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Mathematical model analysis of covid-19 (SARS-Cov-2) using compartmental models in epidemiology and ethical practices to break the chain of infection

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Abstract

The aim of the paper is to mathematically analyze and describe the outbreak of COVID-19 (SARS-CoV-2) using compartmental models in epidemiology and understand the significance of ethical practices to break the chain of infection. A SEQIJR model of epidemic disease transmission which includes compartments each one for susceptible people (S), quarantine (Q) of exposed people (E), isolation (J) of infectious people (I), and a recovered population (R) is studied. The number of COVID-19 positive cases is rising at a significant rate across the globe. The coronavirus generally

spread in two different ways. First, if a person inhale droplet from a person with COVID-19 positive who coughs out or exhales droplets or sneezes. Second, if a person comes in contact with the surface, which was contaminated by droplets or discharge from the nose, and then by touching his nose, mouth, and eyes. The spread of coronavirus can be stopped by interrupting the links of the chain of infection. But this interruption will also lead to multiple effects in terms of economic crisis as well. So, there is a great need to follow ethical practices while breaking the chain of infection.

Keywords: COVID-19, compartmental models in epidemiology, SEQIJR models, SIR models, lockdown, chain of infection

1. Introduction

The COVID-19 (SARS-CoV-2) has created a wide-spread destruction across the globe on individuals, societies, businesses and economy as a whole. The coronavirus is spreading at a significant rate from person to person through both direct and indirect contacts. It was first traced in Wuhan, Hubei, China as a new strain of coronavirus which was given an interim name 2019-nCoV by WHO but was later renamed to SARS-CoV-2 by the International Committee on Taxonomy of Viruses^[7, 8, 9]. Health experts have identified common symptoms of the disease includes fever, cough, fatigue, breathing difficulties, and loss of smell and taste with most people having mild symptoms while a few develops acute respiratory distress syndrome (ARDS) such as cytokine, multi-organ failure, blood clots etc.^[10, 11] The incubation period ranges from 1 to 14 days. The people during incubation period of virus acts as a carrier and are likely to infect other people as well. [6] Mathematical model derivation for COVID-19 using compartmental models is an epidemiological prototype that helps us to understand the progress of people between the compartments. It also helps us to take necessary steps to control and curtail the spread of the diseases. The SEQIJR model of epidemiology has been adopted for our study.

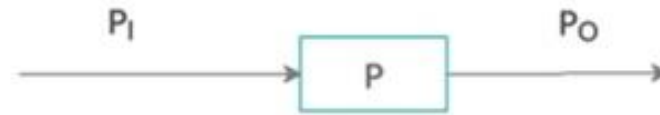
This paper is structured in different sections. Section II describes the Literature Review of compartmental model of epidemiology. Section III is related to Mathematical Model Derivation for COVID-19. Section IV is about Disease-Free Equilibrium. Section V is about Basic Reproduction Number. Section VI describes Sensitivity Analysis of Basic Reproduction Number. Section VII discusses about the SIR Model. Section VIII describes the minimum time period to spread the infection across the country if no restrictions are imposed to curtail and control the spread of infection. Section IX is describing the ethical practices to break the chain of infection. Finally, Section X is conclusion of the study.

2. Literature Review

Compartmental models (also known as *Kermack-McKendrick Model*) is a mathematical modelling technique of infectious diseases. The population in compartmental model is assigned to compartments with labels – S, E, Q, I, J and R (Susceptible, Exposed, Quarantine, Infectious, Isolated and Recovered) with assumptions about the nature and time rate of transfer from one compartment to another. It is also assumed that a recovered individual cannot become infected again. The population progress between compartments. The order of the labels represents the flow patterns between the compartments. These models help to determine things such as how disease spreads, or the total number of infected people, or the duration of an epidemic, and to estimate various other epidemiological parameters such as disease-free equilibrium, basic reproduction number

And sensitivity analysis of basic reproduction number. Such models can also depict how different public health interventions affect the outcome of the epidemic. The mathematical modelling of compartmental models uses concept of ordinary differential equations to analyze the situation and estimate different parameters. The independent variable in our compartmental models is time t and the rate of transfer between compartments are expressed mathematically as derivatives with respect to time of the sizes of the compartments [1, 2, 3, 4].

For E.g. – Let P_1 and P_0 ($P_1 \geq P_0$) represents the number of populations entering and exiting the compartment P at a constant rate respectively. Then, the net rate of change in population in the compartment P will be equal to the difference between the rate at which population enter and exit the compartment. [Figure. 1].



