STABILITY AND BIFURCATION ANALYSIS OF COVID-19 MATHEMATICAL MODEL INCORPORATING CASE DETECTION

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ABSTRACT

COVID-19 became a household name globally in the year 2020 after it was first discovered in Wuhan, China in December 2019. It is a global pandemic that shut the economy of all nations in the larger part of year 2020 by forcing a compulsory holiday on mankind due to its threat of mass death. The menace of this pandemic was combated with the total arsenal in human capacity. One of such weapons is case detection that leads to either self-isolation or quarantine. This weapon helps to reduce the number of new cases that may arise from undetected asymptomatic/symptomatic carriers within a population. In this article, the dynamics of COVID-19 transmission were studied by developing a mathematical model incorporating case detection, the impact of sensitization, and role of early diagnosis in curbing the spread of this disease. The basic properties in terms of existence, uniqueness, and boundedness of solution for the formulated model were discussed. Also, the model was found to exhibit two equilibrium states which are categorised as the disease-free (DFE) and pandemic equilibrium states. The reproductive number for the model was computed and used to establish the stability analysis for both equilibrium states. Center manifold theory was employed to assess the bifurcation analysis of the model and the result shows that the model exhibits forward bifurcation when the reproductive number is greater than and equal to 1.

Keywords: Bifurcation, Case-detection, Covid-19, Pandemic, Reproductive number

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1. Introduction

The coronavirus disease that became a pandemic in the year 2020 is subsiding worldwide with a reduced incidence and fatality compared with the beginning of the epidemic. So far, four variants of novel coronavirus have been discovered, namely, Alpha variant, beta variant, gamma variant and delta variant, with each of these variants affecting some regions more than others and varying degree of fatality. However, some countries are still regarded as epicenters with an increase in newly detected cases, like USA with 1,120,999 new cases in the last seven days according to COVID-19 weekly epidemiological report of 5th October 2021 published by World Health Organization (W.H.O., 2021b). As of April 2021, more than 150 million confirmed cases with over 3 million deaths have been attributed to COVID-19 and the outbreak has spread to more than 220 countries globally (Worldometer, 2021). As the world continues to battle this disease caused by the novel coronavirus, SARS-CoV-2 (a virus regarded as a

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highly virulent one that targets the human respiratory system), it became extremely important to understand its "modus operandi" and transmission mechanisms. Like the other two coronaviruses (SARS-CoV and MERS-CoV), COVID-19 spreads from human to human through direct contact with infected surfaces or objects and through inhalation of droplets from both asymptomatic and symptomatic infected individuals (Riyapan *et al.*, 2021). In a bid to reduce its spread, several preventive methods and policies were adopted from the initial stage of this pandemic. Of such is regular hand-sanitizing, use of protective facemask, socialdistancing and closure of borders. Riyapan *et al.* (2021) studied the effectiveness of these preventive measures using Thailand as a case study and recommended that these policies should be properly enforced if a higher percentage of success is to be recorded.

The fight against this menace does not stop at the preventive stage. Lots of effort were directed towards obtaining a curative drug and prophylactic vaccines to tackle this menace. World Health Organization (W.H.O.) and some other non-governmental agencies made funds available for scientists to come up with effective treatment for this disease. Several drugs were developed with each of them showing a certain percentage of success rate in treating the disease. A remarkable result is the advent of some vaccines, which are believed to be 95% effective with no serious life-threatening side effects. Studies according to John Hopkins Medicine found that the two initial vaccines developed by Pfizer/BioNTech and Moderna is both about 95% effective and reported no serious or life-threatening side effects (Kelen & Maragakis, 2021).

The invention of a prophylactic vaccine in early 2021 brought a greater sigh of relief and hope of total eradication of this pandemic. W.H.O. confirmed that COVID-19 vaccines are safe and getting vaccinated will help protect individual against developing severe COVID-19 disease and dying from COVID-19. It was stated that some individuals, may experience some mild side effects after getting vaccinated, which are signs that the body is building protection (W.H.O., 2021a). However, several myths, conspiracy theories and/or fallacies have followed the advent of this vaccine. One of such is that the vaccine can alter DNA and affect women's fertility (CDC, 2021). These myths undermine the efforts put in place to obtain the vaccine, as the vaccines do not get the desired acceptance rate worldwide. With all the obstacles facing the eradication of this deadly disease globally, the second wave of the disease is not as deadly as forecasted due to the combination and implementation of both preventive and corrective measures, together with the prophylactic vaccine. Some countries are already re-opening their borders once the immigrants present a certificate of vaccination of COVID-19 for economic activities while others are putting mechanisms in place to do so. With all these interventions, the fight against this pandemic is far from being over. Recently, there is a surge in new cases in India. Also, some of the European countries are still combating the second wave of the pandemic. One factor associated with this is the early re-opening of borders to boost the economic situation of the country. However, imported cases of the disease cause a rise in the number of new cases due to inadequate case detection. Some of the strict rules of self-isolation, quarantine and social distancing were relaxed to accommodate immigrants in other to boost the already dwindled economy (Yue et al., 2021). Another situation that increases infection rate is lack of symptoms at the early stage of infection (asymptomatic/exposed stage). Individuals in this category show no signs of the infection but can transmit the virus according to W.H.O. (2020). Report has it that, infected people appear to be most infectious 2 days before the symptoms developed and early in their illness. Thus, this work is centred on analysing the role of case detection (both at asymptomatic and symptomatic stages) in reducing the spread of this coronavirus pandemic.

Mathematical modeling has proven to be an efficient tool to study, scrutinize, analyze, predict and understand the dynamics of an infectious disease. Over the years, several models have evolved from the elementary S-I-R model of Kermack and Mckendrick. Odetunde *et al.* (2021) presented a mathematical model to study the impact of reinfection in the transmission dynamics of COVID-19 using semi-analytical approach. Their result established that no immunity is guaranteed against reinfection from a treated/recovered individual if the preventive

measures are not strictly adhered to. Alqahtani (2021) presented an SIR epidemic model with fractional derivative to model COVID-19 by considering the stability and numerical analysis for the developed model. He concluded that for effective treatment of this epidemic, hospital resources have to be improved. Also, Vytla *et al.* (2021) presented a mathematical model to review COVID-19 pandemic. They affirmed some of the challenges being faced in combating coronavirus by mathematical modelers as pathogen evolution, statistical uncertainties, contact patterns and one model fits to all.

However, in the above cited works, attention was not given to the impact of sensitization, which can result in early diagnosis of the infection at the asymptomatic stage, neither was case detection of the infection examined to establish its role in the transmission dynamics of this pandemic. In this work, a new mathematical model of COVID-19 was developed for analysis by incorporating its multiple transmission pathway as an incidence function. Case detection at symptomatic and asymptomatic states were considered to understand the effect of early diagnosis and sensitization. Qualitative analysis of the model was done by testing the existence, uniqueness and positivity of solution and its boundedness. The basic reproduction number (R_0) for the developed model was computed. Stability analysis of the model was done based on the effective reproduction number and was found to be globally stable at the disease-free equilibrium point whenever $R_0 < 1$. Bifurcation analysis of the model was done using the bifurcation parameter β and was found to possess a forward bifurcation progression from a disease-free equilibrium state to a pandemic equilibrium state whenever $R_0 \geq 1$.

2. Material and Methods

COVID-19 transmits through direct contact with droplets (sweat, saliva, sneeze or cough) from an infected individual. The infectiousness of this disease is so high that even an asymptomatic individual can spread the infection. Thus, case detection at an early stage is one of the significant measures employed by the government of every nation to curb the spread of this disease. In this work, a nonlinear incidence function for disease transmission was employed to model the dynamics of COVID-19 disease by considering the impact of untested/undiagnosed and tested/diagnosed infectious individuals. The method employed is the deterministic modelling approach. The qualitative behaviour of the model shall be studied and analysed.

