Mathematical Modeling Analysis For COVID-19 With Contact Tracing And Quarantine Control Measures

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ABSTRACT

There is currently no approved, recognized and acceptable vaccine or medicine for the treatment of the novel corona virus disease, COVID-19. Thus, non-pharmaceutical interventions such as contact tracing and quarantine are used to control the spread of the infectious disease. Contact tracing and quarantine promptly help to detect new COVID-19 infected persons early before they develop the symptoms and these also help to prevent secondary transmission of the virus in the community. This research study considered a deterministic model for COVI-19 with contact tracing and quarantine as control measure in the dynamics of the COVID-19. The model is developed for the existence of the disease-free equilibrium state. The model shows to be asymptotically stable is less than one and unstable when greater than one. It is then concluded that COVID-19 can be eradicated when contact tracing and quarantine are implemented together.

Keywords: *COVID-19, quarantine, contact tracing, mathematical modeling, disease-free equilibrium state.*

I. INTRODUCTION

Mathematical and Statistical techniques have been used to understand, forecast, and control the spread of infectious diseases like influenza and viral diseases. Some of the techniques have been newly developed, whereas others build upon existing methods from diverse fields which include dynamical systems, stochastic processes, statistical physics, graph theory, statistical inference, probability theory, experimental design methods, operations research, and high performance computing. Mathematically inclined models can be useful in the area of infectious control for two reasons. Firstly, they can be used to predict quantitatively the course of an epidemic, predicting its total size, peak; and time to peak and the impact of infection control interventions including nonlinear interactions that occur when multiple interventions are undertaken. Secondly, they can inform the design of trials and structure statistical analyses to avoid assumptions of serial independence and difficulties with interval censoring and unknown numbers of infectious cases.

It is known very well that mathematical and statistical modeling offers a valuable tool to comprehensively analyze the dynamics of infectious diseases, which reflect population behavior, the availability of public healthcare resources and effectiveness of public health interventions (such as social distancing) [Kiskowski M, Chowell, (2016)]. In the early stages of a new infectious disease outbreak, the transmission dynamics of the infection should be fundamentally understood. The transmission dynamics could offer an insight into the developments in various countries and could determine whether or not the outbreak control measures are exerting a significant effect. However, there are several challenges to such analyses: a delay in symptomatic presentation resulting from the incubation period, the high proportion of unreported cases resulting from limited detection and testing capacity. Furthermore, according to Kucharski et al (2020), data sources might be biased, incomplete or only capture certain aspects of the outbreak dynamics.

Epidemic curves are time series data of the number of infected patients per unit time. They are an essential indication for the seriousness of an epidemic as a function of time. During the preliminary growth phase, the cumulative cases follow on a logarithmic-linear scale an approximately linear relationship with time. Consequently, in the linear range, the number of deaths grows exponentially with time. The number of deaths per unit time is described in the mortality curve and reveals a similar pattern with an approximately exponential growth during the

initial phase of the outbreak, as defined by Ma J (2020). The meaning, on the other hand, is different from the logistic function parameters. The logistical model has been widely used to describe the growth of a population. Similarly, an infectious outbreak can be seen as the growth of a pathogenic agent. Thus, a logistic model seems reasonable since the spread of an infection will stop in the near future [Malato (2020)].

However, several days after the beginning of the disease outbreak, the logistic curve better fitted the description of an infection. The number of persons infected before the end increases, the maximum numbers of new infections often occur on the current or the next day. Although the logistic model appears to be the most sensible one, the shape of the curve would probably shift due to external influences, such as government lockdown actions. Therefore, the prediction models will start to become useful only within a few weeks, presumably after the infection peak as observed by Malato (2020). The ability to understand the effectiveness of lockdown measures in different settings will be crucial in comprehending the dynamics of the epidemic, and increase the likelihood of containing or effectively mitigating the transmission of infectious diseases like SARS-Cov-2.

In December 2019, news emerged about a new flu-like virus affecting people in the city of Wuhan (China). Unfortunately, the virus quickly spread with an exponential increase in the number of confirmed cases in just a few weeks. Despite the strong efforts to contain the virus in Wuhan, it quickly spread to other regions of China, and soon, to other countries in Asia. In January 2020, the World Health Organization (WHO) officially renamed the virus as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and the disease as Coronavirus disease 2019 (COVID-19).

