpha_1(S_a+S_u)}{\delta_1+\beta_1+d_1+\mu} & 0 \\ 0 & \frac{\alpha_2(S_a+S_u)}{\delta_2+\beta_2+d_2+\mu} \end{pmatrix}$

The characteristics equation is given as $(K - \lambda I) = 0$, where I is a 2X2 unit matrix

$$det(K - \lambda I) = \begin{vmatrix} \frac{\alpha_1\bar{S}}{\delta_1+\beta_1+d_1+\mu} - \lambda & 0 \\ 0 & \frac{\alpha_2\bar{S}}{\delta_2+\beta_2+d_2+\mu} - \lambda \end{vmatrix}$$

Where $\bar{S} = S_a + S_u$ the total susceptible

Solving $det(K - \lambda I) = 0$, for λ, we have

$$\lambda = \frac{\alpha_1\bar{S}}{\delta_1+\beta_1+d_1+\mu}, \frac{\alpha_2\bar{S}}{\delta_2+\beta_2+d_2+\mu}$$

The basic reproduction number R_0 is defined as the dominant *eigenvalue* for two strain disease given by

$$R_0 = max(R_1, R_2)$$

Where $R_1 = \frac{\alpha_1\bar{S}}{\delta_1+\beta_1+d_1+\mu}$ and $R_2 = \frac{\alpha_2\bar{S}}{\delta_2+\beta_2+d_2+\mu}$

$S_a + S_u = \frac{\Lambda}{\theta+\mu} + \frac{\Lambda\theta}{(\theta+\mu)(\omega+\mu)} = \frac{\Lambda(\omega+\mu+\theta)}{(\theta+\mu)(\omega+\mu)}$ computed at disease free

Hence, $R_1 = \frac{\alpha_1\Lambda(\omega+\mu+\theta)}{(\delta_1+\beta_1+d_1+\mu)(\theta+\mu)(\omega+\mu)}$, and $R_2 = \frac{\alpha_2\Lambda(\omega+\mu+\theta)}{(\delta_2+\beta_2+d_2+\mu)(\theta+\mu)(\omega+\mu)}$ (14)

Sensitivity Analysis

In this section, we present the local sensitivity analysis of our model which enables us to check how changes in any of the model parameters affect the outputs of the basic reproduction number.

The local stability L. S. Γ of any output R_i and parameter p is given as

$$\Gamma_p^{R_i} = \frac{\partial R_i}{\partial p} \cdot \frac{p}{R_i} \quad (15)$$

L.S. of R_1 w.r.t. α_1: where $R_1 = \frac{\alpha_1\Lambda(\omega+\mu+\theta)}{(\delta_1+\beta_1+d_1+\mu)(\theta+\mu)(\omega+\mu)}$

$\frac{\partial R_1}{\partial \alpha_1} = \frac{\Lambda(\omega+\mu+\theta)}{(\delta_1+\beta_1+d_1+\mu)(\theta+\mu)(\omega+\mu)}$

Thus we have $\Gamma_{\alpha_1}^{R_1} = \frac{\partial R_i}{\partial \alpha_1} \cdot \frac{\alpha_1}{R_1}$

$$= \frac{\Lambda(\omega + \mu + \theta)}{(\delta_1 + \beta_1 + d_1 + \mu)(\theta + \mu)(\omega + \mu)} \times \frac{\alpha_1}{\frac{\alpha_1 \Lambda(\omega+\mu+\theta)}{(\delta_1+\beta_1+d_1+\mu)(\theta+\mu)(\omega+\mu)}}$$

Which simplifies to give $\Gamma_{\alpha_1}^{R_1} = 1$ (16)

Similarly, L.S. of R_1 w.r.t. Λ, $\Gamma_{\Lambda}^{R_1} = 1$

We use the same procedure to compute the L.S. for all the other parameters in R_1 and R_2 and substituting values as it is in table 3

RESULTS AND INTERPRETATION

The table below gives the numerical values of the sensitivity analysis SA obtained using tables 2 and numerical values obtained from [11, 12 and 13].