3. Model Formulation

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In order to analyze the epidemiological characteristics of coronavirus disease, as well as factors triggering its spread, a mathematical model to study COVID-19 dynamics was built by stratifying the total human population at any time t, denoted as N(t) into seven mutually exclusive sub-epidemiological classes of Susceptible individuals S(t), undiagnosed $E_u(t)$ and diagnosed $E_s(t)$ asymptomatic individuals (i.e., those infected without clinical symptoms), undiagnosed $I_u(t)$ and diagnosed $I_s(t)$ symptomatic individuals (i.e., infectious individuals with clinical symptoms), quarantined Q(t) and recovered R(t) individuals. Thus,

$$N(t) = S(t) + E_u(t) + E_s(t) + I_u(t) + I_s(t) + Q(t) + R(t)$$
(1)

Two forms of recruitment are assumed in the formulation of this model. Major recruitment into the population either by birth or immigration increases the population of the susceptible class at the rate π , while minimal number of individuals immigrated into the population as an undetected asymptomatic carrier of the infection at the rate χ_1 . Natural death rate is assumed across all compartments at the rate μ . Susceptible population is further reduced by newly acquired infection through effective contact with infectious individuals in

 E_u, E_s, I_u, I_s and Q subpopulation. The total force of infection ∇ (which is a major factor in disease pandemic) is given as:

$$\nabla = \beta (E_u + \delta_1 E_s + \delta_2 I_u + \delta_3 I_s + \delta_4 Q) \tag{2}$$

where β denotes contact that is sufficient to result in new infection, δ_1 , δ_2 , δ_3 and δ_4 are the modification parameters associated with infected individuals in E_s , I_u , I_s and Q subpopulation, respectively. It is intuitive to assume that the modification parameter satisfies

$$\delta_4 < \delta_3 < \delta_1 < \delta_2.$$

Thus, the rate of change of susceptible compartment is given as:

$$\frac{dS}{dt} = \pi - \nabla S - \mu S$$

The population of the undiagnosed asymptomatic individuals is increased by the infection of susceptible individual at the rate ∇ , recruitment of undetected immigrant (at the rate χ_1) and is decreased by progression to symptomatic stage at ε_1 , detection (at the rate α) and natural death rate μ . Thus,

$$\frac{dE_u}{dt} = \chi_1 E_u + (1 - \sigma)\nabla S - (\varepsilon_1 + \alpha + \mu)E_u$$

where σ denotes the impact of sensitization and testing on case detection of the infection at the early stage. It is important to logically assume that $0 \le \sigma \le 1$, where zero denotes no impact and one assumed hundred percent impact of sensitization to detect and quarantine infected individual at early stage. Diagnosed asymptomatic population is generated by newly detected case from susceptible compartment due to testing (at the rate σ) and detecting undiagnosed asymptomatic individuals (at the rate α). It is reduced by disease progression (at the rate ε_2), quarantine rate (ω_1), recovery rate (η_1) and natural death rate μ , so that

$$\frac{dE_s}{dt} = \sigma \nabla S + \alpha E_u - (\omega_1 + \varepsilon_2 + \eta_1 + \mu)E_s$$

Undiagnosed symptomatic population is increased by disease progression of undiagnosed asymptomatic individuals at ε_1 and is decreased by quarantine rate (ω_2), recovery rate (due to treatment at the rate η_2), natural death rate μ and death arising from COVID-19 complications at the rate τ_1 . Thus,

$$\frac{dI_u}{dt} = \varepsilon_1 E_u - (\omega_2 + \eta_2 + \mu + \tau_1)I_u$$

Similarly, diagnosed symptomatic population increased by disease progression of diagnosed asymptomatic individuals at ε_2 . It is decreased by quarantine rate (ω_3), recovery rate (due to treatment at the rate η_3), natural death rate μ and death arising from COVID-19 complications at the rate τ_2 , so that,

$$\frac{dI_s}{dt} = \varepsilon_2 E_s - (\omega_3 + \eta_3 + \mu + \tau_2)I_s$$

Quarantined population is increased by detection and quarantining of infected individuals (at the rate ω_i , i = 1,2,3 for diagnosed asymptomatic, undiagnosed and diagnosed symptomatic classes respectively). It is decreased by; effective recovery from treatment (at the rate η_4), natural death rate (μ) and COVID-19 induced death (at the rate τ_3). Hence,

$$\frac{dQ}{dt} = \omega_1 E_s + \omega_2 I_u + \omega_3 I_s - (\eta_4 + \mu + \tau_3)Q$$

The recovered population is generated by the recovery of diagnosed and undiagnosed infectious, as well as that of the quarantined individuals, whereas it decreased by natural death rate. Thus, the dynamics of the recovered compartment is such that:

$$\frac{dR}{dt} = \eta_1 E_s + \eta_2 I_u + \eta_3 I_s + \eta_4 Q - \mu R$$

Combining all the above differential equations for each subpopulation, the dynamics of COVID-19 transmission in the presence of undiagnosed immigrants and case detection is given by:

$$\frac{dS}{dt} = \pi - \nabla S - \mu S$$

$$\frac{dE_u}{dt} = (1 - \sigma)\nabla S - (\varepsilon_1 + \alpha + \mu - \chi_1)E_u$$

$$\frac{dE_s}{dt} = \sigma\nabla S + \alpha E_u - (\omega_1 + \varepsilon_2 + \eta_1 + \mu)E_s$$

$$\frac{dI_u}{dt} = \varepsilon_1 E_u - (\omega_2 + \eta_2 + \tau_1 + \mu)I_u$$

$$\frac{dI_s}{dt} = \varepsilon_2 E_s - (\omega_3 + \eta_3 + \tau_2 + \mu)I_s$$

$$\frac{dQ}{dt} = \omega_1 E_s + \omega_2 I_u + \omega_3 I_s - (\eta_4 + \tau_3 + \mu)Q$$

$$\frac{dR}{dt} = \eta_1 E_s + \eta_2 I_u + \eta_3 I_s + \eta_4 Q - \mu R$$

$$(3)$$

System of equations in eq. (3) is pictorially represented as a flow diagram by using boxes (circle) to denote each epidemiological sub-class while arrows are used to represent the in-flow and out-flow (in-flow brings addition to the compartment, while out-flow reduces the population) within the classes. The flowchart as in Figure 1 is for the transmission dynamics of the above model that given as:



Figure 1. Flow chart for the Model.

4. Model Solution

4.1 Existence and uniqueness of solution

Theorem 1: For all non-negative initial conditions, the solutions of system (3) exist and are unique for all time $t \ge 0$.

Proof: Lipschitz criteria for existence and uniqueness of solution as adopted by Sowole *et al.* (2019) shall be adopted. It is sufficient to establish that the partial derivative of the above system (1) exists and are continuous. Consider

$$\begin{cases}
f_{1} = \pi - \nabla S - \mu S \\
f_{2} = (1 - \sigma) \nabla S - k_{1} E_{u} \\
f_{3} = \sigma \nabla S + \alpha E_{u} - k_{2} E_{s} \\
f_{4} = \varepsilon_{1} E_{u} - k_{3} I_{u} \\
f_{5} = \varepsilon_{2} E_{s} - k_{4} I_{s} \\
f_{6} = \omega_{1} E_{s} + \omega_{2} I_{u} + \omega_{3} I_{s} - k_{5} Q \\
f_{7} = \eta_{1} E_{s} + \eta_{2} I_{u} + \eta_{3} I_{s} + \eta_{4} Q - \mu R
\end{cases}$$
(4)

where $k_1 = (\varepsilon_1 + \alpha + \mu - \chi_1), k_2 = (\omega_1 + \varepsilon_2 + \eta_1 + \mu), k_3 = (\omega_2 + \eta_2 + \tau_1 + \mu),$

