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Epidemiological Modelling and Analysis of COVID-19 Pandemic with Treatment

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Abstract: In this paper, Mathematical Model of COVID-19 Pandemic is formulated and discussed. The positivity, boundedness, and existence of the solutions of the model equations are stated and proved. The Disease-free equilibrium point & endemic equilibrium points are identified. Stability Analysis of the model is done with the concept of Next generation matrix. we have investigated that Disease-free equilibrium point (DFEP) of the model is locally asymptotically stable if $\alpha \leq \beta+\delta+\mu$ & unstable if $\alpha > \beta+\delta+\mu$, The basic reproduction number (threshold value) R_0 is the largest eigen value in spectral radius matrix ρ. Thus, eigen values of spectral radius Matrix ρ are determined from the roots of characteristic polynomial equation, $\det[\rho-\lambda I]=0$, Hence, the basic reproduction number is $R_0=\alpha / \beta$. It is shown that if reproduction number is less than one, then COVID-19 cases will be reduced in the community. However, if reproduction number is greater than one, then covid-19 continue to persist in the Community. Lastly, numerical simulations are done with DEDiscover 2.6.4. Software. It is observed that with Constant treatment, increase or decrease contact rate among persons leads great variation on the basic reproduction number which is directly implies that infection rate plays a vital role on decline or persistence of COVID-19 pandemic.

Keywords: COVID-19, PANDEMIC, Model, Stability, Next Generation Matrix, Reproduction Number, Simulation

1. Introduction

Mathematical modeling is an important tool to understand and analyze real world problems, for instance modeling infectious disease transmission dynamics in human and animals. Infectious disease is one of the most important factors in creating illness and even death in hundreds thousands people all over the world. In particular COVID-19 (Corona virus Disease 2019) is a family of RNA Beta virus in Nido viral order. This beta virus is medium size Viruses enveloping a positive-stranded RNA which Contain very large viral RNA genome. Corona prefix Comes from Latin word for Crown named for "crown-like" appearance of virus. This virus first reported in Wuhan Huanan seafood wholesale market that contain aquatic products, and some wild animals [1-3].

It is the seventh Corona virus found to cause illness in humans. Some researchers believed that the virus transmitted from either snakes to humans or from bats to humans. There is animal market in Wuhan that seems to be center of this out break and it is suggested that there was exposure to live and dead animals. Right now, peoples are suspecting bats are sources of COVID-19. [1, 3, 5] Corona virus infect birds and mammals. Bats are hosts to the large number of viral genotype of corona virus. Epidemic occur when viruses transmit from ones pieces to another species. The species that hosts the severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) is probably bat, containing 96% identical at the whole-genome sequence level [1, 2, 5].

Severe acute respiratory syndrome (SARS) is a beta corona virus that occur in Guangdong province of china 2003. Initially the virus transmitted from bats to civets to humans. Due to SARS illness, more than 8000 total cases, 774 deaths, and approximately 9.6% fatality rate are recorded. Middle East respiratory Syndrome (MERS) is beta Corona virus that Started at Saudi Arabian 2012. This virus transmitted from Camels to humans through eating Camels meat, drinking camels milk, exposure to camels. In this epidemic more than 2400 Cases, 858 deaths, and around 34.4% of fatality rate are recorded.

Novel corona virus 2019 may include signs of fever, cough,

shortness of breath and general breathing difficulties, organ failures or even death a severe threat to the whole society. It can be transmitted from person to person even before any actual signs appeared, which is difficult to prevent and control [4, 5, 7]. Researchers all around the world have been trying to know how the virus spreads and find out the effective ways to put this out break quickly under control. Compared there production number R_0 of SARS 2.2 to 3.6, the R_0 of COVID-19 shows awful transmission as 2.2, 3.8 and 2.6 by different research in the world. WHO published an estimated R_0 of COVID-19 is 1.4 to 2.5, the larger R_0 the higher power the transmission rate [1-5].

There is no specific medicine to prevent or treat corona virus disease (COVID-19). People may need supportive care to help them breathe. If you have mild symptoms, stay at home until you have recovered. You can relieve your symptoms if you: (i) rest and sleep, (ii) keep warm, (iii) drink plenty of liquids, and (iv) use a room humidifier or take a hot shower to help eases sore throat and cough [6, 7, 16] Most people infected with the COVID-19 virus will experience mild to moderate respiratory illness and recover without requiring special treatment. Older people, and those with underlying medical problems are more likely to develop serious illness [7, 8, 16]. Novel Corona virus (2019-nCoV), Situation Report 1, Initially the Disease spread in china, republic of Korea, and Thailand and It was 282 number of confirmed cases reported globally up to 21 January 2020. Corona virus disease 2019 (COVID-19) Situation Report–94, shows that there are 2,695,418 peoples are infected and 188,804 peoples are died and 739,871 peoples are recovered from Corona virus disease (Covid-19) pandemic up to 23 April 2020 in which this paper is organized [16].

