



## **Basic Reproduction Number of a Mathematical Model of Corona Virus Disease 2019 (Covid-19)**

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### ***Abstract***

*This study aimed at proposing a new model regarding the transmission of Coronavirus Disease 2019 (COVID-19) in human population. The mathematical model was constructed by taking into consideration several epidemiology parameters that are closely identical with the real condition. In the study, an analysis was conducted to determine the presence of disease-free equilibrium (DFE) point. The basic reproduction number was obtained and can be used to determine what happen next in the population with regard to the disease.*

***Keywords:*** *Mathematical Model; Coronavirus Disease; COVID-19; Basic Reproductive Number*

## **Introduction**

The corona virus disease 2019 (COVID-19) pandemic has since December 2019 put so many things at stand still in the world resulting in many losing their livelihood as it is very rapid in its spread. It was first identified to occur in Wuhan city of China and has since become one of the main talking points as it reached the whole world and took thousands of death tolls in a very short period with

uncertainty to its end in all countries. This has necessitated all parties to devise measures in finding treatment and/or vaccine in anticipatory for means to prevent damage on a much wider scale. In mathematical perspective, the concern is closely related to implementation of mathematical model to identify potential solutions. Mathematicians been one of stakeholders who are

always at the forefront of finding solutions to pandemic like this, this time around too they have not been left out. Several mathematical models have since been proposed by many researchers in the field of Mathematics in a bit to contribute toward finding solutions [4, 5]. Mathematical modeling is one of the key tools in epidemic preparation, including the COVID-19 pandemic. The system allows one to comprehend and identify the correlation between COVID-19 spread and several epidemiology parameters, conduct preparatory measures for future planning, and implement best practices of pandemic treatment [4].

At the moment, little studies on the disease transmission are available in the [2][4][5]. The model involved accurate and effective public health interventions. Other authors have proposed mathematical models for predicting COVID-19 cases in different countries [4][5].

Most discussion in most of these proposed models in the previous studies suggest that the virus started from an unknown source and eventually began to spread to human population. In this present study different approach was introduced on mathematical modeling to the virus transmission by also involving the epidemiology parameters adopted from [4].

The work in this model focused mainly on discussion on the basic reproduction number, which is a threshold that determine the spread or not of the virus.

In the following sections we shall elaborate on the construction of the proposed mathematical model and research results in the form of model analysis. The last section proposes several conclusions to the research findings and discussion.

### **Model Formulation**

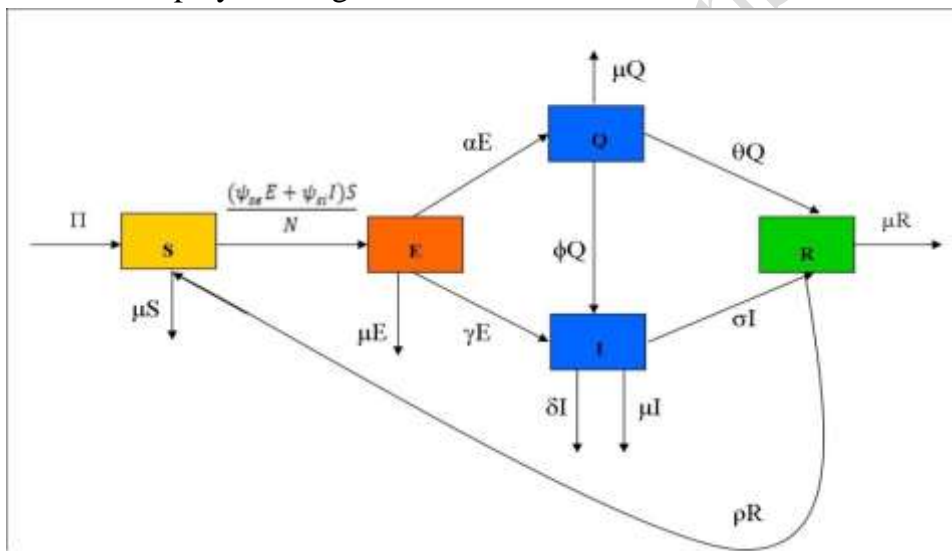
Model of the corona virus (COVID-19) disease using simple rates of transmission is proposed in this research work. Let  $N(t)$  be the total population of human. This population is divided into five classes: susceptible individuals  $S(t)$ , exposed individuals  $E(t)$ , infected individuals  $I(t)$ , quarantined individuals  $Q(t)$ , and individuals that have recovered/remove from COVID-19  $R(t)$ . Based on this consideration, the total population is  $N(t) = S(t) + E(t) + Q(t) + I(t) + R(t)$ . For simplicity, we shall use  $S = S(t), E = E(t), Q = Q(t), I = I(t), R = R(t), N = N(t)$  henceforth.