Although many mathematical models have been developed and used in investigating the impact and control of the dynamics of COVID-19, none have considered the combined effects of quarantine and contact tracing. These models have been proved to be helpful in controlling some diseases, specifically Tuberculosis, Severe Acute Respiratory Syndrome (SARS), and Human Immunodeficiency Virus (HIV) [Mubayi et al (2010), Hsieh et al (2010) and Begun et al (2013)]. Hence, this research study considers a mathematical model with contact tracing and quarantine as control measures in the dynamics of COVID-19.

II. MODEL FORMULATION

The deterministic model of corona virus disease (COVID-19) with contact tracing and quarantine is considered. The model is based on the following assumptions:

i. The population is homogeneous
ii. Immigrants from COVID-19 affected population are quarantined for a period of time equivalent to the incubation period of the virus
iii. Treated individuals may become susceptible again when they recover since COVID-19 is not known to confer permanent immunity
iv. Individuals who died of the disease are immediately cremated/buried, thus preventing transmission after death
v. Exposed class of individuals is ignored since incubation period of the disease is short
vi. A natural death rate is assumed in all classes of the model except the quarantined class in which the death rate is assumed a smaller value since quarantined individuals have short stay in the quarantine, that is fourteen days

Table 1: Model variables and parameters

Variable/Parameter	Variable/Parameter Description
$S(t)$	Total number of susceptible individuals at t
$Q(t)$	Total number of quarantined individuals at t
$I(t)$	Total number of infected individuals at t
$T(t)$	Total number of treated individuals at t
β	Disease transmission rate
c_1	Contact tracing rate for susceptible that are exposed individuals
c_2	Contact tracing rate for infected individuals
d_1	Corona Virus Disease induced death rate for infected class
γ	Human recruitment rate

σ	Transfer rate from quarantined class to susceptible class after incubation period without developing symptoms
$\emptyset$	Rate at which treated individuals recover and become susceptible again
ϵ	Immigration rate from Corona Virus Disease affected area
μ	Natural death rate for susceptible, infected and treated classes
μ_1	Death rate for quarantined class
φ	Treatment rate of quarantined persons
α	Treatment rate of individuals other than the quarantined persons

In view of the assumptions of the models stated above, the model equations are derived as follows:

$$\frac{dS}{dt} = \gamma - \frac{\beta SI}{N} + \sigma Q + \emptyset T - \mu S - c_1 S, S(0) = S_0 \quad (1)$$

$$\frac{dQ}{dt} = \epsilon + c_1 S - \sigma Q - \varphi Q - \mu_1 Q, \; Q(0) = Q_0 \quad (2)$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - (\mu + \alpha + d_1)I - c_2 I, \; I(0) = I_0 \quad (3)$$

$$\frac{dT}{dt} = \alpha I - \varphi Q + c_2 I - \mu T - \emptyset T, \; T(0) = T \quad (4)$$

where $S_0, \; Q_0, I_0 \; and \; T_0$ are assumed to be non-negative

III. MODEL ANALYSIS

A. Invariant Rgion

Every solution of the models (1, 2, 3 and 4) with initial conditions in $\mathbb{R}_+^4$ remain or enter the region Ω at all time t. This is essential in the proof of stability analysis of the model. The following lemma is hereby stated.

Lemma: The models (1, 2, 3 and 4) have solutions which are contained in the feasible region $\Omega = \left\{(S, Q, I, T) \epsilon \mathbb{R}_+^4 : N \leq \frac{\epsilon+\gamma}{\mu}\right\}$

Proof: The proof is done that the population of humans at time t, $N(t)$ satisfies the inequality $N(t) \leq \frac{\epsilon+\gamma}{\mu}$. Adding the right sides of the models (1, 2, 3 and 4),

$$\frac{dN}{dt} = \varepsilon + \gamma - \mu(S + I + T) - \mu_1 Q - d_1 I \quad (5)$$

and this gives

$$\frac{dN}{dt} \leq \varepsilon + \gamma - \mu(S + I + T) - \mu_1 Q \quad (6)$$

Since $\mu_1 \geq \mu$, equation (6) can be rewritten as:

$$\frac{dN}{dt} + \mu N \leq \varepsilon + \gamma \quad (7)$$

Using the method of integrating factor to solve equation (7) and applying the initial condition $N(0) = N_0$, this results in:

$$N(t) = \frac{\epsilon+\gamma}{\mu} + \left[N_0 - \frac{\epsilon+\gamma}{\mu}\right] e^{-\mu t} \quad (8)$$