It is urgent to study and provide more scientific information for a better understanding of the novel corona virus (nCoV) or COVID-19. Thus susceptible-infectious-Treated-recovered (SITR) model is adopted to understand the transmission dynamics or potential spread of COVID-19 based on the current data. The basic reproduction number R_0 of the COVID-19 pandemic will be computed for different infection rates and conclusions drawn depending on the value of the reproduction number.

The paper Contain the following sections: Insection 2, Mathematical model formulation: Model assumptions, description of variables and parameters, Model diagram and Model equations are presented. In section 3, Mathematical Model Analysis: positivity, Boundedness, and existence of solution, Equilibrium points are Discussed. In section 4, Stability Analysis of Equilibrium points; Next Generation matrix, *Local Stability of DFEP*, Global Stability of endemic equilibrium point, Basic Reproduction number will be presented. In Section 5, Simulation Study of our model equations are performed with initial conditions given for the variables and some values are assigned for the parameters. results and discussion are presented in section 6. In Section 7, Conclusions and Recommendations are drawn depend on the stability analysis and simulation study.

2. Mathematical Model Formulation and Assumptions

In this paper mathematical model of COVID-19 with treatment will be discussed. The total populations are divided in to four compartments:(i) Susceptible Compartment denoted by S consists persons which are capable of becoming infected (ii) Infected compartment denoted by I consists of persons which are infected with COVID-19 and are also infectious (iii) Treatment compartment denoted by T consists of persons being treated and (iv) Recovered compartment denoted by R consists of recovered persons from COVID-19. A system of differential equation is formulated based on the following assumptions.

1. Suppose total population is constant $N = S(t) + I(t) + T(t) + R(t)$.
2. The number of births and death may not be equal, the population is well mixed, immigration and migration is not considered in the model.
3. Susceptible persons are recruited in to the compartment $S(t)$ at constant rate Λ
4. Susceptible persons will be infected, if they come in to contact to infective & transmitted at rate α
5. The infected persons join treatment compartment and treated at rate β.
6. The treated persons join recovery compartment at rate γ.
7. Recovered persons revert to the susceptible person after losing their immunity at rate ρ.
8. All types of persons suffer natural mortality at rate μ.
9. Infected persons die due to COVID-19 Pandemic at rate δ.
10. Assume that all parameters are positive.

Table 1. *Notations and description of model variables.*

Variables	Descriptions
S(t)	Population size of susceptible person
I(t)	Population size of infected & infectious person
T(t)	Population size of under treatment person
R(t)	Population size of recovered person

Table 2. *Notations and description of model parameters.*

Parameters	Descriptions
Λ	*Recruitment rate. susceptible* person enter in to susceptible compartment with this rate.
α	*Infection rate*. susceptible persons become infected to COVID-19 with this rate
β	*Treatment rate*. With this rate infective person move from compartment I to T for treatment.
γ	Recovery rate. With this rate treated class moves from compartment T to R
ρ	re-infection rate. recovered persons infected with rate and moves from compartment R to S
δ	*Death rate due COVID-19*. Infected person under infected I & treatment T Compartments are die.
μ	*Natural death rate.* With this rate all Compartment are suffering from natural death rate.

Having the above assumptions the model diagram shown in Figure 1.

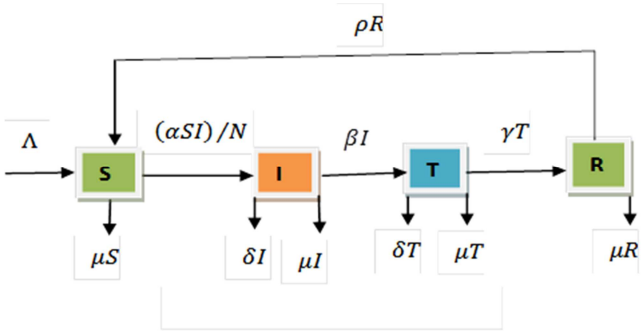

Figure 1. *Model Diagram.*

Based on the assumptions and Model diagram, the following system of differential equations are obtained.

$$dS/dt = \Lambda + \rho R - [(\alpha SI)/N] - \mu S \quad (1)$$

$$dI/dt = [(\alpha SI)/N] - \beta I - \delta I - \mu I \quad (2)$$

$$dT/dt = \alpha I - \gamma T - \delta T - \mu T \quad (3)$$

$$dR/dt = \gamma T - \rho R - \mu R \quad (4)$$

with initial conditions $S(0) > 0, I(0) \geq 0, T(0) \geq 0, R(0) \geq 0$.

3. Mathematical Analysis of the Model

To show the formulated model is meaningful and valid, it is necessary to prove that the solutions of the system of differential equations (1)–(4) are positive, bounded for all time. This properties of the model can be considered as primary results.

Theorem 1 [Positivity] All Solutions of the mathematical model (1)–(4) are always positive with initial conditions $S(0) > 0, I(0) \geq 0, T(0) \geq 0, R(0) \geq 0$. That is the model variables $S(t), I(t), T(t)$, and $R(t)$ are positive for all t and will remain in $\mathbb{R}^4_+$.

Proof: Positivity is shown separately for each variables $S(t), I(t), T(t)$, and $R(t)$.