The natural human natality and mortality rates are denoted by  $\Pi$  and  $\mu$  respectively. Susceptible individuals ( $S$ ) gets exposed from enough contact with exposed individuals ( $E$ ) at the rate of  $\psi_{se}$  and infected individuals  $I(t)$  at the rate

of  $\psi_{si}$ . The exposed individuals ( $E$ ) may move to quarantined ( $Q$ ) class first or get infected and move to infected class ( $I$ ) at the rates of  $\alpha$  and  $\gamma$  respectively. Also quarantined individuals ( $Q$ ) may be confirmed infected through test and move to infected class ( $I$ ) at the rate of  $\phi$  or move to recovery class ( $R$ ) at the rate of  $\theta$ . The infected individuals ( $I$ ) may recover at the rate of  $\sigma$  or die as a result of the disease at the rate of  $\delta$ . The possibility of recovered individuals moving to susceptible class and get re-infected was also considered at the rate of  $\rho$ .

Each of these classes may decrease as a result of natural mortality  $\mu$ , while the class of individuals infected ( $I$ ) may also decrease as a result of death from the disease at the rate of  $\delta$ .

The schematic diagram showing the transmission pattern of COVID-19 in this model is displayed in figure 1.



**Figure 1: Schematic diagram of the proposed model**

### Model equations

The model equations are given as follow:

$$S' = \Pi - \frac{(\psi_{se}E + \psi_{si}I)S}{N} - \mu S + \rho R \quad (1)$$

$$E' = \frac{(\psi_{se}E + \psi_{si}I)S}{N} - (\alpha + \gamma + \mu)E \quad (2)$$

$$Q' = \alpha E - (\mu + \phi + \theta)Q \quad (3)$$

$$I' = \gamma E + \phi Q - (\delta + \mu + \sigma)I \quad (4)$$

$$R' = \theta Q + \sigma I - (\mu + \rho)R \quad (5)$$

With  $S \geq 0, E \geq 0, Q \geq 0, I \geq 0, R \geq 0$  and initial conditions  $S(0) = S_0, E(0) = E_0, Q(0) = Q_0, I(0) = I_0, R(0) = R_0$ .

## Qualitative properties of the model

### Invariant region

Since the model (1) – (5) describes human population it is necessary to show that all the state variables  $S, E, Q, I, R$  are nonnegative for all  $t \geq 0$ . Solutions with positive initial data remains positive for all  $t \geq 0$  and are bounded.

It is easy to see from system (1) – (6) that  $\frac{dN(t)}{dt} = \Pi - \mu N(t) - \delta I$  and  $\text{Sup}_{t \rightarrow \infty} N(t) \leq \frac{\Pi}{\mu}$ . As such we can study the system (1) – (5) in the following feasible region:

$$\Omega = \left\{ (S, E, Q, I, R) \in \mathbb{R}_+^5 : 0 \leq N(t) \leq \frac{\Pi}{\mu} \right\}$$

This is positively invariant with respect to the system (1) – (6). Meaning our system is epidemiologically well posed and all solutions of the system with  $(S_0, E_0, Q_0, I_0, R_0) \in \mathbb{R}_+^5$  remain in  $\Omega$ .

## Model Analysis

### Disease Free Equilibrium Point ( $E_0$ )

The disease free equilibrium point is obtained by setting  $E = Q = I = R = 0$ .

Therefore, the system (1) – (5) indicates that the DFE point is given by

$$DFE = (S_0, 0, 0, 0, 0) = \left( \frac{\Pi}{\mu}, 0, 0, 0, 0 \right)$$

### Basic Reproduction Number

In this proposed model, the basic reproductive number denoted by  $R_0$  is the expected value of infection rate per time unit. The infection occurs in a susceptible population, caused by an infected individual and/exposed individual. Based on the system (1) – (5), the article generates equation that involves the classes of exposed and infected population.