Source: Compiled by Author

Fig 1: Compartment models transfer diagram in Epidemiology

$$\left[\begin{array}{c} \text{Net rate} \\ \text{of change} \\ \text{in population} \\ \text{in the compartment} \end{array} \right] = \left[\begin{array}{c} \text{Rate at which} \\ \text{population enters} \\ \text{into the compartment} \end{array} \right] - \left[\begin{array}{c} \text{Rate at which} \\ \text{population exit} \\ \text{from the compartment} \end{array} \right]$$

$$\frac{dP}{dt} = \lim_{\Delta t \rightarrow 0} \frac{P_0 - P_1}{\Delta t} \quad \dots (1)$$

3. Mathematical Model Derivation for Covid-19

3.1 Mathematical modeling of susceptible population [S(t)]:

$S(t)$ represents the number of susceptible individuals at time t . When a susceptible individual and an infectious individual come into an "infectious contact", the susceptible individual gets infected with the disease and the person transitions into the infectious compartment. The new susceptible individuals enter in the susceptible zone population at a rate Π . The susceptible individual will be infected through sufficient contact with infectious individual with the transmission rate at α (average number of contacts per person per day). These susceptible population is augmented and condensed by natural death μ_1 . This population is also decreased by constant rates β_1 and σ_1 and converted into quarantined individual and recovered individual respectively. This is due to fear factor pre-dominating among the people. This situation arises due to inadequate facility for treatment or testing at a large scale of populations. Therefore, the net rate of change of susceptible population are governed by the following ordinary differential equation:

$$\frac{dS}{dt} = \Pi - \alpha \cdot S \cdot I - \beta_1 \cdot S - \sigma_1 \cdot S - \mu_1 \cdot S \quad \dots (2)$$

3.2 Mathematical modeling of exposed population (infected but not detected by testing) [E(t)]:

$E(t)$ represents the number of exposed individuals at time t . The exposed individuals are the individuals who are infected but their infection is not detected due to inadequate testing facilities. This population in the exposed zone increases at a rate α when susceptible individual makes a contact with individual who are infected but not detected by testing. This population is further decreased at a rate β_2 and converted into quarantine individual. This population is also condensed by natural death at a rate μ_1 . If the exposed population density is too large to send all of them for quarantine period then the remaining population is also directly decreased by exposed population at a rate λ_1 . Therefore, the net rate of change of exposed population is governed by the following ordinary differential equation:

$$\frac{dE}{dt} = \alpha \cdot S \cdot I - \beta_2 \cdot E - \lambda_1 \cdot E - \mu_1 \cdot E \quad \dots (3)$$

3.3 Mathematical modeling of quarantine population [Q(t)]

The incubation period of the virus is the time between the exposure and the display of symptoms. The incubation period of coronavirus ranges from 1 to 12.5 days (with median estimates of 5 to 6 days), but can also get extend to 14 days [6]. This period is very crucial as the transmission of virus may occur during the incubation period even much before a person shows signs of sickness. $Q(t)$ represents the number of quarantine individuals at time t . These are the susceptible and exposed population who are infected but have not shown symptoms yet. These populations are isolated for 14 days to curtail the spread of coronavirus. Quarantined population is increased at a rate β_1 and β_2 from susceptible and exposed population respectively. This population is further decreased at a rate λ_2 and σ_2 as some of them get infected with virus and some are recovered correspondingly. This population is also condensed by natural death at a rate μ_1 . Therefore, the net rate of change of quarantined population is governed by the following ordinary differential equation:

$$\frac{dQ}{dt} = \beta_1 \cdot S + \beta_2 \cdot E - \sigma_2 \cdot Q - \lambda_2 \cdot Q - \mu_1 \cdot Q \quad \dots (4)$$

3.4 Mathematical modeling of confirmed infected population [I(t)]:

I(t) represent the number of infectious individuals at time t. These are individuals who have been infected with the COVID-19 and are capable of spreading the disease to those in the susceptible category. These infected individuals belong to the population who have been reported COVID-19 positive based on the symptoms and are not detected by testing. These population is increased at a rate λ_1 and λ_2 from exposed population and quarantined population respectively. The infected and detected by testing population is decreased at a rate δ as they are kept in isolation for treatment. These infected population is further decreased at rate σ_3 due to recovered population. This population is also condensed by natural death at a rate μ_1 and death due to Covid-19 infection at a rate μ_2 . Therefore, the net rate of change of infected population is governed by the following ordinary differential equation:

$$\frac{dI}{dt} = \lambda_1 \cdot E + \lambda_2 \cdot Q - \sigma_3 \cdot I - \delta \cdot I - \mu_1 \cdot I - \mu_2 \cdot I \quad \dots (5)$$