Positivity of $S(t)$*:* Equation (1) given by $dS/dt = \Lambda + \rho R - [(\alpha SI)/N] - \mu S$ can be expressed without loss of generality, eliminating the positive terms $(\Lambda + \rho R)$, as inequality as $dS/dt \geq -\left(\left[{}^{\alpha I}/_{N}\right] + \mu\right)S$. Using separable of variable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $S(t) \geq e^{-([\alpha I/N]+\mu)t}$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent, Hence, it can be concluded that $S(t) \geq 0$. Positivity of $I(t)$: Equation (2) arranged $dI/dt = [(\alpha SI)/N] - (\beta + \delta + \mu)I$ can be expressed without loss of generality, after eliminating the positive term $((\alpha SI)/N)$ which are appearing on the right hand side, inequality as $dI/dt \geq -(\beta + \delta + \mu)I$. Using variables separable method and on applying integration, the solution of the foregoing differential inequality can be obtained as $I(t) \geq e^{-(\beta+\delta+\mu)t}$. Hence, it can be concluded that $I(t) \geq 0$.

Positivity of $T(t)$*:* Equation (3) arranged $dT/dt = \beta I - (\gamma + \delta + \mu)T$ can be expressed without loss of generality, after eliminating the positive term(βI)which are appearing on the right hand side, inequality as $dT/dt \geq -(\gamma + \delta + \mu)T$. Using variables separable method and on applying integration, the solution of the fore going differential inequality can be obtained as $T(t) \geq e^{-(\gamma+\delta+\mu)t}$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent. Hence, it can be concluded that $T(t) \geq 0$.

Positivity of $R(t)$*:* Equation (4) arranged $dR/dt = \gamma T - (\rho + \mu)R$ can be expressed without loss of generality, after eliminating the positive term(γT)which are appearing on the right hand side, inequality $dR/dt \geq -(\rho + \mu)R$. Using variables separable method and on applying integration, the solution of the foregoing differential inequality can be obtained as $R(t) \geq e^{-(\rho+\mu)t}$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent. Hence, it can be concluded that $R(t) \geq 0$.

Thus variables $S(t), I(t), T(t)$, and $R(t)$ represent persons at different compartment which are positive quantities and will remain in $\mathbb{R}^4_+$ for all time [9, 10, 13, 16].

Theorem 2 [Boundedness] The positive solutions of mathematical models (1)–(4) are bounded. That is variables S(t), I(t), T(t), & R(t) are bounded for all t.

Proof: each population size of variable is bounded if and only if the total population size N is bounded. Hence, it is sufficient to show that total population size $N = S(t) + I(t) + T(t) + R(t)$ is bounded for all t. This can be depicted that all feasible solutions are uniformly bounded in a proper subset $\Omega \in \mathbb{R}^4_+$ where the feasible region Ω isgivenby $\Omega = \{(S, I, T, R) \in \mathbb{R}^4_+; N \leq (\Lambda/\mu)\}$.

It is trivial that $dN/dt = [dS/dt] + [dI/dt] + [dT/dt] + [dR/dt]$ Then adding all four equations (1)–(4) results $dN(t)/dt = \Lambda - \mu(S + I + T + R) - \delta(I + T)$ which implies $dN(t)/dt = \Lambda - \mu N(t) - \delta(I + T)$. after eliminating negative term $[-\delta(I + T)]$ resultsinequality $dN(t)/dt \leq [\Lambda - \mu N(t)]$. Equivalently this inequality can be expressed as $dN(t)/dt + \mu N(t) \leq \Lambda$ solving this differential equation yields $N(t) \leq (\Lambda/\mu) + Ae^{-\mu t}$ general solution. But the term $N(0)$ represents initial values of variable $N(t) = N(0)$ at $t = 0$. Thus, particular solution can be written as $N(t) \leq (\Lambda/\mu) + [N(0) - (\Lambda/\mu)]e^{-\mu t}$. Furthermore, $N(t) \to (\Lambda/\mu)$ as $t \to \infty$. Thus, the total population size of $N(t)$ takes off from the value $N(0)$at $t = 0$and ends up with bounded value (Λ/μ) astime t goestoinfinity. hence $N(t)$ is bounded as $0 \leq N(t) \leq (\Lambda/\mu)$. Hence, feasible solution of the system of differential equations (1)–(4) remains in the region Ωwhich is positively invariant set. Thus, the given mathematical model is meaningful and mathematically well posed in the domain of region Ω. hence, variables $S(t), I(t), T(t)$, &$R(t)$ are bounded for all t [9, 10, 13, 16].

Theorem 3 [Existence] All Solutions of differential equations (1)–(4) exist in $\mathbb{R}^4_+$ with the initial conditions $S(0) > 0, I(0) \geq 0, T(0) \geq 0, R(0) \geq 0$. That is variables $S(t), I(t), T(t)$, &$R(t)$ exist for all t and remain in $\mathbb{R}^4_+$.