 $k_4 = (\omega_3 + \eta_3 + \tau_2 + \mu)$ and $k_5 = (\eta_4 + \tau_3 + \mu)$. Using system (4) together with eq. (2), the partial derivative of f_i , i = 1, 2, ..., 7 with respect to compartments S, E_u, E_s, I_u, I_s, Q and R are obtained as:

$$\begin{split} \left|\frac{\partial f_{1}}{\partial S}\right| &= \left|-\nabla - \mu\right| < \infty, \left|\frac{\partial f_{1}}{\partial E_{u}}\right| = \left|-\beta S\right| < \infty, \left|\frac{\partial f_{1}}{\partial E_{s}}\right| = \left|-\beta \delta_{1} S\right| < \infty, \\ \left|\frac{\partial f_{1}}{\partial I_{u}}\right| &= \left|-\beta \delta_{2} S\right| < \infty, \left|\frac{\partial f_{1}}{\partial I_{s}}\right| = \left|-\beta \delta_{3} S\right| < \infty, \left|\frac{\partial f_{1}}{\partial Q}\right| = \left|-\beta \delta_{4} S\right| < \infty, \left|\frac{\partial f_{1}}{\partial R}\right| = 0 < \infty, \\ \left|\frac{\partial f_{2}}{\partial S}\right| &= \left|(1 - \sigma)\nabla\right| < \infty, \left|\frac{\partial f_{2}}{\partial E_{u}}\right| = \left|(1 - \sigma)\beta S - k_{1}\right| < \infty, \left|\frac{\partial f_{2}}{\partial E_{s}}\right| = \left|(1 - \sigma)\beta \delta_{1} S\right| < \infty, \\ \left|\frac{\partial f_{2}}{\partial I_{u}}\right| &= \left|(1 - \sigma)\beta \delta_{2} S\right| < \infty, \left|\frac{\partial f_{2}}{\partial I_{s}}\right| = \left|(1 - \sigma)\beta \delta_{3} S\right| < \infty, \left|\frac{\partial f_{2}}{\partial Q}\right| = \left|(1 - \sigma)\beta \delta_{4} S\right| < \infty, \\ \left|\frac{\partial f_{2}}{\partial R}\right| &= 0 < \infty, \left|\frac{\partial f_{3}}{\partial S}\right| = \left|\sigma\nabla\right| < \infty, \left|\frac{\partial f_{3}}{\partial E_{u}}\right| = \left|\sigma\beta S + \alpha\right| < \infty, \left|\frac{\partial f_{3}}{\partial E_{s}}\right| = \left|\sigma\beta\delta_{1} S - k_{2}\right| < \infty, \\ \left|\frac{\partial f_{3}}{\partial I_{u}}\right| &= \left|\sigma\beta\delta_{2} S\right| < \infty, \left|\frac{\partial f_{3}}{\partial I_{s}}\right| = \left|\sigma\beta\delta_{3} S\right| < \infty, \left|\frac{\partial f_{3}}{\partial Q}\right| = \left|\sigma\beta\delta_{4} S\right| < \infty, \\ \left|\frac{\partial f_{3}}{\partial R}\right| &= 0 < \infty, \left|\frac{\partial f_{4}}{\partial S}\right| = 0 < \infty, \left|\frac{\partial f_{4}}{\partial E_{u}}\right| = \left|\varepsilon_{1}\right| < \infty, \left|\frac{\partial f_{4}}{\partial E_{s}}\right| = 0 < \infty, \left|\frac{\partial f_{5}}{\partial H_{u}}\right| = \left|-k_{3}\right| < \infty, \\ \left|\frac{\partial f_{5}}{\partial E_{s}}\right| &= 0 < \infty, \left|\frac{\partial f_{4}}{\partial Q}\right| = 0 < \infty, \left|\frac{\partial f_{4}}{\partial E_{u}}\right| = \left|-k_{4}\right| < \infty, \left|\frac{\partial f_{5}}{\partial S}\right| = 0 < \infty, \left|\frac{\partial f_{5}}{\partial R}\right| = 0 < \infty, \\ \left|\frac{\partial f_{5}}{\partial E_{s}}\right| &= 0 < \infty, \left|\frac{\partial f_{5}}{\partial H_{u}}\right| = 0 < \infty, \left|\frac{\partial f_{5}}{\partial E_{s}}\right| = \left|\omega_{1}\right| < \infty, \left|\frac{\partial f_{5}}{\partial H_{u}}\right| = \left|\omega_{3}\right| < \infty, \\ \left|\frac{\partial f_{6}}{\partial E_{s}}\right| &= \left|-k_{5}\right| < \infty, \left|\frac{\partial f_{6}}{\partial R}\right| = 0 < \infty, \left|\frac{\partial f_{7}}{\partial E_{s}}\right| = 0 < \infty, \left|\frac{\partial f_{5}}{\partial H_{u}}\right| = \left|\omega_{3}\right| < \infty, \\ \left|\frac{\partial f_{6}}{\partial Q}\right| &= \left|-k_{5}\right| < \infty, \left|\frac{\partial f_{6}}{\partial R}\right| = 0 < \infty, \left|\frac{\partial f_{7}}{\partial S}\right| = \left|0 < \infty, \left|\frac{\partial f_{7}}{\partial E_{u}}\right| = \left|0 < \infty, \left|\frac{\partial f_{7}}{\partial E_{s}}\right| = \left|\mu_{3}\right| < \infty, \\ \left|\frac{\partial f_{6}}{\partial H_{u}}\right| &= \left|\lambda_{2}\right| < \infty, \left|\frac{\partial f_{7}}{\partial E_{s}}\right| = \left|\lambda_{3}\right| < \infty, \left|\frac{\partial f_{7}}{\partial Q}\right| = \left|\mu_{4}\right| < \infty, \left|\frac{\partial f_{7}}{\partial R}\right| = \left|-\mu\right| < \infty \right\}$$

Since all the partial derivatives exist and are continuous, then f_i , i = 1, 2, ..., 7 is locally continuous in \mathbb{R}^7_+ with a unique solution by Theorem 1, Lemma 3 and Theorem 2 of Sowole *et al.* (2019).

4.2 Boundedness of the Model

Lemma 1: The closed set

$$\Omega = \left\{ (S, E_u, E_s, I_u, I_s, Q, R) \in \mathbb{R}^7_+ : 0 \le S + E_u + E_s + I_u + I_s + Q + R \le \frac{\pi}{\mu} \right\}$$

is positively invariant with respect to system (3).

Proof: From eq. (1), it is obvious to state that:

$$\frac{dN(t)}{dt} = \frac{dS(t)}{dt} + \frac{dE_u(t)}{dt} + \frac{dE_s(t)}{dt} + \frac{dI_u(t)}{dt} + \frac{dI_s(t)}{dt} + \frac{dQ(t)}{dt} + \frac{dQ(t)}{dt}$$

So that,

$$\frac{dN(t)}{dt} = \pi - \mu N + \chi_1 E_u \tag{6}$$

Applying theorem by Birkhoff and Rota (1989) on eq. (6) to obtain:

$$\frac{dN(t)}{dt} \le \pi - \mu N \tag{7}$$

Solving eq. (7) to obtain,

$$N(t) \le N(0)e^{-\mu t} + \frac{\pi}{\mu}(1 - e^{-\mu t})$$
(8)

Obviously from eq. (8), as $t \to \infty$, $0 \le N(t) \le \frac{\pi}{u}$.

This completes the proof.

4.3 Disease-free Equilibrium state (DFE)

In the absence of COVID-19 infection, the disease-free equilibrium state for the model denoted as Δ_0 is obtained as:

$$\Delta_0 = \left(S^0, E_u^0, E_s^0, I_u^0, I_s^0, Q^0, R^0\right) = \left(\frac{\pi}{\mu}, 0, 0, 0, 0, 0, 0\right)$$
(9)

4.4 Computation of Reproduction Number (R_0) for the Model

The approach of next generation matrix method as adopted by Ibrahim *et al.* (2016) shall be used to compute the effective reproduction number. The associated incidence matrix (F) and transition matrix (V) to system (3), are obtained respectively as:

Thus, the basic reproduction number is obtained from the spectral radius $\rho(FV^{-1})$ as:

$$R_0 = \frac{\beta \pi [A_1 k_3 (\sigma k_1 + \alpha (1 - \sigma)) + A_2 k_2 k_4 (1 - \sigma)]}{\mu k_1 k_2 k_3 k_4 k_5}$$
(10)

where $A_1 = k_4 k_5 \delta_1 + k_4 \omega_2 \delta_4 + \varepsilon_2 k_5 \delta_3 + \omega_4 \varepsilon_2 \delta_4$ and $A_2 = \varepsilon_1 k_5 \delta_2 + \varepsilon_1 \omega_3 \delta_4 + k_3 k_5$