Table 3: Sensitivity Analysis result

Parameter	Parameter Values	Sensitivity R_1	Sensitivity R_2	Remark
Λ	6/day	1.00000	1.00000	Maximum positive effect on $R_1$and R_2
α_1	0.05	1.00000	0.00000	Maximum effect on R_1 and non on R_2
α_2	0.07	0.00000	1.0000000	Maximum effect on R_2 and non on R_1
ω	0.18	-0.714848	-0.714848	High negative effect on $R_1$and R_2
β_1	0.97	-0.733021	0.00000	High negative effect on $R_1$and no effect R_2
β_2	0.97	0.00000	-0.069017	High negative effect on $R_2$and no effect R_1
τ	0.01	0.00000	0.00000	No effect on $R_1$and R_2
δ_1	0.33	-0.249378	0.00000	Low negative effect on $R_1$and no effect R_2
δ_2	0.5	0.00000	-0.313111	Low negative effect on $R_2$and no effect R_1

γ	0.99	0.00000	0.00000	No effect on R_1 and R_2
ϕ	0.98	0.00000	0.00000	No effect on R_1 and R_2
μ	0.011	-0.070001	-0.069017	Low negative effect on R_1 and R_2
d_1	0.01229	-0.009287	0.00000	Low negative effect on R_1 and no effect R_2
d_2	0.02	0.00000	-0.013324	Low negative effect on R_2 and no effect R_1

From the table above we see that the values of SA lies between *-1* and $+1$. While some of the parameters have strong positive/negative values, others have weak or no values. This indicates the strength of their influence on the basic reproduction number. Those parameters with positive values indicate a direct relationship with R_0 whille those with negative values indicate negative relationship with R_0.

Graphical representation of the sensitivity analysis: The following figures present the graphical representation of the sensitivity analysis

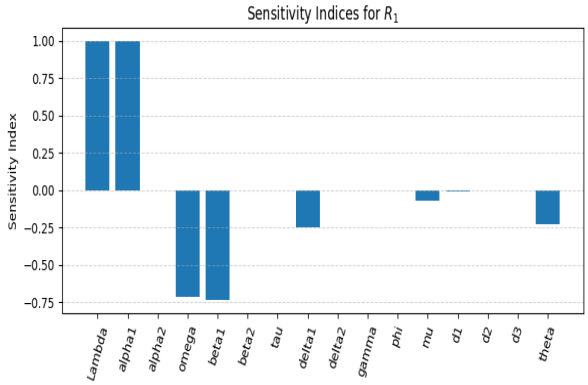

Figure 1: Sensitivity analysis for R_1

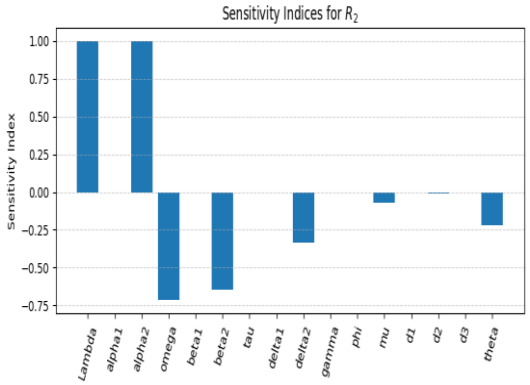

Figure 2: Sensitivity analysis for R_2

Figures 1 and 2 shows the sensitivity analyses of R_1 and R_2 respectively. We observe that the recruitment rate Λ and the infection rates α_1 and α_2 the only parameters with strong positive effect on the basic reproduction number. This means that any increase in their values will lead to the growth of the disease. Also, vaccination rate ω and the natural recovery rates β_1 and β_2 have strong negative effect on the basic reproduction number. This means increasing the vaccination rate will reduce the growth (spread) of the disease within the population.