3.5 Mathematical modeling of isolated population [J(t)]:

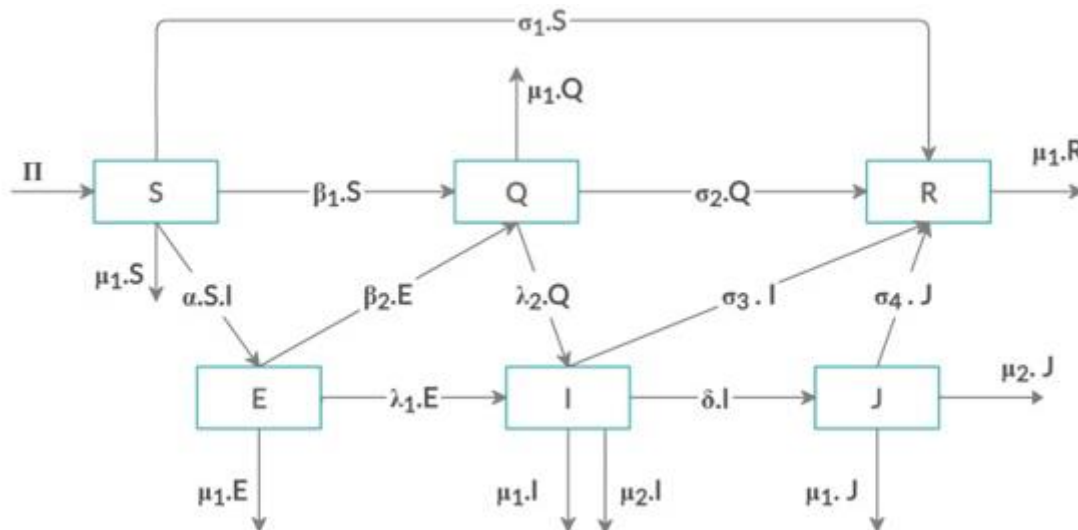
J(t) represent the number of isolated individuals at time t. These are individuals who have been infected with the COVID-19 and detected by testing. These individuals are capable of spreading the disease to those in the susceptible category and therefore they are kept isolated. These population is increased at a rate δ from infected population and further decreased at rate σ_4 due to recovered population. This population is also condensed by natural death at a rate μ_1 and death due to Covid-19 infection at a rate μ_2 . Therefore, the net rate of change of isolated population is governed by the following ordinary differential equation:

$$\frac{dJ}{dt} = \delta \cdot I - \sigma_4 \cdot J - \mu_1 \cdot J - \mu_2 \cdot J \quad \dots (6)$$

3.6 Mathematical modeling of recovered zone population [R(t)]

R(t) represents the number of recovered individuals at time t. These are the individuals who was infected and have either recovered from the disease and entered the recovered zone population compartment either due to immunization or due to death. Those in this category are not able to get reinfected and transmit the infection to others. This compartment is also be called "resistant". These population is increased at a rate σ_1 , σ_2 , σ_3 and σ_4 from susceptible, quarantined, infected and isolated individuals respectively. This population is also condensed by natural death at a rate μ_1 . Therefore, the net rate of change of recovered population is governed by the following ordinary differential equation:

$$\frac{dR}{dt} = \sigma_1 \cdot S + \sigma_2 \cdot Q + \sigma_3 \cdot I + \sigma_4 \cdot J - \mu_1 \cdot R \quad \dots (7)$$



Source: Compiled by Author

Fig 2: Compartmental model transfer diagram SEQIJR of covid-19

The mathematical model formulation of SEQIJR is

$$\frac{dS}{dt} = \Pi - \alpha \cdot S \cdot I - \beta_1 \cdot S - \sigma_1 \cdot S - \mu_1 \cdot S$$

$$\frac{dE}{dt} = \alpha \cdot S \cdot I - \beta_2 \cdot E - \lambda_1 \cdot E - \mu_1 \cdot E$$

$$\frac{dQ}{dt} = \beta_1 \cdot S + \beta_2 \cdot E - \sigma_2 \cdot Q - \lambda_2 \cdot Q - \mu_1 \cdot Q \quad \dots (8)$$

$$\frac{dI}{dt} = \lambda_1 \cdot E + \lambda_2 \cdot Q - \sigma_3 \cdot I - \delta \cdot I - \mu_1 \cdot I - \mu_2 \cdot I$$

$$\frac{dJ}{dt} = \delta \cdot I - \sigma_4 \cdot J - \mu_1 \cdot J - \mu_2 \cdot J$$

$$\frac{dR}{dt} = \sigma_1 \cdot S + \sigma_2 \cdot Q + \sigma_3 \cdot I + \sigma_4 \cdot J - \mu_1 \cdot R$$

With initial population densities

$$S(0) > 0; \quad E(0) \geq 0; \quad Q(0) \geq 0; \quad I(0) \geq 0; J(0) \geq 0; \quad R(0) > 0$$

The above SEQIJR model formulation (8) can be rewritten as

$$\frac{dS}{dt} = \Pi - \alpha \cdot S \cdot I - A \cdot S$$

$$\frac{dE}{dt} = \alpha \cdot S \cdot I - B \cdot E$$

$$\frac{dQ}{dt} = \beta_1 \cdot S + \beta_2 \cdot E - C \cdot Q \quad \dots (9)$$

$$\frac{dI}{dt} = \lambda_1 \cdot E + \lambda_2 \cdot Q - D \cdot I$$

$$\frac{dJ}{dt} = \delta \cdot I - G \cdot J$$

$$\frac{dR}{dt} = \sigma_1 \cdot S + \sigma_2 \cdot Q + \sigma_3 \cdot I + \sigma_4 \cdot J - \mu_1 \cdot R$$