The reproduction number  $R_0$  of the proposed model (1) - (5) is defined herein in the infected classes. This threshold quantity has been described in [1,3]. In all cases,  $R_0 < 1$  implies that disease will decline, whereas  $R_0 > 1$  implies that disease will persist within a community and  $R_0 = 1$  requires further investigation.  $R_0$  is obtained using the next generation matrix approach [1] where several authors have used it.

We implore the use of next-generation matrix to find the basic reproduction number for the model (1) – (5). Without much of the formalities, it is clear from the model (1) – (5), the article generates equation that involves the classes of exposed population, infected population, as follows:

$$E' = \frac{(\psi_{se}E + \psi_{si}I)S}{N} - (\alpha + \gamma + \mu)E \quad (2a)$$

$$Q' = \alpha E - (\mu + \phi + \theta)Q \quad (3a)$$

$$I' = \gamma E + \phi Q - (\delta + \mu + \sigma)I \quad (4a)$$

Based on [1], from the equations (2a) – (4a), the study generates matrix  $\mathcal{F}$  and  $\mathcal{V}$ , i.e.

$$\mathcal{F} = \begin{pmatrix} \frac{(\psi_{se}E + \psi_{si}I)S}{N} \\ 0 \\ 0 \end{pmatrix}, \quad \mathcal{V} = \begin{pmatrix} (\alpha + \gamma + \mu)E \\ (\mu + \phi + \theta)Q - \alpha E \\ (\delta + \mu + \sigma)I - \gamma E - \phi Q \end{pmatrix}$$

The Jacobian matrix of  $\mathcal{F}$  and  $\mathcal{V}$  at  $DFE$ , denoted by  $F$  and  $V$  are given as follow:

$$F = \begin{pmatrix} \psi_{se} & 0 & \psi_{si} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} \alpha + \gamma + \mu & 0 & 0 \\ -\alpha & \mu + \phi + \theta & 0 \\ -\gamma & -\phi & \delta + \mu + \sigma \end{pmatrix}$$

Therefore,  $FV^{-1}$  is the next generation matrix of the model structure (1) - (5). So, as described in [Inset ref]  $R_0 = \rho(FV^{-1})$  where  $\rho$  is the spectral radius of the next-generation matrix  $FV^{-1}$ .

$$\text{Now, } FV^{-1} = \begin{pmatrix} \frac{\psi_{se}[(\gamma + \delta + \mu + \sigma)(\mu + \phi + \theta) + \alpha\phi]}{(\alpha + \gamma + \mu)(\mu + \phi + \theta)(\delta + \mu + \sigma)} & \frac{\psi_{se}\phi}{(\mu + \phi + \theta)(\delta + \mu + \sigma)} & \frac{\psi_{se}}{(\delta + \mu + \sigma)} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}.$$

$$\text{Thus, } \rho(FV^{-1}) = \frac{\psi_{se}[(\gamma + \delta + \mu + \sigma)(\mu + \phi + \theta) + \alpha\phi]}{(\alpha + \gamma + \mu)(\mu + \phi + \theta)(\delta + \mu + \sigma)} = R_0.$$

Therefore,  $R_0 = \frac{\psi_{se}[(\gamma+\delta+\mu+\sigma)(\mu+\phi+\theta)+\alpha\phi]}{(\alpha+\gamma+\mu)(\mu+\phi+\theta)(\delta+\mu+\sigma)} > 0$

## Conclusion

We developed a simple mathematical model to investigate the the existence of basic reproduction number on a population for the novel corona virus diseases 2019 (COVID-19). Principles drawn from the literature of mathematical epidemiology have been used to model how individuals became infected with COVID-19 and their possible recovery. The growth and decrease of each subpopulation was driven by the disease reproduction number,  $R_0$ , just as in the case of any epidemic models. This basic reproduction number can be used to make generalization when further analysis is conducted and more information on how best the disease can be curtailed may be obtained.

This is an undergoing research and the finding of the basic reproduction number is one of the preliminaries for further analysis.

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