CONCLUSION

This work presented the basic reproduction numbers and the sensitivity analysis of two strains of Covid-19 disease model. The most important parameters that can lead to the persistence or other wise of the disease are the recruitment and infection rates. Thus preventive measures such as vaccination, quarantine and lock-down will help control the spread of the disease. Also, effective awareness campaign will lead to taking measures that will reduce contact rates

REFERENCES

[1]. Kermack, W. O., & McKendrick, A. G. (1991). Contributions to the mathematical theory of epidemics—I. *Bulletin of Mathematical Biology, 53*(1–2), 33–55. https://doi.org/10.1007/BF02464423

[2]. Brauer, F., & Castillo-Chavez, C. (2001). *Mathematical models in population biology and epidemiology*. Springer. https://doi.org/10.1007/978-1-4757-3516-1

[3]. Branswell, H. (2020, March 11). WHO declares the coronavirus outbreak a pandemic. *STAT*. https://www.statnews.com/2020/03/11/who-declares-the-coronavirus-outbreak-a-pandemic/

[4]. Di Gennaro, F., Pizzol, D., Marotta, C., Antunes, M., Racalbuto, V., Veronese, N., & Smith, L. (2020). Coronavirus diseases (COVID-19) current status and future perspectives: A narrative review. *International Journal of Environmental Research and Public Health, 17*(8), 2690. https://doi.org/10.3390/ijerph17082690

[5]. World Health Organization. (n.d.). *WHO COVID-19 dashboard*. Retrieved April 24, 2020, from https://covid19.who.int/

[6]. Ferretti, L., Wymant, C., Kendall, M., Zhao, L., Nurtay, A., Parker, M., Abeler-Dörner, L., Bonsall, D., & Fraser, C. (2020). Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. *Science, 368*(6491), eabb6936. https://doi.org/10.1126/science.abb6936

[7]. Powell, D. R., Fair, J., LeClaire, R. J., Moore, L. M., & Thompson, D. (2005). Sensitivity analysis of an infectious disease model. In *Proceedings of the 23rd International System Dynamics Conference* (pp. 1–20). https://proceedings.systemdynamics.org/2005/proceed/papers/LECLA330.pdf

[8]. Diekmann, O., Heesterbeek, J. A. P., & Metz, J. A. J. (1990). On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations. *Journal of Mathematical Biology, 28*(4), 365–382. https://doi.org/10.1007/BF00178324

[9]. Fosu, G. O., Akweittey, E., & Adu-Sackey, A. (2020). Next-generation matrices and basic reproductive numbers for all phases of the coronavirus disease. *Open Journal of Mathematical Sciences, 4*(1), 261–272. https://doi.org/10.30538/oms2020.0117

[10]. van den Driessche, P., & Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission.

Mathematical Biosciences, 180(1–2), 29–48. https://doi.org/10.1016/S0025-5564(02)00108-6

[11]. Nigeria Centre for Disease Control. (2020, February 28). *First case of corona virus disease confirmed in Nigeria*. https://ncdc.gov.ng/news/227/first-case-of-corona-virus-disease-confirmed-in-nigeria

[12]. Eegunjobi, A. S., & Makinde, O. D. (2022). Mathematical analysis of two strains COVID-19 disease using SEIR model. *Journal of Mathematical and Fundamental Sciences, 54*(2), 211–232. https://doi.org/10.5614/j.math.fund.sci.2022.54.2.1

[13]. Akinwande, N. I., Ashezua, T. T., Gweryina, R. I., Somma, S. A., Oguntolu, F. A., Usman, A., Abdurrahman, O. N., Kaduna, F. S., Adajime, T. P., Kuta, F. A., Abdulrahman, S., Olayiwola, R. O., Enagi, A. I., Bolarin, G. A., & Shehu, M. D. (2022). Mathematical model of COVID-19 transmission dynamics incorporating booster vaccine program and environmental contamination. *Heliyon, 8*(11), e11513. https://doi.org/10.1016/j.heliyon.2022.e11513