The population size, $N(t) \rightarrow \frac{\epsilon+\gamma}{\mu}$, as $t \rightarrow \infty$ in equation (8), which implies that $0 \leq N(t) \leq \frac{\epsilon+\gamma}{\mu}$. If $N_0 < \frac{\epsilon+\gamma}{\mu}$ then as $t \rightarrow \infty$, the trajectories approach $\frac{\epsilon+\gamma}{\mu}$. If $N_0 > \frac{\epsilon+\gamma}{\mu}$, the solution N(t) decreases to $\frac{\epsilon+\gamma}{\mu}$ as $t \rightarrow \infty$. In either case, the solution approaches $N(t) = \frac{\epsilon+\gamma}{\mu}$ as $t \rightarrow \infty$. Hence, the feasible solution set of the models (1, 2, 3 and 4) enter the region $\Omega = \left\{(S, Q, I, T) \epsilon \mathbb{R}_+^4 : N \leq \frac{\epsilon+\gamma}{\mu}\right\}$, which is a positive invariant set. According to Hethcote (2000), the models (1, 2, 3 and 4) are biologically meaningful and epidemiologically well posed in the region Ω. Therefore, it is sufficient to consider the stability analysis of the models (1, 2, 3 and 4).

B. The Disease Free Equilibrium State And Its Stability

The disease-free equilibrium (DFE), E_0, is a steady state solution where there is no corona virus disease in the population. This is calculated by setting the right hand side of the models (1, 2, 3 and 4) to zero. This gives the following:

$$\gamma - \frac{\beta SI}{N} + \sigma Q + \emptyset T - \mu S - c_1 S = 0 \quad (9)$$

$\epsilon + c_1 S - \sigma Q - \varphi Q - \mu_1 Q = 0$ (10)

$\frac{\beta SI}{N} - (\mu + \alpha + d_1)I - c_2 I = 0$ (11)

$\alpha I - \varphi Q + c_2 I - \mu T - \emptyset T = 0$ (12)

Solving models (9, 10, 11 and 12) simultaneously and simplifying, we have:

$E_0 = \left[\frac{\gamma fg + g\sigma\epsilon + \emptyset\varphi\epsilon}{\mu gf + c_1\varphi\mu + gc_1\mu_1}, \frac{\gamma gc_1 + gc_1\epsilon + g\mu\epsilon}{\mu gf + c_1\varphi\mu + gc_1\mu_1}, 0, \frac{\gamma\varphi c_1 + \varphi c_1\epsilon + \mu\varphi\epsilon}{\mu gf + c_1\varphi\mu + gc_1\mu_1}\right]$ ` (13)

where $f = \sigma + \varphi + \mu_1,\ g = \emptyset + \mu, h = \mu + \alpha + d_1 + c_2$

In order to examine the stability of the DFE, the effective reproduction number R_e is first computed. The effective number is defined in the presence of a control measure whereas the basic reproduction number denoted by R_0 is defined as the absence of controls. The basic reproduction number is the average number of secondary infections produced when one infected person is introduced into a host population where everyone is susceptible; this is as stated by Benyah (2007). R_0 determines whether or not an infectious disease will spread in a given population. If $R_0 < 1$, the disease will die out and when $R_0 > 1$, the disease will become endemic in the population. In the same vein, the effective reproduction number, R_e as defined by Shaban and Mofi (2014) is the average number of new infections generated by a typical infectious individual introduced in a population where contact tracing and quarantine are introduced as measure controls. It is a threshold parameter that governs the spread of disease in a population where control measures are in place. When $R_e < 1$, it means COVID-19 can be eliminated from the population in the presence of contact tracing and quarantine. However, when $R_e > 1$, it implies that COVID-19 will persist in the population where contact tracing and quarantine are implemented. R_e is computed using next generation method described by Driessche and Watmough (2002). Based on the notations in Driessche and Watmough (2002), the effective reproduction number is given by $R_e = \rho(CU^{-1})$, where ρ is the spectral radius of the matrix CU^{-1}.

From the model equations (1 to 4), $F = \frac{\beta SI}{N}$ is the rate of new COVID-19 in I while $V = hI$ is the transfer of individuals in and out of the compartment I by all other means except new infection since we have one infected compartment I.