Where,

$$A = \beta_1 + \sigma_1 + \mu_1; B = \beta_2 + \lambda_1 + \mu_1; C = \sigma_2 + \lambda_2 + \mu_1; D = \sigma_3 + \delta + \mu_1 + \mu_2; G = \sigma_4 + \mu_1 + \mu_2$$

Table 1: Explanation of parameters exploited in our proposed SEQIJR model structure

Parameters	Meaning
Π	The rate at which new susceptible individuals enter in the susceptible zone population.
σ_1	The transmission rate from susceptible population to recovered zone population.
σ_2	The transmission rate from quarantine population to recovered zone population.
σ_3	The transmission rate from symptomatic (infected but not detected by testing) population to recovered zone population.
σ_4	The transmission rate from asymptomatic (isolated and detected by testing) population to recovered zone population.
μ_1	The natural death rate of all sub-population.
μ_2	The death rate of symptomatic and asymptomatic population due to Covid-19 infection.
λ_1	The transmission rate from exposed (infected but not detected by testing) population to infected population for treatment.
λ_2	The transmission rate from quarantine population to infected population for treatment.
α	The transmission rate from susceptible population to infected but not detected by testing population. (α = Average number of contacts per person per day).
β_1	The transmission rate from susceptible population to quarantine population.
β_2	The transmission rate from exposed (infected but not detected by testing) population to quarantine population.
δ	The transmission rate from infected and detected by testing population to isolated population for treatment.

Source: Compiled by Author

3.7 Non-Negativity Constraints of Solution

The system of equation (9) is non-linear algebraic equation. Therefore, we can obtain its analytic solution in implicit form. From first equation of system of equation (9) with initial condition, we have

$$\frac{dS}{dt} = \Pi - \alpha \cdot S \cdot I - A \cdot S$$

$$\frac{dS}{dt} + A \cdot S = \Pi - \alpha \cdot S \cdot I$$

$$\frac{dS}{dt} + A \cdot S \geq 0$$

Solving above differential equation and applying initial condition, we get

$$S(t) \geq S(0) \cdot e^{-At} > 0; \forall t \geq 0 \quad \dots (10)$$

Similarly, we can obtain the non-negativity constraints of remaining equations of system of equations (9)

$$E(t) \geq E(0) \cdot e^{-B \cdot t} \geq 0; \forall t \geq 0 \quad \dots (11)$$

$$Q(t) \geq Q(0) \cdot e^{-C \cdot t} \geq 0; \forall t \geq 0 \quad \dots (12)$$

$$I(t) \geq I(0) \cdot e^{-D \cdot t} \geq 0; \forall t \geq 0 \quad \dots (13)$$

$$J(t) \geq J(0) \cdot e^{-G \cdot t} \geq 0; \forall t \geq 0 \quad \dots (14)$$

$$R(t) \geq R(0) \cdot e^{-\mu_1 \cdot t} \geq 0; \forall t \geq 0 \quad \dots (15)$$

Although the basic SEQIJR model only contains 6 equations, one each for S, E, Q, I, J, R, we have found it convenient to add one extra equations for easy computation of the total population size N(t) at time t.

$$N = N(t) = S(t) + E(t) + Q(t) + I(t) + J(t) + R(t) \quad \dots (16)$$

Differentiating equation,

$$\frac{dN(t)}{dt} = \frac{dS(t)}{dt} + \frac{dE(t)}{dt} + \frac{dQ(t)}{dt} + \frac{dI(t)}{dt} + \frac{dJ(t)}{dt} + \frac{dR(t)}{dt} \quad \dots (17)$$

Substituting set of equations (9) in equation (17),

$$\frac{dN}{dt} = \Pi - \mu_1 \cdot [S + E + Q + I + J + R] - \mu_2 \cdot [I + J]$$

$$\frac{dN}{dt} = \Pi - \mu_1 \cdot N - \mu_2 \cdot [I + J]$$

$$\frac{dN}{dt} + \mu_1 \cdot N = \Pi - \mu_2 \cdot [I + J]$$

$$\frac{dN}{dt} + \mu_1 \cdot N \leq \Pi$$

Solving above differential equation and applying initial condition, we get

$$0 < N(t) \leq N(0) \cdot e^{-\mu_1 \cdot t} + \frac{\Pi}{\mu_1}; \forall t \geq 0 \quad \dots (18)$$

At $\rightarrow \infty$, the equation becomes

$$0 < N(t) \leq \frac{\Pi}{\mu_1} \quad \dots (19)$$

Therefore, all solution of the model structure (9) enters in the region

$$\Psi = \left\{ (S, E, Q, I, J, R) \in \mathbb{R}_+ : 0 < N(t) \leq \frac{\Pi}{\mu_1} \right\} \quad \dots (20)$$

4. Disease Free Equilibrium (E₀)

Disease-free equilibrium (E₀) is the point at which there is no disease present in the population. The disease-free equilibrium (E₀) points are solutions of the system of nonlinear algebraic equations (9) and (17) obtained by setting

$$\frac{dN(t)}{dt} = \frac{dS(t)}{dt} = \frac{dE(t)}{dt} = \frac{dQ(t)}{dt} = \frac{dI(t)}{dt} = \frac{dJ(t)}{dt} = \frac{dR(t)}{dt} = 0$$