4.5 Pandemic Equilibrium State

The point at which the disease break-out and is persistent in a population is called the pandemic equilibrium state. Let Δ_1 denote COVID-19 persistent equilibrium state for system (3). Solving (3) at steady state gives

$$S^{*} = \frac{\pi}{\nabla^{*} + \mu}, E_{u}^{*} = \frac{(1 - \sigma)\nabla^{*}\pi}{k_{1}(\nabla^{*} + \mu)}, E_{s}^{*} = \frac{[\sigma(\varepsilon_{1} + \mu) + \alpha]\nabla^{*}\pi}{k_{1}k_{2}(\nabla^{*} + \mu)}, I_{u}^{*} = \frac{\varepsilon_{1}(1 - \sigma)\nabla^{*}\pi}{k_{1}k_{3}(\nabla^{*} + \mu)}$$

$$I_{s}^{*} = \frac{\varepsilon_{2}[\sigma(\varepsilon_{1} + \mu) + \alpha]\nabla^{*}\pi}{k_{1}k_{2}k_{4}(\nabla^{*} + \mu)}, Q^{*} = \frac{\{(k_{3}k_{4}\omega_{1} + k_{3}\omega_{3}\varepsilon_{2})[\sigma(\varepsilon_{1} + \mu) + \alpha] + k_{2}k_{4}\omega_{2}\varepsilon_{1}(1 - \sigma)\}\nabla^{*}\pi}{k_{1}k_{2}k_{3}k_{4}k_{5}(\nabla^{*} + \mu)}$$

$$R^{*} = \frac{\{(\eta_{1}k_{3}k_{4}k_{5} + \eta_{3}k_{3}k_{5}\varepsilon_{2} + \eta_{4}(k_{3}k_{4}\omega_{1} + k_{3}\omega_{3}\varepsilon_{2}))[\sigma(\varepsilon_{1} + \mu) + \alpha] + [\eta_{2}k_{2}k_{4}k_{5} + \eta_{4}k_{2}k_{4}\omega_{2}]\varepsilon_{1}(1 - \sigma)\}\nabla^{*}\pi}{\mu k_{1}k_{2}k_{3}k_{4}k_{5}(\nabla^{*} + \mu)}\right\}$$
(11)

Substituting eq. (11) into eq. (2), with further simplification to obtain

$$\nabla^* + \mu = \mu R_0$$

$$\nabla^* = \mu (R_0 - 1)$$
(12)

Substituting eq. (12) into eq. (11), to obtain the pandemic equilibrium state as:

$$S^{*} = \frac{\pi}{\mu R_{0}}$$

$$E_{u}^{*} = \frac{\pi(1-\sigma)(R_{0}-1)}{k_{1}R_{0}}$$

$$E_{s}^{*} = \frac{[\sigma(\varepsilon_{1}+\mu)+\alpha]\pi(R_{0}-1)}{k_{1}k_{2}R_{0}}$$

$$I_{u}^{*} = \frac{\varepsilon_{1}(1-\sigma)\pi(R_{0}-1)}{k_{1}k_{3}R_{0}}$$

$$I_{s}^{*} = \frac{\varepsilon_{2}[\sigma(\varepsilon_{1}+\mu)+\alpha]\pi(R_{0}-1)}{k_{1}k_{2}k_{4}R_{0}}$$

$$Q^{*} = \frac{\{(k_{3}k_{4}\omega_{1}+k_{3}\omega_{3}\varepsilon_{2})[\sigma(\varepsilon_{1}+\mu)+\alpha]+k_{2}k_{4}\omega_{2}\varepsilon_{1}(1-\sigma)\}\pi(R_{0}-1)}{k_{1}k_{2}k_{3}k_{4}k_{5}R_{0}}$$

$$R^{*} = \frac{\{A_{3}[\sigma(\varepsilon_{1}+\mu)+\alpha]+[\eta_{2}k_{2}k_{4}k_{5}+\eta_{4}k_{2}k_{4}\omega_{2}]\varepsilon_{1}(1-\sigma)\}\pi(R_{0}-1)}{\mu k_{1}k_{2}k_{3}k_{4}k_{5}R_{0}}$$

$$(13)$$

Such that $A_3 = \eta_1 k_3 k_4 k_5 + \eta_3 k_3 k_5 \varepsilon_2 + \eta_4 (k_3 k_4 \omega_1 + k_3 \omega_3 \varepsilon_2).$

4.6 Local stability analysis of the Model at DFE

Theorem 2: The disease-free equilibrium of system (3) is locally asymptotically stable if

 $R_0 < 1$ and unstable otherwise.

Proof: Consider the Jacobian matrix of system (4) evaluated at the disease-free equilibrium state Δ_0 , given as:

$$J_{\Delta_{0}} = \begin{pmatrix} -\mu & -\frac{\beta\pi}{\mu} & -\frac{\beta\delta_{1}\pi}{\mu} & -\frac{\beta\delta_{2}\pi}{\mu} & -\frac{\beta\delta_{3}\pi}{\mu} & -\frac{\beta\delta_{4}\pi}{\mu} & 0\\ 0 & \frac{\beta(1-\sigma)\pi}{\mu} - k_{1} & \frac{\beta(1-\sigma)\delta_{1}\pi}{\mu} & \frac{\beta(1-\sigma)\delta_{2}\pi}{\mu} & \frac{\beta(1-\sigma)\delta_{3}\pi}{\mu} & \frac{\beta(1-\sigma)\delta_{4}\pi}{\mu} & 0\\ 0 & \frac{\beta\sigma\pi}{\mu} + \alpha & \frac{\beta\sigma\delta_{1}\pi}{\mu} - k_{2} & \frac{\beta\sigma\delta_{2}\pi}{\mu} & \frac{\beta\sigma\delta_{3}\pi}{\mu} & \frac{\beta\sigma\delta_{4}\pi}{\mu} & 0\\ 0 & \varepsilon_{1} & 0 & -k_{3} & 0 & 0 & 0\\ 0 & 0 & \varepsilon_{2} & 0 & -k_{4} & 0 & 0\\ 0 & 0 & \omega_{1} & \omega_{2} & \omega_{3} & -k_{5} & 0\\ 0 & 0 & \eta_{1} & \eta_{2} & \eta_{3} & \eta_{4} & -\mu \end{pmatrix}$$
(14)

Evaluating $|J_{\Delta_0} - \lambda I| = 0$, to obtain the eigenvalues. Clearly, the first two eigenvalues are obtained from the first and last columns as $\lambda_1 = -\mu$ and $\lambda_2 = -\mu$. The remaining 5 × 5 matrix is given as:

$$\begin{vmatrix} \frac{\beta(1-\sigma)\pi}{\mu} - k_1 - \lambda & \frac{\beta(1-\sigma)\delta_1\pi}{\mu} & \frac{\beta(1-\sigma)\delta_2\pi}{\mu} & \frac{\beta(1-\sigma)\delta_3\pi}{\mu} & \frac{\beta(1-\sigma)\delta_4\pi}{\mu} \\ \frac{\beta\sigma\pi}{\mu} + \alpha & \frac{\beta\sigma\delta_1\pi}{\mu} - k_2 - \lambda & \frac{\beta\sigma\delta_2\pi}{\mu} & \frac{\beta\sigma\delta_3\pi}{\mu} & \frac{\beta\sigma\delta_4\pi}{\mu} \\ \varepsilon_1 & 0 & -k_3 - \lambda & 0 & 0 \\ 0 & \varepsilon_2 & 0 & -k_4 - \lambda & 0 \\ 0 & \omega_1 & \omega_2 & \omega_3 & -k_5 - \lambda \end{vmatrix} = 0$$
(15)