The associated generation matrices C and U can be found by taking the partial derivatives of F and V with respect to infected compartment I at $DFE\ E_0$. That is $G = \frac{\beta S_0}{N_0}$ is the rate of new infection at $DFE\ E_0$. $U = h$ is the remaining transition terms at $DFE\ E_0$ and $N_0 = S_0 + Q_0 + T_0$. It follows that the effective reproduction number with contact tracing and quarantine measures is given by:

$R_e = \rho(CU^{-1}) = \frac{\beta S_0}{hN_0} = \frac{\beta}{h}\left[\frac{\gamma fg + g\sigma\epsilon + \emptyset\varphi\epsilon}{\gamma fg + g\sigma\epsilon + \emptyset\varphi\epsilon + \mu gf + c_1\varphi\mu + gc_1\mu_1 + \mu gf + c_1\varphi\mu + gc_1\mu_1}\right]$ (14)

The effective reproduction number with quarantine only ($c_1 = 0, c_2 = 0$), R_{eq} is given by

$R_{eq} = \frac{\beta}{h^*}\left[\frac{\gamma fg + g\sigma\epsilon + \emptyset\varphi\epsilon}{\gamma fg + g\sigma\epsilon + \emptyset\varphi\epsilon + \mu gf + \mu gf}\right]$ (15)

where $h^* = \mu + \sigma + d_1$.

While the basic reproduction number R_0 is computed when there is no control measure in the population. That is when $Q = 0, c_1 = 0, c_2 = 0, \sigma = 0, \mu_1 = 0$ and $\varphi = 0$.

Therefore, $R_0 = \frac{\beta}{h^*}$ (16)

From equations (14), (15) and (16), this inequality $R_e < R_{eq} < R_0$ may hold. This means that quarantine as a control measure may reduce the spread of COVID-19 in the population, but not as much as when it is combined with contact tracing measure.

We will examine the local stability of $DFE\ E_0$ using linearization method at E_0 with the following theorem.

Theorem: The disease-free equilibrium state E_0 of the model is locally asymptotically stable if $R_e < 1$ and unstable if $R_e > 1$.

Proof: By linearization method, the Jacobian matrix I_{E0} of the models (1, 2, 3 and 4) evaluated at E_0 is given as:

$$I_{E0} = \begin{bmatrix} -\mu - c_1 & \alpha & -\frac{\beta S_0}{N_0} & \emptyset \\ c_1 & -f & 0 & 0 \\ 0 & 0 & \frac{\beta S_0}{N_0} - h & 0 \\ 0 & \varphi & \alpha + c_2 & -g \end{bmatrix} \quad (17)$$

The characteristics equation of the Jacobian matrix I_{E0} is given as

$$\left(\lambda - \frac{\beta S_0}{N_0} + h\right)(\lambda^3 + A\lambda^2 + B\lambda + C) = 0 \quad (18)$$

where $N_0 = S_0 + Q_0 + T_0$. λ is an eigenvalue of the Jacobian matrix I_{E0}.

$A = g + f + \mu + c_1$, $B = fg + c_1 g + \mu g + \mu f + c_1(\varphi + \mu_1)$, $C = \mu fg + c_1\mu_1 g + c_1\varphi\mu$

For the $DFE\ E_0$ to be locally asymptotically stable, it means that all the eigenvalues of Jacobian matrix I_{E0} (17) will be negative. One of the eigenvalues of the characteristic equation (18), $\lambda = \frac{\beta S_0}{N_0} - h$ is negative if $\frac{\beta S_0}{hN_0} < 1$ where $R_e = \frac{\beta S_0}{hN_0}$ from the definition of R_e in equation (14). The other three eigenvalues are found by solving the equation

$$\lambda^3 + A\lambda^2 + B\lambda + C = 0 \quad (19)$$

Using the Routh-Hurwitz criteria, all roots of the polynomial equation (19) have negative real part, if

i. $A > 0, B > 0, C > 0$

ii. $AB - C > 0$

Condition (i) is satisfied. For (ii), we have $AB - C = c_1\mu(\varphi + 2\mu_1) + c_1^2(g + \mu_1 + \varphi) + g\mu(g + \mu) + fg(2\mu + g + 2c_1 + f) + c_1 f(\varphi + \mu + \mu_1) + c_1 g(g + \mu + \varphi) + f\mu(\mu + f)$. Therefore, all the eigenvalues of Jacobian matrix I_{E0} (17) are negative when $R_e < 1$. Thus, the disease-free equilibrium E_0 is locally asymptotically stable if $R_e < 1$.

IV. CONCLUSION

A deterministic model for the dynamics of COVID-19 is presented as developed and analyzed in this research paper. The mathematical model incorporates quarantine and contact tracing of the infected persons as control measures to evaluate their impact on the COVID-19 dynamics. The existence and stability of the disease-free state is established when the effective reproduction number is less than unity. Therefore, the combined implementation of quarantine and contact tracing measures are seen to have most significant impact in eradicating the COVID-19 in the human population.

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