The obtained Disease-Free Equilibrium is

$$E_0 = (S_1^*, E_1^*, Q_1^*, I_1^*, J_1^*, R_1^*, N_1^*) = \left(\frac{\Pi}{A}, 0, 0, 0, 0, 0, \frac{\Pi}{\mu_1}\right) \quad \dots (21)$$

5. Basic Reproduction Number (R_0):

Basic Reproduction Number (R_0) represents the number of new cases that an existing case generates on an average over the infectious period in a susceptible population at disease free equilibrium (E_0) point.

$$R_0 = \frac{\text{Average number of new cases}}{\text{Average number of existing case}} \quad \dots (22)$$

In compartmental model of epidemiology, the basic reproduction number is calculated by using next-generation matrix method [12].

Let us assume,

$$y = (S, E, Q, I, J, R)^T \quad \dots (23)$$

As, an infected person always enters the Exposed population (E) first and then later enters the Quarantine (Q), Infected (I), Isolated (J) and Recovery (R) populations. Therefore, we regard Exposed population (E) as the next-generation “infected” population and $(S, Q, I, J, R)^T$ can be regarded as the remaining populations. Therefore, the model can be written in the next-generation form as,

$$\frac{dy}{dt} = F(y) - V(y) \quad \dots (24)$$

Where,

$$F(y) = \frac{\text{Average number of new cases}}{\text{Average number of existing cases}} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \alpha \cdot S \cdot I & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$V(y) = \begin{bmatrix} \Pi - \alpha \cdot S \cdot I - A \cdot S & 0 & 0 & 0 & 0 & 0 \\ 0 & B & 0 & 0 & 0 & 0 \\ -\beta_1 & -\beta_2 & C & 0 & 0 & 0 \\ 0 & -\lambda_1 & -\lambda_2 & D & 0 & 0 \\ 0 & 0 & 0 & -\delta & G & 0 \\ -\sigma_1 & 0 & -\sigma_2 & -\sigma_3 & -\sigma_4 & \mu_1 \end{bmatrix}$$

At disease free equilibrium point (E_0), the Jacobian Matrices $F(y)$ and $V(y)$ is given by

$$F(y) = \frac{\text{Average number of new cases}}{\text{Average number of existing cases}} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \alpha \cdot \Pi / A & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$V(y) = \begin{bmatrix} \alpha \cdot \Pi / A & 0 & 0 & 0 & 0 & 0 \\ 0 & B & 0 & 0 & 0 & 0 \\ -\beta_1 & -\beta_2 & C & 0 & 0 & 0 \\ 0 & -\lambda_1 & -\lambda_2 & D & 0 & 0 \\ 0 & 0 & 0 & -\delta & G & 0 \\ -\sigma_1 & 0 & -\sigma_2 & -\sigma_3 & -\sigma_4 & \mu_1 \end{bmatrix}$$

Therefore,
 $F \cdot V^{-1} =$

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\alpha \cdot \Pi}{AB} & \frac{\alpha \cdot \Pi \cdot \beta_2}{ABC} & \frac{\alpha \cdot \Pi \cdot \left[\frac{\beta_2 \cdot \lambda_2}{+ C \cdot \lambda_1} \right]}{ABCD} & \frac{\alpha \cdot \Pi \cdot \left[\frac{\beta_2 \cdot \lambda_2}{+ C \cdot \lambda_1} \right] \cdot \delta}{ABCDG} & \frac{\alpha \cdot \Pi \cdot \left[\left(\frac{\beta_2 \cdot \lambda_2}{+ C \cdot \lambda_1} \right) \cdot \left(\frac{\delta \cdot \sigma_4}{+ G \cdot \sigma_3} \right) \right]}{+ \beta_2 \cdot \sigma \cdot D \cdot G}{ABCDG\mu_1} \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

The characteristic equation of the matrix $F \cdot V^{-1}$ is given by,

$$\det(F \cdot V^{-1} - \eta \cdot U) = 0 \quad \dots (25)$$

where, 'U' is Identity Matrix of order 6 x 6 and 'η' is eigen value of matrix $F \cdot V^{-1}$.

$$(-\eta) \cdot \left(\frac{\alpha \cdot \Pi}{AB} - \eta \right) \cdot (-\eta) \cdot (-\eta) \cdot (-\eta) \cdot (-\eta) = 0 \quad \dots (26)$$

Therefore, roots of the equation (26) i.e. eigen values of the matrix $F \cdot V^{-1}$ are,

$$\eta_S = \eta_Q = \eta_I = \eta_J = \eta_R = 0 \quad ; \quad \eta_E = \frac{\alpha \cdot \Pi}{A \cdot B} \quad \dots (27)$$

Therefore, the basic reproduction number will be given by,

$$R_0 = \frac{\alpha \cdot \Pi}{A \cdot B} = \frac{\alpha \cdot \Pi}{(\beta_1 + \sigma_1 + \mu_1) \cdot (\beta_2 + \lambda_1 + \mu_1)} > 0 \quad \dots (28)$$

If $R_0 > 1$, the infection will spread exponentially. If $R_0 < 1$, the infection will spread slowly, and it will eventually die out after some time. The higher the value of R_0 , the faster an epidemic will progress ^[1, 2, 3, 4]. Basic Reproduction Number (R_0) of COVID – 19 (SARS-CoV-2) ranges between 2 and 6 ^[13, 14].