It is important to emphasize that the matrix in eq. (15) is a Metzler matrix. For simplification, using $c_1 = \frac{\beta(1-\sigma)\pi}{\mu}$, $c_2 = \frac{\beta\sigma\pi}{\mu}$ and applying row-echelon form on eq. (15) to obtain the matrix in eq. (16) below:

$$\begin{vmatrix} c_{1} - k_{1} - \lambda & c_{1}\delta_{1} & c_{1}\delta_{2} & c_{1}\delta_{3} & c_{1}\delta_{4} \\ 0 & -\frac{A_{9}}{c_{1} - k_{1}} - \lambda & -\frac{c_{2}(c_{1}\delta_{2} - c_{1}\delta_{3} + \delta_{3}k_{1})}{c_{1} - k_{1}} & -\frac{c_{2}\delta_{3}k_{1}}{c_{1} - k_{1}} & -\frac{c_{2}\delta_{4}k_{1}}{c_{1} - k_{1}} \\ 0 & 0 & -\frac{A_{4}}{A_{9}} - \lambda & -\frac{\varepsilon_{1}c_{1}\delta_{3}A_{5}}{A_{9}} & -\frac{\varepsilon_{1}c_{1}\delta_{4}A_{5}}{A_{9}} \\ 0 & 0 & 0 & 0 & -\frac{A_{6}}{A_{4}} - \lambda & \frac{A_{7}}{A_{4}} \\ 0 & 0 & 0 & 0 & 0 & -\frac{A_{8}}{A_{6}} - \lambda \end{vmatrix} = 0$$
(16)

where

$$\begin{aligned} A_4 &= c_1 c_2 \delta_1 \delta_3 \varepsilon_1 - c_1 c_2 \delta_2^2 \varepsilon_1 + c_1 c_2 \delta_1 k_3 - c_1 c_2 \delta_2 k_3 + c_1 \delta_2 \varepsilon_1 k_2 + c_2 \delta_2 k_1 k_3 + c_1 k_2 k_3 \\ A_5 &= c_2 \delta_1 - c_2 \delta_2 + k_2; \\ A_6 &= c_1 c_2 \delta_1 \delta_3 \varepsilon_1 k_4 - c_1 c_2 \delta_2^2 \varepsilon_1 k_4 - c_1 c_2 \delta_2 \delta_3 \varepsilon_1 \varepsilon_2 + c_1 c_2 \delta_3^2 \varepsilon_1 \varepsilon_2 + c_1 c_2 \delta_1 k_3 k_4 - c_1 c_2 \delta_2 k_3 k_4 + c_2 \delta_2 k_1 k_3 k_4 + c_2 \delta_3 \varepsilon_2 k_1 k_3 + c_1 k_2 k_3 k_4 - k_1 k_2 k_3 k_4; \\ A_7 &= (c_1 \delta_2 \varepsilon_1 - c_1 \delta_3 \varepsilon_1 - k_1 k_3) \varepsilon_2 c_2 \delta_4; \\ A_8 &= c_1 c_2 \delta_1 \delta_3 \varepsilon_1 k_4 k_5 + c_1 c_2 \delta_1 \delta_4 \varepsilon_1 k_4 \omega_2 - c_1 c_2 \delta_2^2 \varepsilon_1 k_4 k_5 - c_1 c_2 \delta_2 \delta_3 \varepsilon_1 \varepsilon_2 k_5 - c_1 c_2 \delta_2 \delta_4 \varepsilon_1 \omega_2 k_4 + c_1 c_2 \delta_3 \delta_4 \varepsilon_1 \omega_2 k_4 + c_1 c_2 \delta_3^2 \varepsilon_1 \varepsilon_2 k_5 + c_1 c_2 \delta_3 \delta_4 \varepsilon_1 \varepsilon_2 \omega_3 + c_1 c_2 \delta_3 \delta_4 \varepsilon_1 \omega_1 k_4 + c_1 c_2 \delta_1 k_3 k_4 k_5 - c_1 c_2 \delta_2 k_3 k_4 k_5 + c_1 \delta_2 \varepsilon_1 k_2 k_4 k_5 + c_2 \delta_3 \varepsilon_2 k_1 k_3 k_4 k_5 - c_1 c_2 \delta_2 k_3 k_4 k_5 + c_1 \delta_2 \varepsilon_1 k_2 k_4 k_5 + c_1 \delta_2 \varepsilon_1 k_2 k_4 k_5 + c_2 \delta_3 \varepsilon_2 k_1 k_3 k_4 k_5 - c_1 c_2 \delta_2 k_2 k_4 k_5 + c_1 \delta_2 \varepsilon_1 k_2 k_4 k_5 + c_2 \delta_3 \varepsilon_2 k_1 k_3 k_4 k_5 - c_1 c_2 \delta_2 \delta_4 \varepsilon_1 k_1 k_3 k_4 \omega_1 + c_1 k_2 k_3 k_4 k_5 - c_1 c_2 \delta_2 \delta_4 \varepsilon_1 k_1 k_3 k_4 \omega_1 + c_1 k_2 k_3 k_4 k_5 - k_1 k_2 k_3 k_4 k_5 + c_2 \delta_3 \varepsilon_2 k_1 k_3 k_5 + c_2 \delta_4 \varepsilon_2 k_1 k_3 \omega_3 + c_2 \delta_4 k_1 k_3 k_4 \omega_1 + c_1 k_2 k_3 k_4 k_5 - k_1 k_2 k_3 k_4 k_5 + c_1 \delta_2 \varepsilon_1 k_2 k_4 k_5 + c_2 \delta_3 \varepsilon_2 k_1 k_3 k_4 k_5 + c_2 \delta_4 \varepsilon_2 k_1 k_3 \omega_3 + c_2 \delta_4 k_1 k_3 k_4 \omega_1 + c_1 k_2 k_3 k_4 k_5 - k_1 k_2 k_3 k_4 k_5 + c_1 \delta_2 \varepsilon_1 k_2 k_4 k_5 + c_1 k_2 k_3 k_4 k_5 + c_1 \delta_2 \varepsilon_1 k_2 k_4 k_5 + c_1 k_2 k_3 k_4 k_5 + c_1 \delta_2 \varepsilon_1 k_2 k_4 k_5 + c_1 \delta_2 \varepsilon_1 k_4$$

From evaluation, A_8 is the determinant of the reduced 5 × 5 matrix which is positive by the properties of Metzler-matrix (Corentin & Khammash, 2015). For stability criteria to be satisfied, A_6 must be negative. $A_6 < 0$ implies;

$$c_{1}c_{2}\delta_{1}\delta_{3}\varepsilon_{1}k_{4} - c_{1}c_{2}\delta_{2}^{2}\varepsilon_{1}k_{4} - c_{1}c_{2}\delta_{2}\delta_{3}\varepsilon_{1}\varepsilon_{2} + c_{1}c_{2}\delta_{3}^{2}\varepsilon_{1}\varepsilon_{2} + c_{1}c_{2}\delta_{1}k_{3}k_{4} - c_{1}c_{2}\delta_{2}k_{3}k_{4} + c_{1}\delta_{2}\varepsilon_{1}k_{2}k_{4} + c_{2}\delta_{2}k_{1}k_{3}k_{4} + c_{2}\delta_{3}\varepsilon_{2}k_{1}k_{3} + c_{1}k_{2}k_{3}k_{4} - k_{1}k_{2}k_{3}k_{4} < 0$$
(17)
$$c_{1}c_{2}\delta_{1}\delta_{3}\varepsilon_{1}k_{4} - c_{1}c_{2}\delta_{2}^{2}\varepsilon_{1}k_{4} - c_{1}c_{2}\delta_{2}\delta_{3}\varepsilon_{1}\varepsilon_{2} + c_{1}c_{2}\delta_{3}^{2}\varepsilon_{1}\varepsilon_{2} + c_{1}c_{2}\delta_{1}k_{3}k_{4} - c_{1}c_{2}\delta_{2}k_{3}k_{4} + c_{1}\delta_{2}\varepsilon_{1}k_{2}k_{4} + c_{2}\delta_{2}c_{1}k_{3}k_{4} + c_{2}\delta_{3}\varepsilon_{2}k_{1}k_{3} + c_{1}k_{2}k_{3}k_{4} < k_{1}k_{2}k_{3}k_{4}$$
(18)