Proof: Define the differential equation (1)–(4) as follows:

$$f_1 = \Lambda + \rho R - [(\alpha SI)/N] - \mu S$$

$$f_2 = [(\beta IS)/N] - (\beta + \delta + \mu)I$$

$$f_3 = \beta I - (\gamma + \delta + \mu)T$$

$$f_4 = \gamma T - (\rho + \mu)R$$

Suppose Ω represent a region $\Omega = \{(S,\ I,\ T,\ R) \in \mathbb{R}^4_+;\ N \leq (\Lambda/\mu)\}$. Then According to Derrick & Groosman theorem, the differential equations (1)–(4) have a unique solution if$(\partial f_i)/(\partial x_j)$are continuous & bounded in a region Ω for $i,j = 1,2,3,4$ Here $x_1 = S, x_2 = I, x_3 = T, x_4 = R$, Continuity and the boundedness can be verified as follows:

Table 3. *Partial derivatives of model with respect to variables.*

For f_1:	For f_3:
$\lvert(\partial f_1)/(\partial S)\rvert = \lvert-[(\alpha I/N) + \mu]\rvert < \infty$	$\lvert(\partial f_3)/(\partial S)\rvert = 0 < \infty$
$\lvert(\partial f_1)/(\partial I)\rvert = \lvert-(\alpha S/N)\rvert < \infty$	$\lvert(\partial f_3)/(\partial I)\rvert = \lvert\beta\rvert < \infty$
$\lvert(\partial f_1)/(\partial T)\rvert = 0 < \infty$	$\lvert(\partial f_3)/(\partial T)\rvert = \lvert-(\gamma + \delta + \mu)\rvert < \infty$
$\lvert(\partial f_1)/(\partial R)\rvert = \lvert\rho\rvert < \infty$.	$\lvert(\partial f_3)/(\partial R)\rvert = 0 < \infty$
For f_2:	For f_4:
$\lvert(\partial f_2)/(\partial S)\rvert = \lvert\alpha I/N\rvert < \infty$	$\lvert(\partial f_4)/(\partial S)\rvert = 0 < \infty$
$\lvert(\partial f_2)/(\partial I)\rvert = \lvert(\alpha S/N) - (\beta + \delta + \mu)\rvert < \infty$	$\lvert(\partial f_4)/(\partial I)\rvert = 0 < \infty$
$\lvert(\partial f_2)/(\partial T)\rvert = 0 < \infty$	$\lvert(\partial f_4)/(\partial T)\rvert = \lvert\gamma\rvert < \infty$
$\lvert(\partial f_2)/(\partial R)\rvert = 0 < \infty$	$\lvert(\partial f_4)/(\partial R)\rvert = \lvert-(\rho + \mu)\rvert < \infty$

Thus, all the partial derivatives $(\partial f_i)/(\partial x_j), i,j = 1,2,3,4$ exist, continuous and bounded in Ω. Hence the solution of differential equations (1)–(4) exists and unique by Derrick & Groosman theorem [9, 10, 14, 16].

4. Equilibrium Points of the Model

4.1. Disease-free Equilibrium Points of the Model

Disease-free equilibrium points are solutions of model equations where$I(t) = T(t) = R(t) = 0$ due to no disease in the population and the right hand side of differential equation (1)-(4) is equal to zero. Thus $\Lambda - \mu S = 0$ which results $S = \Lambda/\mu$. hence, the disease-free equilibrium point of differential equation (1)–(4) is given by $E(S,\ I,\ T,\ R) = (\Lambda/\mu,\ 0,\ 0,\ 0)$

4.2. Positive or Endemic Equilibrium of the Model

The endemic equilibrium point $E^*\{S^*, I^*, T^*, R^*\}$ is a positive equilibrium point solutions, where the disease persists in the population. The endemic equilibrium point is obtained by taking rates of changes of variables with respect to time is zero. hence $dS/dt = dI/dt = dT/dt = dR/dt = 0$, then differential equations (1)-(4) can be written as the system differential equations;

$$\Lambda + \rho R - [(\alpha SI)/N] - \mu S = 0 \quad (5)$$

$$[(\alpha SI)/N] - pI = 0 \quad (6)$$

$$\beta I - qT = 0 \quad (7)$$

$$\gamma T - rR = 0 \quad (8)$$

Where $p = \beta + \delta + \mu, q = \gamma + \delta + \mu, r = \rho + \mu$. Then Equation (6) arranged as $[(\alpha S/N) - p]I = 0$ which results$(\alpha S/N) - p = 0$ or$I = 0$. but Idoes not vanish due to the disease is assumed to exist in the system. Then the only meaningful solution of the system is $(\alpha S/N) - p = 0$ solving for S yields:

$$S^* = [pN]/\alpha \quad (9)$$

In Similarly fashion, solving equations (7) & (8) results expression for T& R interms of variable I

$$T = [\beta I]/q \quad (10)$$

$$R = ([\gamma T]/r) = (\gamma/r)([\beta I]/q) = [\beta\gamma I]/[qr] \quad (11)$$