6. Sensitivity Analysis (Δ) of Basic Reproduction Number (R_0)

Sensitivity analysis (Δ) is a model that helps to determine how target variable i.e. R_0 are affected based on changes in other variables known as input variables i.e. ($\alpha, \beta_1, \beta_2, \sigma_1, \lambda_1, \mu_1$). It predicts the outcome of a decision given a certain range of variables.

$$\Delta_\alpha = \frac{\frac{\partial R_0}{R_0}}{\frac{\partial \alpha}{\alpha}} = \frac{\alpha}{R_0} \frac{\partial R_0}{\partial \alpha} = \frac{\alpha}{R_0} \cdot \frac{\Pi}{(\beta_1 + \sigma_1 + \mu_1) \cdot (\beta_2 + \lambda_1 + \mu_1)} = \frac{R_0}{R_0} = 1$$

$$\Delta_{\beta_1} = \frac{\frac{\partial R_0}{R_0}}{\frac{\partial \beta_1}{\beta_1}} = \frac{\beta_1}{R_0} \frac{\partial R_0}{\partial \beta_1} = \left| \frac{-\beta_1}{(\beta_1 + \sigma_1 + \mu_1)} \right| < 1$$

$$\Delta_{\beta_2} = \frac{\frac{\partial R_0}{R_0}}{\frac{\partial \beta_2}{\beta_2}} = \frac{\beta_2}{R_0} \frac{\partial R_0}{\partial \beta_2} = \left| \frac{-\beta_2}{(\beta_2 + \lambda_1 + \mu_1)} \right| < 1 \quad \dots (29)$$

$$\Delta_{\sigma_1} = \frac{\frac{\partial R_0}{R_0}}{\frac{\partial \sigma_1}{\sigma_1}} = \frac{\sigma_1}{R_0} \frac{\partial R_0}{\partial \sigma_1} = \left| \frac{-\sigma_1}{(\beta_1 + \sigma_1 + \mu_1)} \right| < 1$$

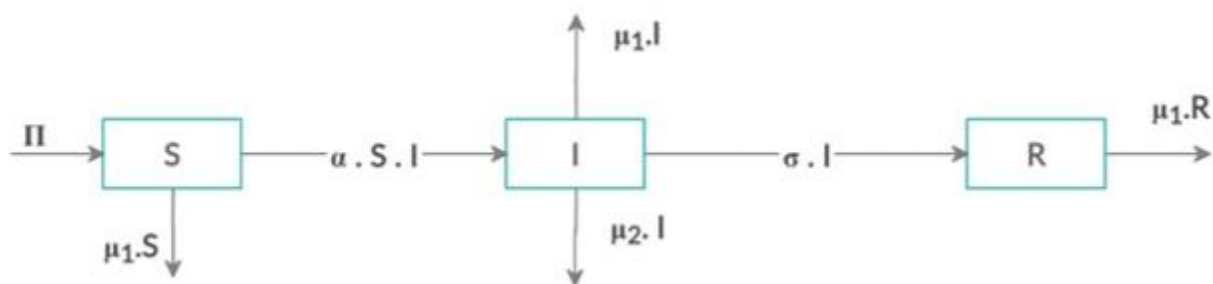
$$\Delta_{\lambda_1} = \frac{\frac{\partial R_0}{R_0}}{\frac{\partial \lambda_1}{\lambda_1}} = \frac{\lambda_1}{R_0} \frac{\partial R_0}{\partial \lambda_1} = \left| \frac{-\lambda_1}{(\beta_2 + \lambda_1 + \mu_1)} \right| < 1$$

$$\Delta_{\mu_1} = \frac{\frac{\partial R_0}{\partial \mu_1}}{\frac{R_0}{\mu_1}} = \frac{\mu_1}{R_0} \frac{\partial R_0}{\partial \mu_1} = \left| \frac{-\mu_1}{(\beta_1 + \sigma_1 + \mu_1)} + \frac{-\mu_1}{(\beta_2 + \lambda_1 + \mu_1)} \right| < 1$$

Above results, clearly interprets that the basic reproduction number (R_0) is actually sensitive to α . The value of R_0 increases with increase in the value of α . Similarly, the value of R_0 decreases with decrease in the value of α in the same proportion. It is also noticed from the above expressions, that the parameters β_1 , β_2 , σ_1 , λ_1 , μ_1 are inversely related to R_0 . Therefore, for any increase in value of β_1 , β_2 , σ_1 , λ_1 , μ_1 will lead to reduction in the value of R_0 . However, the decrease in value of R_0 will be comparatively smaller. Therefore, it will be wise enough to put efforts in reducing α which means that the sensitivity analysis of R_0 emphasize that prevention is always better than treatment. Thus, prevention is very much effective way in controlling the spread of COVID-19 disease as yet there is no proper vaccine developed to control the spread of coronavirus disease across the globe.