Replacing c_1 , c_2 and multiply both sides of inequality in eq. (18) by k_5 with further simplification to obtain

$$\beta \pi [(k_4 k_5 \delta_1 + k_4 \omega_2 \delta_4 + \varepsilon_2 k_5 \delta_3 + \omega_4 \varepsilon_2 \delta_4) k_3 (\sigma k_1 + \alpha (1 - \sigma)) + (\varepsilon_1 k_5 \delta_2 + \varepsilon_1 \omega_3 \delta_4 + k_3 k_5) k_2 k_4 (1 - \sigma)] / \mu < k_1 k_2 k_3 k_4 k_5$$
Dividing eq. (19) by the RHS to obtain $R_0 < 1$ which complete the proof. (19)

4.7 Global Stability at DFE

Consider a time-dependent Lyapunov function

$$L = b_1 E_u + b_2 E_s + b_3 I_u + b_4 I_s + b_5 Q,$$
(20)

where the parameters b_i , i = 1, 2, ..., 5 are given as:

$$b_{1} = \frac{\mu R_{0}}{\pi}$$

$$b_{2} = \frac{\langle \eta_{1}k_{3}k_{4}k_{5} + \eta_{4}(k_{3}k_{4}\omega_{1} + k_{3}\omega_{3}\varepsilon_{2})\rangle[\sigma(\varepsilon_{1} + \mu) + \alpha] + [\eta_{2}k_{2}k_{4}k_{5} + \eta_{4}k_{2}k_{4}\omega_{2}]\varepsilon_{1}}{\eta_{1}k_{1}k_{2}k_{4}}$$

$$b_{3} = \frac{(\sigma\delta_{2}\delta_{3} + \delta_{4}\varepsilon_{1}\omega_{1} + \omega_{1}\delta_{2}\varepsilon_{1} + \omega_{2}\delta_{3}\varepsilon_{1} + \eta_{4}k_{1}k_{3})}{\tau_{1}k_{1}k_{2}k_{3}k_{4}k_{5}}$$

$$b_{4} = \frac{\beta\delta_{3}}{\tau_{2}}$$

$$b_{5} = \frac{\beta\delta_{3}}{\tau_{3}k_{5}}$$

$$(21)$$

Differentiating eq. (20) and substituting eq. (3) and eq. (2) in turn to obtain:

$$\frac{dL}{dt} = b_1 \frac{dE_u}{dt} + b_2 \frac{dE_s}{dt} + b_3 \frac{dI_u}{dt} + b_4 \frac{dI_s}{dt} + b_5 \frac{dQ}{dt}$$
$$\frac{dL}{dt} = b_1 ((1 - \sigma)\nabla S - k_1 E_u) + b_2 (\sigma \nabla S + \alpha E_u - k_2 E_s) + b_3 (\varepsilon_1 E_u - k_3 I_u) + b_4 (\varepsilon_2 E_s - k_4 I_s) + b_5 (\omega_1 E_s + \omega_2 I_u + \omega_3 I_s - k_5 Q)$$

 $= b_1 ((1 - \sigma)[\beta(E_u + \delta_1 E_s + \delta_2 I_u + \delta_3 I_s + \delta_4 Q)]S - k_1 E_u) + b_2 (\sigma[\beta(E_u + \delta_1 E_s + \delta_2 I_u + \delta_3 I_s + \delta_4 Q)]S + \alpha E_u - k_2 E_s) + b_3 (\varepsilon_1 E_u - k_3 I_u) + b_4 (\varepsilon_2 E_s - k_4 I_s) + b_5 (\omega_1 E_s + \omega_2 I_u + \omega_3 I_s - k_5 Q)$

 $= (b_{1}(1-\sigma)\beta S + b_{2}\sigma\beta S + b_{3}\varepsilon_{1} - b_{1}k_{1})E_{u} + (b_{1}(1-\sigma)\delta_{1}\beta S + b_{2}\sigma\delta_{1}\beta S + b_{4}\varepsilon_{2} + b_{5}\omega_{1} - b_{2}k_{2})E_{s} + (b_{1}(1-\sigma)\delta_{2}\beta S + b_{2}\sigma\delta_{2}\beta S + \omega_{2}b_{5} - b_{3}k_{3})I_{u} + (b_{1}(1-\sigma)\delta_{3}\beta S + b_{2}\sigma\delta_{3}\beta S + \omega_{3}b_{5} - b_{4}k_{4})I_{s} + (b_{1}(1-\sigma)\delta_{4}\beta S + b_{2}\sigma\delta_{4}\beta S - b_{5}k_{5})Q$ (22)

Obviously, from eq. (9), $S(t) \le N(t) \le \frac{\pi}{\mu'}$, so that eq. (22) becomes:

$$\frac{dL}{dt} \le \left(\frac{b_1(1-\sigma)\beta\pi}{\mu} + \frac{b_2\sigma\beta\pi}{\mu} + b_3\varepsilon_1 - b_1k_1\right)E_u + \left(\frac{b_1(1-\sigma)\delta_1\beta\pi}{\mu} + \frac{b_2\sigma\delta_1\beta\pi}{\mu} + b_4\varepsilon_2 + b_5\omega_1 - b_2k_2\right)E_s + \left(\frac{b_1(1-\sigma)\delta_2\beta\pi}{\mu} + \frac{b_2\sigma\delta_2\beta\pi}{\mu} + \omega_2b_5 - b_3k_3\right)I_u + \left(\frac{b_1(1-\sigma)\delta_3\beta\pi}{\mu} + \frac{b_2\sigma\delta_3\beta\pi}{\mu} + \omega_3b_5 - b_4k_4\right)I_s + + \left(\frac{b_1(1-\sigma)\delta_4\beta\pi}{\mu} + \frac{b_2\sigma\delta_4\beta\pi}{\mu} - b_5k_5\right)Q$$
(23)

Inserting eq. (21) into eq. (23) with further simplification, to obtain:

$$\frac{dL}{dt} \le \left(\beta(E_u + \delta_1 E_s + \delta_2 I_u + \delta_3 I_s + \delta_4 Q)\right)(R_0 - 1)$$
(24)

From eq. (24), it can be observed that whenever $R_0 \le 1$ then $\frac{dL}{dt} \le 0$. It follows from LaSalle's principle (LaSalle & Lefschetz, 1961) that every solution of the system (3) with initial conditions in Lemma 1 approaches Ω as $t \to \infty$. Thus, since the region Ω is positively-

invariant, the disease-free equilibrium Δ_0 of the COVID-19 model is globally asymptotically stable in Ω if $R_0 \leq 1$.

4.8 Bifurcation analysis of the model

Bifurcation theory primarily deals with the change in stability criteria of a system of differential equations. A bifurcation value is the point where changes in stability occurs. The bifurcation property for the developed model shall be studied using center manifold theory described in Theorem 4.1 of Castillo-Chavez and Song (2004). To establish the local stability of COVID-19 pandemic equilibrium, bifurcation analysis is performed at the disease-free equilibrium Δ_0 . For easy representation, let $S(t) = y_1(t)$, $E_u(t) = y_2(t)$, $E_s(t) = y_3(t)$,

$$I_u(t) = y_4(t), I_s(t) = y_5(t), Q(t) = y_6(t) \text{ and } R(t) = y_7(t), \text{ and the system (3) becomes}$$

$$\frac{dy_{1}}{dt} = \pi - (\nabla + \mu)y_{1}
\frac{dy_{2}}{dt} = (1 - \sigma)\nabla y_{1} - k_{1}y_{2}
\frac{dy_{3}}{dt} = \sigma\nabla y_{1} + \alpha y_{2} - k_{2}y_{3}
\frac{dy_{4}}{dt} = \varepsilon_{1}y_{2} - k_{3}y_{4}
\frac{dy_{5}}{dt} = \varepsilon_{2}y_{3} - k_{4}y_{5}
\frac{dy_{6}}{dt} = \omega_{1}y_{3} + \omega_{2}y_{4} + \omega_{3}y_{5} - k_{5}y_{6}
\frac{dy_{7}}{dt} = \eta_{1}y_{3} + \eta_{2}y_{4} + \eta_{3}y_{5} + \eta_{4}y_{6} - \mu y_{7}$$
(25)