Then plug equations (9), (10) & (11) into (5) results;

$$\Lambda + \rho([\beta\gamma I]/[qr]) - (\alpha I/N)([pN]/\alpha) - \mu([pN]/\alpha) = 0 \quad (12)$$

plug the value of total population size$N = (\Lambda/\mu)$ on equation (12) and solving for I, will yield expression for I^*. hence the endemic equilibrium points are

$$I^* = [(\alpha - p)qr\Lambda]/[\alpha(pqr - \beta\gamma\rho)] \quad (13)$$

Now substitute I^* in (10) & (11) will result expressions for T^* and R^* interms of parameters.

$$T^* = [(\alpha - p)\beta r\Lambda]/[\alpha(pqr - \beta\gamma\rho)] \quad (14)$$

$$R^* = [(\alpha - p)\beta\gamma\Lambda]/[\alpha(pqr - \beta\gamma\rho)] \quad (15)$$

Hence, the positive equilibrium point is given by

$$E^*\{S^*,\ I^*,\ T^*,\ R^*\} = \{[pN]/\alpha,\ [(\alpha - p)qr\Lambda]/[\alpha(pqr - \beta\gamma\rho)],\ [(\alpha - p)\beta r\Lambda]/[\alpha(pqr - \beta\gamma\rho)],\ [(\alpha - p)\beta\gamma\Lambda]/[\alpha(pqr - \beta\gamma\rho)]\}$$

5. Stability Analysis of Equilibrium Points of the Model

In this section the Local Stability of Disease-free equilibrium point (LSDFEP) of the model is established and proved as follows in theorem 4.

Theorem 4 The differential equations (1)–(4) is locally asymptotically stable at DFEP E_0 if $\alpha \leq \beta + \delta + \mu$ & unstable if $\alpha > \beta + \delta + \mu$

Proof: Define the differential equations (1)–(4) as follows;

$dS/dt = \Lambda + \rho R - [(\alpha SI)/N] - \mu S \equiv f(S,\ I,\ T,\ R)$

$dI/dt = [(\alpha SI)/N] - pI \equiv g(S,\ I,\ T,\ R)$

$dT/dt = \beta I - qT \equiv h(S,\ I,\ T,\ R)$

$dR/dt = \gamma T - rR \equiv k(S,\ I,\ T,\ R)$, Where $p = \beta + \delta + \mu, q = \gamma + \delta + \mu, r = \rho + \mu$

Now, Next generation matrix of the functions (f, g, h, k) with respect to variables $(S,\ I,\ T,\ R)$ is

$$J(S\quad I\quad T\quad R) = \begin{bmatrix} -(\alpha I/N) - \mu & (\alpha S/N) & 0 & \rho \\ (\alpha I/N) & (\alpha S/N) - p & 0 & 0 \\ 0 & \beta & -q & 0 \\ 0 & 0 & \gamma & -r \end{bmatrix}$$

Therefore, the Next generation matrix evaluated at disease-free equilibrium point (DFEP) E_0 yields

$$J[(\Lambda/\mu)\quad 0,\quad 0,\quad 0] = \begin{bmatrix} -\mu & -\alpha & 0 & \rho \\ 0 & (\alpha - p) & 0 & 0 \\ 0 & \beta & -q & 0 \\ 0 & 0 & \gamma & -r \end{bmatrix}$$

Then eigen values of the next generation matrix $J(E_0)$will be computed from the roots of characteristic equation $\det[J(E_0) - \lambda I] = 0$. That is

$$\begin{vmatrix} -\mu - \lambda & -\alpha & 0 & \rho \\ 0 & (\alpha - p) - \lambda & 0 & 0 \\ 0 & \beta & -q - \lambda & 0 \\ 0 & 0 & \gamma & -r - \lambda \end{vmatrix} = 0$$

$$((\alpha - p) - \lambda)\begin{vmatrix} -\mu - \lambda & 0 & 0 \\ 0 & -q - \lambda & 0 \\ 0 & \gamma & -r - \lambda \end{vmatrix} = 0$$

$$(\alpha - p - \lambda)(-q - \lambda)\left|\begin{matrix} -\mu - \lambda & \delta \\ 0 & -r - \lambda \end{matrix}\right| = 0$$

$(\alpha - p - \lambda)(-q - \lambda)(-\mu - \lambda)(-r - \lambda) = 0$ Thus, the four eigen values of the next generation matrix are

$$\lambda_1 = \alpha - p, \lambda_2 = -q, \lambda_3 = -\mu, \lambda_4 = -r$$

plug value of p, q and r yields: $\lambda_1 = \alpha - (\beta + \delta + \mu), \lambda_2 = -(\gamma + \delta + \mu), \lambda_3 = -\mu,\ \lambda_4 = -(\rho + \mu)$ Hence disease-free equilibrium point (DFEP) E_0 of the system of differential equations (1)–(4) is locally asymptotically stable if $\alpha - p \leq 0$ & unstable if $\alpha - p > 0$ which means the DFEP E_0 of the system of differential equation is locally asymptotically stable if $\alpha \leq \beta + \delta + \mu$ & unstable if $\alpha > \beta + \delta + \mu$

Global Stability Analysis of Endemic Equilibrium Point (GSEEP) of the model.

The Global stability analysis of positive or endemic equilibrium point of the model $E^*(S^*,\ I^*,\ T^*,\ R^*)$ is established and proved as follows in theorem 5.