7. SIR Model

SIR model is a special case which indicates that all susceptible individuals progress from susceptible compartment S to the infective compartment I to the recovered compartment R . The exposed compartment E , quarantine compartment Q and isolation compartment J are neglected in this case. [1, 2, 3, 4].



Source: Compiled by Author

Fig 3: Compartmental model transfer diagram SIR of covid-19

$$\frac{dS}{dt} = \Pi - \alpha.S.I - \mu_1.S$$

$$\frac{dI}{dt} = \alpha.S.I - \sigma.I - \mu_1.I - \mu_2.I \quad \dots (30)$$

$$\frac{dR}{dt} = \sigma.I - \mu_1.R$$

Table 2: Explanation of parameters exploited in our proposed SIR model structure

Parameters	Meaning
Π	The rate at which new susceptible individuals enter in the susceptible zone population.
σ	The transmission rate from infected population to recovered zone population.
μ_1	The natural death rate of all sub-population.
μ_2	The death rate of symptomatic and asymptomatic population due to Covid-19 infection.
α	The transmission rate from susceptible population to infected but not detected by testing population. (α = Average number of contacts per person per day).

Source: Compiled by Author

The solution of confirmed infected population $[I(t)]$ in sir model is,

$$\frac{dI}{dt} = \alpha.S.I - \sigma.I - \mu_1.I - \mu_2.I$$

$$\frac{dI}{dt} = [\alpha.S - \sigma - \mu_1 - \mu_2].I$$

$$\frac{dI}{dt} \leq [\alpha.S - \sigma].I$$

$$\frac{dI}{dt} - [\alpha.S - \sigma].I \leq 0$$

Solving above differential equation and applying initial condition, we get

$$I \leq I(0). e^{(\alpha.S.-\sigma).t} ; \forall t \geq 0, I(0) \geq 0 \quad \dots (31)$$

The equation (31) clearly shows that the number of infected individual increases exponentially over the period of time. Basic reproduction number in SIR model will get reduced to,

$$R_0 = \frac{\alpha. \Pi}{\sigma} \quad \dots (32)$$

8. Minimum Time Period to Spread Infection across the Country

Let us assume,

- 1) The virus is spreading at minimum possible rate. (Assuming, $R_0 = 2$).
- 2) The susceptible individual follows SIR model of epidemiology.
- 3) The model starts with 1 susceptible and 1 infected person i.e., $\Pi = S(0) = I(0) = 1$.
- 4) There is no pre-existing immunity i.e., everyone is susceptible.
- 5) There is no vaccine developed for the treatment of coronavirus.
- 6) There is no restriction imposed to curtail and control the spread of virus.

Since,

$$R_0 = \frac{\alpha. \Pi}{\sigma} = 2 \quad \Rightarrow \quad \sigma = \frac{\alpha. \Pi}{2}$$

Substituting above values in equation (31), we get

$$t \geq \frac{2}{\alpha} * \ln \left[\frac{I}{I(0)} \right] \text{ days}$$

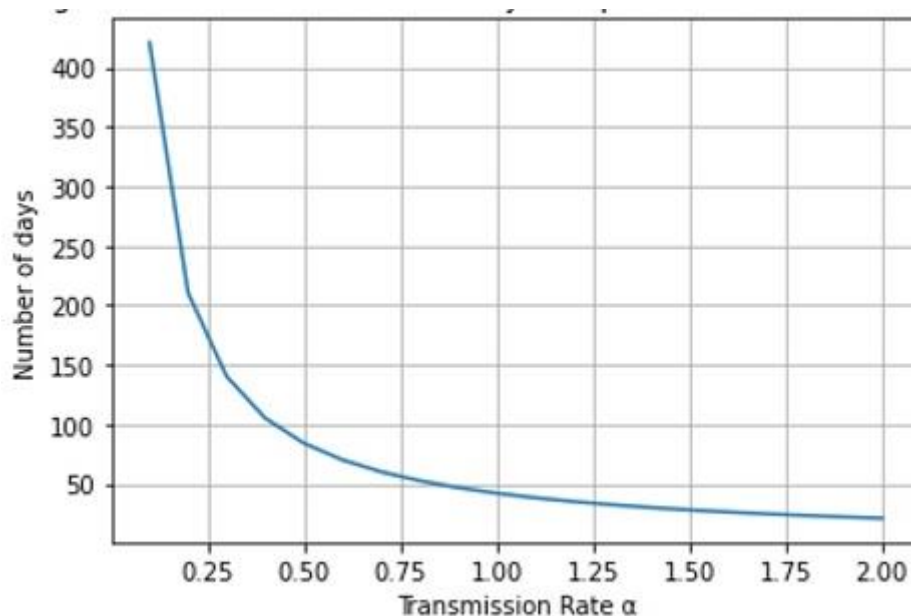
$$t \propto \frac{1}{\alpha} \quad \dots (33)$$

The value of time period 't' to spread infection is inversely proportional to the transmission rate from susceptible population to infected people ' α '. Higher the number of people coming into the contact of infected people, faster the infection will spread.