Chosen the bifurcation parameter when $R_0 = 1$ as $\beta = \beta^*$, then, from eq. (10),

$$\beta^* = \frac{\mu k_1 k_2 k_3 k_4 k_5}{\pi [A_1 k_3 (\sigma k_1 + \alpha (1 - \sigma)) + A_2 k_2 k_4 (1 - \sigma)]}.$$
(26)

If we denote the left eigenvector of matrix in eq. (14) at the DFE equilibrium point as

 $V = (v_1, v_2, v_3, v_4, v_5, v_6, v_7)$, then:

$$J_{left} = \begin{pmatrix} v_1 \\ v_2 \\ v_3 \\ v_4 \\ v_5 \\ v_6 \\ v_7 \end{pmatrix}^T \begin{pmatrix} -\mu & -\frac{\beta\pi}{\mu} & -\frac{\beta\delta_1\pi}{\mu} & -\frac{\beta\delta_2\pi}{\mu} & -\frac{\beta\delta_3\pi}{\mu} & -\frac{\beta\delta_4\pi}{\mu} & 0 \\ 0 & \frac{\beta(1-\sigma)\pi}{\mu} - k_1 & \frac{\beta(1-\sigma)\delta_1\pi}{\mu} & \frac{\beta(1-\sigma)\delta_2\pi}{\mu} & \frac{\beta(1-\sigma)\delta_3\pi}{\mu} & \frac{\beta(1-\sigma)\delta_4\pi}{\mu} & 0 \\ 0 & \frac{\beta\sigma\pi}{\mu} + \alpha & \frac{\beta\sigma\delta_1\pi}{\mu} - k_2 & \frac{\beta\sigma\delta_2\pi}{\mu} & \frac{\beta\sigma\delta_3\pi}{\mu} & \frac{\beta\sigma\delta_4\pi}{\mu} & 0 \\ 0 & \varepsilon_1 & 0 & -k_3 & 0 & 0 & 0 \\ 0 & 0 & \varepsilon_2 & 0 & -k_4 & 0 & 0 \\ 0 & 0 & \omega_1 & \omega_2 & \omega_3 & -k_5 & 0 \\ 0 & 0 & \eta_1 & \eta_2 & \eta_3 & \eta_4 & -\mu \end{pmatrix} = 0$$
(27)

Solving eq. (27) to obtain:

$$\begin{array}{l} \left. \begin{array}{l} v_{1}=0, \quad v_{2}>0 \; (free), \quad v_{3}=-\left(\frac{\varepsilon_{1}k_{5}c_{1}\delta_{2}+c_{1}k_{3}k_{5}+\varepsilon_{1}\omega_{3}c_{1}\delta_{4}}{\varepsilon_{1}k_{5}c_{2}\delta_{2}+c_{2}k_{3}k_{5}+ak_{3}k_{5}+\varepsilon_{1}\omega_{2}c_{2}\delta_{4}}\right) v_{2}, \\ v_{4}=\left(\frac{(c_{2}+\alpha)[\varepsilon_{1}k_{5}c_{1}\delta_{2}+c_{1}k_{3}k_{5}+k_{1}\omega_{3}c_{1}\delta_{4}]-(c_{1}-k_{1})[\varepsilon_{1}k_{5}c_{2}\delta_{2}+c_{2}k_{3}k_{5}+ak_{3}k_{5}+\varepsilon_{1}\omega_{2}c_{2}\delta_{4}}]}{\varepsilon_{1}k_{5}c_{2}\delta_{2}+c_{2}k_{3}k_{5}+ak_{3}k_{5}+\varepsilon_{1}\omega_{2}c_{2}\delta_{4}}\right) v_{2} \\ v_{5}=\left(\frac{k_{5}(c_{2}\delta_{1}-k_{3})[\varepsilon_{1}k_{5}c_{1}\delta_{2}+c_{1}k_{3}k_{5}-k_{1}k_{3}k_{5}+\varepsilon_{1}\omega_{3}c_{1}\delta_{4}]-(c_{1}\delta_{1}k_{5}+\omega_{1}c_{1}\delta_{4})[\varepsilon_{1}k_{5}c_{2}\delta_{2}+c_{2}k_{3}k_{5}+ak_{3}k_{5}+\varepsilon_{1}\omega_{2}c_{2}\delta_{4}]}{\varepsilon_{2}k_{5}(\varepsilon_{1}k_{5}c_{2}\delta_{2}+c_{2}k_{3}k_{5}+ak_{3}k_{5}+\varepsilon_{1}\omega_{2}c_{2}\delta_{4}]}\right) v_{2} \\ v_{6}=\left(\frac{c_{1}\delta_{4}(\varepsilon_{1}k_{5}c_{2}\delta_{2}+c_{2}k_{3}k_{5}+ak_{3}k_{5}+\varepsilon_{1}\omega_{2}c_{2}\delta_{4})-c_{2}\delta_{4}[\varepsilon_{1}k_{5}c_{1}\delta_{2}-c_{1}k_{3}k_{5}-k_{1}k_{3}k_{5}+\varepsilon_{1}\omega_{3}c_{1}\delta_{4}]}{k_{5}(\varepsilon_{1}k_{5}c_{2}\delta_{2}+c_{2}k_{3}k_{5}+ak_{3}k_{5}+\varepsilon_{1}\omega_{2}c_{2}\delta_{4})}\right) v_{7}=0 \end{array} \right) \\ \end{array}$$

Similarly, the right eigenvector for matrix in eq. (14) denoted as

 $U = (u_1, u_2, u_3, u_4, u_5, u_6, u_7)^T$ is obtained by solving eq. (29) below.

$$J_{right} = \begin{pmatrix} -\mu & -\frac{\beta\pi}{\mu} & -\frac{\beta\delta_{1}\pi}{\mu} & -\frac{\beta\delta_{2}\pi}{\mu} & -\frac{\beta\delta_{3}\pi}{\mu} & -\frac{\beta\delta_{4}\pi}{\mu} & 0\\ 0 & \frac{\beta(1-\sigma)\pi}{\mu} - k_{1} & \frac{\beta(1-\sigma)\delta_{1}\pi}{\mu} & \frac{\beta(1-\sigma)\delta_{2}\pi}{\mu} & \frac{\beta(1-\sigma)\delta_{3}\pi}{\mu} & \frac{\beta(1-\sigma)\delta_{4}\pi}{\mu} & 0\\ 0 & \frac{\beta\sigma\pi}{\mu} + \alpha & \frac{\beta\sigma\delta_{1}\pi}{\mu} - k_{2} & \frac{\beta\sigma\delta_{2}\pi}{\mu} & \frac{\beta\sigma\delta_{3}\pi}{\mu} & \frac{\beta\sigma\delta_{4}\pi}{\mu} & 0\\ 0 & \varepsilon_{1} & 0 & -k_{3} & 0 & 0 & 0\\ 0 & 0 & \varepsilon_{2} & 0 & -k_{4} & 0 & 0\\ 0 & 0 & \omega_{1} & \omega_{2} & \omega_{3} & -k_{5} & 0\\ 0 & 0 & \eta_{1} & \eta_{2} & \eta_{3} & \eta_{4} & -\mu \end{pmatrix} \begin{pmatrix} u_{1}\\ u_{2}\\ u_{3}\\ u_{4}\\ u_{5}\\ u_{6}\\ u_{7} \end{pmatrix} = 0$$
(29)