Theorem 5

The endemic equilibrium point $E^*(S^*,\ I^*,\ T^*,\ R^*)$ is globally asymptotically stable.

Proof: To prove the theorem take appropriate liapunove function [9, 10, 13, 15, 16].

Suppose that $L(S,\ I,\ T,\ R) = m_1(s - s^*)^2/2 + m_2(I - I^*)^2/2 + m_3(T - T^*)^2/2 + m_4(R - R^*)^2/2$

$$dL/dt = m_1(s - s^*)\{ds/dt\} + m_2(I - I^*)\{dI/dt\} + m_3(T - T^*)\{dT/dt\} + m_4(R - R^*)\{dR/dt\} \quad (16)$$

Then plug the differential equations (1)-(4) into (16)

$$dL/dt = m_1(s - s^*)\{\Lambda + \rho R - [(\alpha SI)/N] - \mu S\} + m_2(I - I^*)\{[(\alpha SI)/N] - pI\} + m_3(T - T^*)\{\beta I - qT\} + m_4(R - R^*)\{\gamma T - rR\}$$

Take the variables S, I, T, R out of each bracket as follows

$$dL/dt = m_1(s - s^*)(s - s^*)$$

$$\left\{\left[\frac{\Lambda}{S}\right] + \left[\frac{\rho R}{S}\right] - [(\alpha I)/N] - \mu\right\} + m_2(I - I^*)(I - I^*)\{[(\alpha S)/N] - p\}$$

$$+m_3(T - T^*)(T - T^*)\{[\beta I/T] - q\} + m_4(R - R^*)(R - R^*)\{[\gamma T/R] - r\}$$

Take negative sign out from each bracket, then observe resulting equations to complete the proof.

$$dL/dt = -m_1(s - s^*)^2$$

$$\left\{-\left[\frac{\Lambda}{S}\right] - \left[\frac{\rho R}{S}\right] + [(\alpha I)/N] + \mu\right\} - m_2(I - I^*)^2\{-[(\alpha S)/N] + p\} - m_3(T - T^*)^2\{-[\beta I/T] + q\} - m_4(R - R^*)^2\{-[\gamma T/R] + r\}$$

Thus, it is possible to conclude that $dL/dt \leq 0$, for non negative integers m_1, m_2, m_3, m_3 and hence endemic equilibrium point is globally stable.

6. Basic Reproduction Number

The basic reproduction number denoted by $R_0$and defined as the expected number of people getting secondary infection among the whole susceptible population. This number shows a potential for spread of disease within a given population. When $R_0 < 1$ each infected individual produces on average less than one new infected individual so that the disease is expected to die out. On the other hand if $R_0 > 1$, then each individual produces more than one new infected individual so that the disease is expected to continue spreading in the population [11, 12, 14].

The basic reproductive numberR_0can be determined using the next generation matrix. In this method, R_0 is defined as the largest eigen value of the next generation matrix. Constructing the next generation matrix involves classifying

all compartments of differential equation (1)-(4) into two classes: infected and non-infected class. Thus, basic reproduction number could not be found from structure of model equation alone but rather from definition of infected & uninfected compartments.

Assume that there are n compartments in the model of which the first m compartments are with infected individuals [3]. From the system (1)–(4) the first three equations are considered and decomposed into two groups; F contains newly infected cases, V contains the remaining terms, and Let $X = [I, T, S]^t$ be a column vector and the differential equations of the first three compartments are rewritten as $F(X) - V(X)$.

Let $F(X) = [F_1, F_2, F_3]^t$. Here (i) $F_1 = (\alpha SI\ /\ N)$ denote newly infected cases which arrive in to the infected compartment; (ii) $F_2 = 0$ denotes newly infected cases arrived in to the treated compartment, and (iii) $F_3 = 0$denotes newly infected case from susceptible compartment. let $V(X) = [V_1, V_2, V_3]^t$. Here $V_1 = pI$; $V_2 = -\alpha I + qT, V_3 = -\Lambda + (\alpha SI\ /\ N) + \mu S$, where parameters $p = (\beta + \delta + \mu)$ & $q = (\gamma + \delta + \mu)$.

Then next step is the computation of the square matrices F and V of order $m \times m$, where m is the number of infected classes, defined by $F = [\partial F_i(E_0)/\partial x_j]$ and $V = [\partial V_i(E_0)/\partial x_j]$ with $1 \le i, j \le m$, such that F is non-negative, V is a non-singular matrix and E_0 is the disease free equilibrium point DFE. If F is non-negative and V non-singular, then V^{-1} is non-negative and thus FV^{-1} is also non-negative. The matrix FV^{-1} is called the next generation matrix for the model. The basic reproduction number $R_0 = \rho(FV^{-1})$. where $\rho(A)$ denotes the spectral radius of matrix A and the spectral radius is the biggest non-negative eigen value of the next generation matrix. The Jacobian matrices for $F(X)$ and $V(X)$ at $(I,\ T,\ S)$ can be Computed as

$$J_F(X) = \begin{bmatrix} (\alpha S/N) & 0 & (\alpha I/N) \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \text{ and}$$

$$J_V(X) = \begin{bmatrix} p & 0 & 0 \\ -\beta & q & 0 \\ (\alpha S/N) & 0 & (\mu + [\alpha I/N]) \end{bmatrix}.$$