Table 3: Minimum number of days to spread infection in entire population of some top populated countries when no restrictions are imposed to control the spread ($R_0 = 2$, $\Pi = S(0) = I(0) = 1$)

Country	Population (March 2020) [5]	Number of Days			
		$\alpha = 0.5$	$\alpha = 1$	$\alpha = 1.5$	$\alpha = 2$
China	143.93 Crore	85	43	29	22
India	138.54 Crore	85	43	29	22
USA	33.17 Crore	79	40	27	20
Indonesia	27.64 Crore	78	39	26	20
Pakistan	22.26 Crore	77	39	26	20
Brazil	21.31 Crore	77	39	26	20
Nigeria	20.81 Crore	77	39	26	20
Bangladesh	16.53 Crore	76	38	26	19
Russia	14.59 Crore	76	38	26	19
Mexico	12.94 Crore	75	37	25	19
Japan	12.63 Crore	75	37	25	19
Ethiopia	11.60 Crore	74	37	25	19
Philippines	11.01 Crore	74	37	25	19
Egypt	10.31 Crore	74	37	25	18
Vietnam	9.76 Crore	74	37	25	18
World	778 Crore	92	46	31	23

Source: Compiled by author



Source: Compiled by author

Fig 4: Minimum number of days to spread infection across India

9. Ethical Practices to Break the Chain of Infection

Table 3 and Figure 4 show the minimum number of days to spread infection in entire population of some top populated countries when no restrictions are imposed by the government to break the chain of infection. The coronavirus disease can spread from person to person through a series of events. This virus spread through small droplets of saliva or discharge from the nose which are spread when a person with COVID-19 coughs or sneezes. These droplets or discharge lands on the surface and contaminate it. The virus may remain alive for days and weeks depending upon the type of surface and environmental condition. The susceptible individual catches coronavirus when they come in contact with that surface and then touches their eyes, nose or mouth. The susceptible individual can also catch coronavirus if they inhale droplets from a person with COVID-19 positive who coughs out or exhales droplets and discharge from nose. Therefore, it is very important to prevent spreading of coronavirus and infecting other people. This is why there is a need to break the chain of infection. The only way to stop spreading of coronavirus is by interrupting this chain at any link. This can be done by imposing lockdown, follow Social Distancing, diagnosis and treatment of disease, educating people about the virus and disease, running immunization program, cleaning and disinfecting surrounding environment, sterilizing medical instruments and equipment, framing infection prevention policies, frequent hand hygiene, maintaining personal hygiene, following good respiratory hygiene, avoid touching eyes, nose and mouth, covering face with mask, using personal protective equipment in the right way, proper waste disposal, food safety, following quarantine and isolation rules strictly, keeping up to date on the updated COVID-19 hotspots zone, avoid self-medication, increase testing & fast contact tracing and finally immunization. There is also need to recognize individual circumstances, react with empathy and maintain transparency when feeling out of control, avoid taking advantage of the situation to push other agendas and finally remember the power of healthcare and benefit coverage while not abusing them. If these steps are followed strictly, it will contribute to delayed peak and to an extent in flattening of the curve by breaking the chain of infection. India imposed the lockdown much earlier than many other countries across the world which failed to contain the initial spread of virus. That's why India has reported lowest fatality rate due to COVID-19 across the world.

10. Conclusion

In this paper mathematical model is used to study COVID-19. The number of COVID-19 positive cases across the globe is increasing exponentially day by day. With no immediate permanent solution to eradicate this disease, the government of all the countries decided to impose full scale lockdown barring essential activities. But due to this lockdown the nations entered into the phase of economic crisis and consequently their GDP have experienced drastic fall even much higher as had happened between 2007-2009. Manufacturing and service industries are severely hit. People have lost their job. Unorganized sector is in extreme painful condition. People are coming out in search of job. They are facing difficulty to maintain social distancing. And due to which the public health infrastructures are overloaded with positive cases. Therefore, it very important to predict the possible spread of infection so as to make proper arrangement for treatment of infected patients and curtail the spread of disease as soon as possible. It is observed that the virus starts spreading if and only if the basic reproduction number $R_0 > 1$. The basic reproduction number (R_0) is mainly sensitive to α . It is also mathematically proven that if the no restrictions are imposed to control the spread of coronavirus, higher the number of people will come into the contact of infected people resulting in faster spread the infection. In such case countries would have entered into a deep recession. And also, it would have been impossible to get these economies back on the track. To avoid such big trouble, it is very necessary to take stricter measures such as lockdown, quarantine, isolation, immunization program etc. by the government keeping in mind to provide essential commodities in right quantity, in right condition, at right place, at right time and at the right price to each and every individual within that country.

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