Expanding and simultaneously solving eq. (29) to get

$$u_{1} = 0, \quad u_{2} > 0 \ (free), \quad u_{3} = -\left(\frac{k_{1}k_{3}k_{4}k_{5}(c_{1}-k_{1})+c_{1}\delta_{1}\varepsilon_{1}k_{3}k_{4}k_{5}+c_{1}\delta_{4}\varepsilon_{1}\omega_{2}k_{1}k_{4}}{k_{1}k_{3}(c_{1}\delta_{1}k_{4}k_{5}+c_{1}\delta_{3}\varepsilon_{2}k_{5}+c_{1}\delta_{4}\omega_{1}k_{4}+\varepsilon_{2}\omega_{2}c_{1}\delta_{4})}\right)u_{2}$$

$$u_{4} = \frac{\varepsilon_{1}}{k_{3}}u_{2}; \quad u_{5} = \frac{\varepsilon_{2}}{k_{4}}\left(\frac{k_{1}k_{3}k_{4}k_{5}(c_{1}-k_{1})+c_{1}\delta_{1}\varepsilon_{1}k_{3}k_{4}k_{5}+c_{1}\delta_{4}\varepsilon_{1}\omega_{2}k_{1}k_{4}}{k_{1}k_{3}(c_{1}\delta_{1}k_{4}k_{5}+c_{1}\delta_{3}\varepsilon_{2}k_{5}+c_{1}\delta_{4}\omega_{1}k_{4}+\varepsilon_{2}\omega_{2}c_{1}\delta_{4})}\right)u_{2}$$

$$v_{6} = \left(\frac{\omega_{2}\varepsilon_{1}k_{1}k_{3}k_{4}k_{5}(c_{1}\delta_{1}k_{4}k_{5}+c_{1}\delta_{3}\varepsilon_{2}k_{5}+c_{1}\delta_{4}\omega_{1}k_{4}+\varepsilon_{2}\omega_{2}c_{1}\delta_{4})-(\omega_{1}k_{4}+\varepsilon_{2}\omega_{3})[k_{1}k_{3}k_{4}k_{5}(c_{1}-k_{1})+c_{1}\delta_{1}\varepsilon_{1}k_{3}k_{4}k_{5}+c_{1}\delta_{4}\varepsilon_{1}\omega_{2}k_{1}k_{4}]}{k_{1}k_{3}k_{4}k_{5}(c_{1}\delta_{1}k_{4}k_{5}+c_{1}\delta_{3}\varepsilon_{2}k_{5}+c_{1}\delta_{4}\omega_{1}k_{4}+\varepsilon_{2}\omega_{2}c_{1}\delta_{4})}\right)u_{2}$$

$$v_{7} = \left(\frac{k_{1}k_{4}A_{10}(c_{1}\delta_{1}k_{4}k_{5}+c_{1}\delta_{3}\varepsilon_{2}k_{5}+c_{1}\delta_{4}\omega_{1}k_{4}+\varepsilon_{2}\omega_{2}c_{1}\delta_{4})-A_{11}[k_{1}k_{3}k_{4}k_{5}(c_{1}-k_{1})+c_{1}\delta_{1}\varepsilon_{1}k_{3}k_{4}k_{5}+c_{1}\delta_{4}\varepsilon_{1}\omega_{2}k_{1}k_{4}]}{k_{1}k_{3}k_{4}k_{5}(c_{1}\delta_{1}k_{4}k_{5}+c_{1}\delta_{3}\varepsilon_{2}k_{5}+c_{1}\delta_{4}\omega_{1}k_{4}+\varepsilon_{2}\omega_{2}c_{1}\delta_{4})}\right)u_{2}$$

$$(30)$$

where $A_{10} = \eta_1 \varepsilon_2 k_5 + \eta_4 \varepsilon_1 \omega_2$ and $A_{11} = \eta_1 k_4 k_5 - \eta_3 \varepsilon_2 k_5 + \eta_4 (\omega_1 k_4 + \varepsilon_2 \omega_3)$

The local dynamics of system (3) around equilibrium point Δ_0 are totally determined by *a* and *b* denoted as

$$a = \sum_{k,i,j=1}^{n} v_k u_i u_j \frac{\partial^2 g_k(0,0)}{\partial x_i \partial x_j}$$

$$b = \sum_{k,i,j=1}^{n} v_k u_i \frac{\partial^2 g_k(0,0)}{\partial x_i \partial \phi}$$
(31)

For the computations of a and b (Castillo-Chavez & Song, 2004; Mukandavire *et al.*, 2009), the non-zero partial derivatives of system (4) at the DFE are obtained as

Substituting (30) and (32) into (31) to obtain

$$a = \frac{-2v_2k_1\beta^*u_2^2(A_1k_3(\sigma k_1 + \alpha(1 - \sigma)) + A_2k_2k_4(1 - \sigma))}{\mu k_1k_2k_3k_4k_5}$$
(33)

To get *b*, the non-zero second order derivatives of system (4) at DFE is given as:

$$\frac{\partial^2 f_1}{\partial y_2 \partial \beta^*} = \frac{\partial^2 f_1}{\partial \beta^* \partial y_2} = -\frac{\pi}{\mu}$$

$$\frac{\partial^2 f_1}{\partial y_3 \partial \beta^*} = \frac{\partial^2 f_1}{\partial \beta^* \partial y_3} = -\frac{\pi \delta_1}{\mu}$$

$$\frac{\partial^2 f_1}{\partial y_4 \partial \beta^*} = \frac{\partial^2 f_1}{\partial \beta^* \partial y_4} = -\frac{\pi \delta_2}{\mu},$$

$$\frac{\partial^2 f_1}{\partial y_5 \partial \beta^*} = \frac{\partial^2 f_1}{\partial \beta^* \partial y_5} = -\frac{\pi \delta_3}{\mu}$$

$$\frac{\partial^2 f_1}{\partial y_6 \partial \beta^*} = \frac{\partial^2 f_1}{\partial \beta^* \partial y_6} = -\frac{\pi \delta_4}{\mu}$$
(34)

using (34) and (29) in (31) to have

$$b = \frac{v_2 \pi u_2^2 (A_1 k_3 (\sigma k_1 + \alpha (1 - \sigma)) + A_2 k_2 k_4 (1 - \sigma))}{\mu k_1 k_2 k_3 k_4 k_5}$$
(35)

Since a < 0 and b > 0, we conclude by *item iv* of Theorem 4.1 of Castillo-Chavez and Song (2004) that the model exhibits forward bifurcation when $R_0 = 1$. Hence establishing that the unique COVID-19 endemic equilibrium is locally asymptotically stable whenever $R_0 > 1$.

5. Results Discussion

The system in eq. (3) governing the developed COVID-19 model was tested for the existence and uniqueness of the solution using Lipschitz criteria for the solution of a system of differential equations. It was discovered that the solution for the model exists and also unique in the feasible region of the model. The model exhibits positive characteristics and is bounded at all time regardless of the initial population to the carrying capacity $\left(N(t) \leq \frac{\pi}{\mu}\right)$.

The model equations have two distinct equilibrium points, which are; the disease-free and pandemic equilibrium. The qualitative characteristics of the model depend largely on the

reproduction number (which is defined as the number of new cases that may arise from a single infected case that enters a susceptible population). The reproduction number for the model was computed using the next-generation approach. Stability analysis of the model was done based on the reproduction number of the developed model and was obtained to be locally and globally stable for DFE whenever $R_0 < 1$. This implies that, if the number of new case(s) that may arise from an infected individual is less than unity, the disease will be wiped out with little/no intervention. However, the result of bifurcation established the existence of forward bifurcation at the DFE whenever $R_0 \ge 1$. This implies that whenever the basic reproduction number of the developed COVID-19 is greater than or equal to unity, there is a progression from a DFE stable state to a disease persistent state. According to Yue et al. (2021), the estimated basic reproduction number for COVID-19 at the early stage, based on the intrinsic growth rate of the epidemic curve ranged from 2.24 to 3.58. However, their analysis using six countries with the largest cumulative numbers of infected cases around the world with strict implementation measures of prevention (social distancing, use of face mask, hand-sanitizing, total closure of borders, and self-isolation/quarantine) put the reproduction number at a decline rate of \sim 3.0 to 1.0 within forty-eight days in India (Yue, et al., 2021). Their analysis also established that in Germany, due to poor implementation of the measures, the rate of reduction in reproduction number is not as rapid as other countries. From the result obtained in this work, for the reproduction number to be further reduced rapidly, case detection must be properly handled, especially by the medical practitioner. Its effect on the force of infection is significant and when properly enforced, it can help boost the chance of winning the war against the third wave of the infection.

6. Conclusion

In this work, a new deterministic mathematical model was formulated to study the dynamics of coronavirus disease taking cognizance of the impact of preventive measures and case detection. The model was analysed for the existence and uniqueness of the solution. The stability and bifurcation analysis of the model established that the disease-free equilibrium state will be maintained as long as all efforts directed keeps the reproduction number to be less than unity, otherwise, a stable pandemic equilibrium will persist.

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