The respective Jacobian Matrix of F and V at the disease free equilibrium point E_0 takes the form

$$J_F(E_0) = \begin{bmatrix} \alpha & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \text{ and } J_V(E_0) = \begin{bmatrix} p & 0 & 0 \\ -\beta & q & 0 \\ \alpha & 0 & \mu \end{bmatrix}.$$

Clearly $det[J_F(E_0)]$ is non-zero. Thus Matrix $J_V(E_0)$ is invertible and its inverse matrix exists. So after computation of its inverse matrix results;

$$[J_V(E_0)]^{-1} = \begin{bmatrix} (1/p) & 0 & 0 \\ (\beta/pq) & (1/q) & 0 \\ (\alpha/\mu p) & 0 & (1/\mu) \end{bmatrix}.$$

The product of matrices $J_F(E_0)$ and $[J_V(E_0)]^{-1}$ can be given by

$$\rho = [J_F(E_0)][J_V(E_0)]^{-1}$$

$$= \begin{bmatrix} \alpha & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} (1/p) & 0 & 0 \\ (\beta/pq) & (1/q) & 0 \\ (\alpha/\mu p) & 0 & (1/\mu) \end{bmatrix}.$$

$$= \begin{bmatrix} (\alpha/\beta) & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

Recall that the basic reproduction number (threshold value) R_0 is the largest eigen value in spectral radius matrix $\rho = [J_F(E_0)][J_V(E_0)]^{-1}$. Thus, eigen values of spectral radius Matrix ρ are determined from the roots of characteristic polynomial equation $\det[\rho - \lambda I] = 0$ which implies $det\left[[J_F(E_0)][J_V(E_0)]^{-1} - \lambda I\right] = 0$ Hence, the basic reproduction number is $R_0 = (\alpha/\beta)$.

7. Numerical Simulation

In this section, the numerical simulation of model equations (1)–(4) is done, using the software DEDiscover 2.6.4. For Simulation purpose, Model equations are arranged and a set of meaningful values are assigned to the model parameters. These sets of parametric values are given in Table 4.

dS/dt=Lambda+Rho*R-(Alpha*S*I)/N-Mu*S//susceptible class

dI/dt=(Alpha*S*I)/N-(Beta+Delta+Mu)*I//Infected class

dT/dt=Alpha*I-(Gamma+Delta+Mu)*T//Population Class under Treatment

dR/dt=Gamma*T-(Delta+Mu)*R//Recovered class

Table 4. *Parameter values.*

Parameters	Values	References
Λ	0.965	Assumed
α	0.020, 0.043, 0.169	Assumed
β	0.043	Assumed
γ	0.169	Assumed
ρ	0.476	Assumed
δ	0.099	Assumed
μ	0.067	Assumed

Using the parameter values given in Table 2 and the initial conditions $S(0) = 4, I(0) = 1 = T(0), R(0) = 2$in the model equations (1)–(4) a simulation study is conducted and the results are given in Figures 2-4.

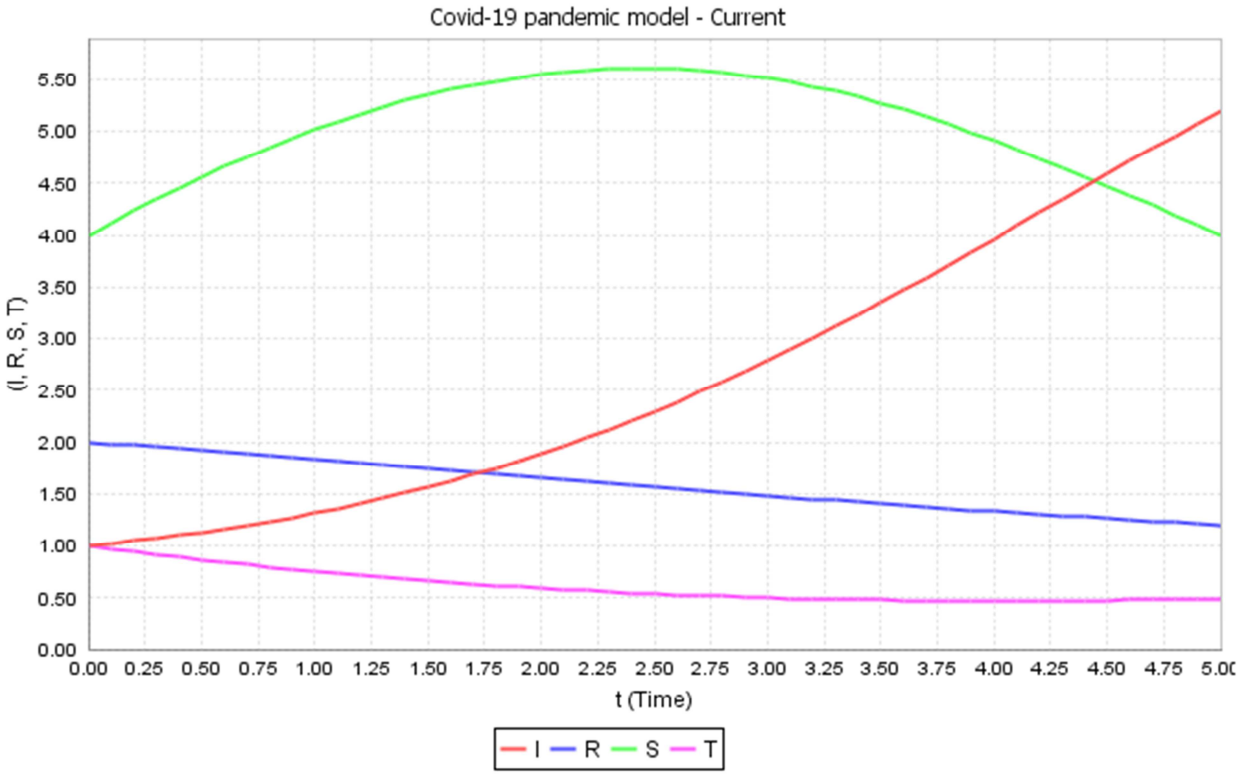

Figure 2. *Time series plot for COVID-19 pandemic at* $\alpha = 0.169$ *with* $R_o = 3.93$

From Figure 2, it is observed that the number of infected individuals looks like exponential curve which tell us Covid-19 expanded rapidly in the community. This phenomenon supplemented by the basic reproduction number $R_o = 3.93$. Thus COVID-19 pandemic will persist in the community for some period of time. The remaining population gradually decrease in number as shown above.

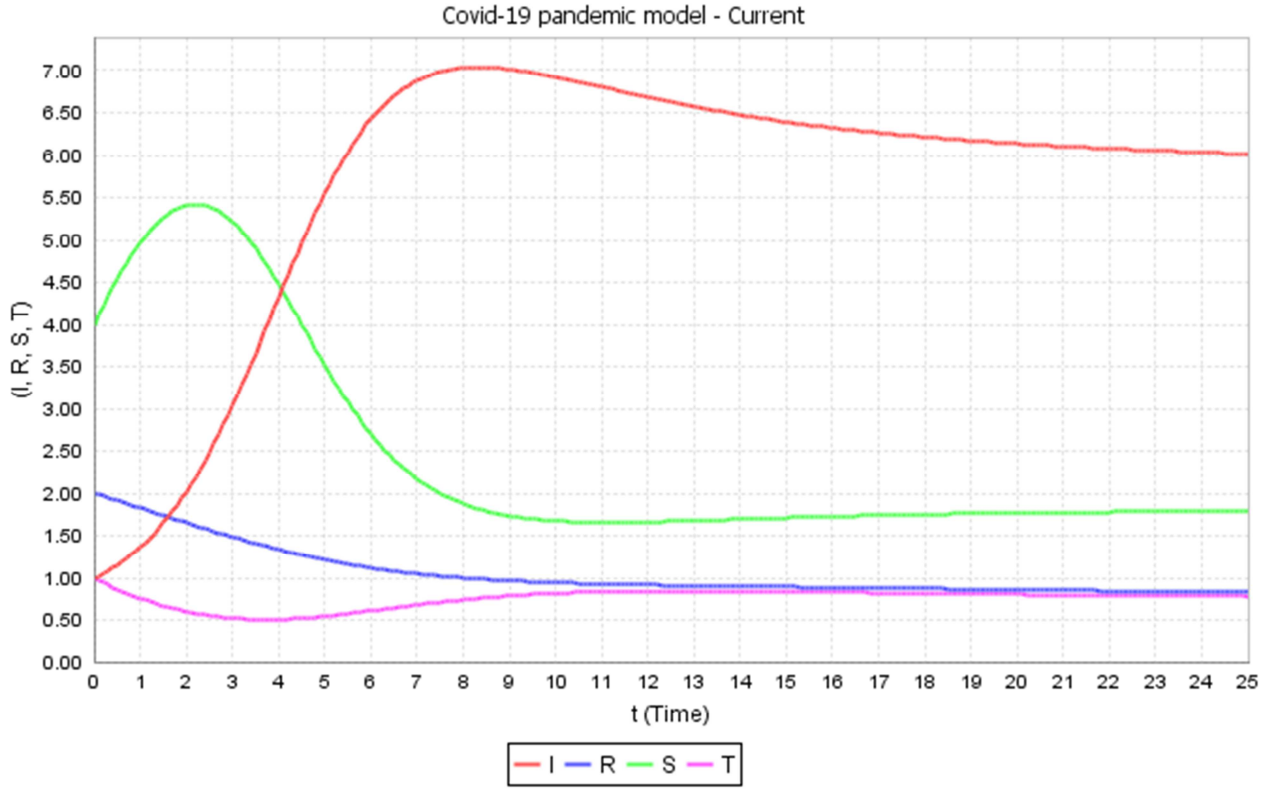

Figure 3. *Time series plot for COVID-19 pandemic at* $\alpha = 0.043$ *with* $R_o = 1$.

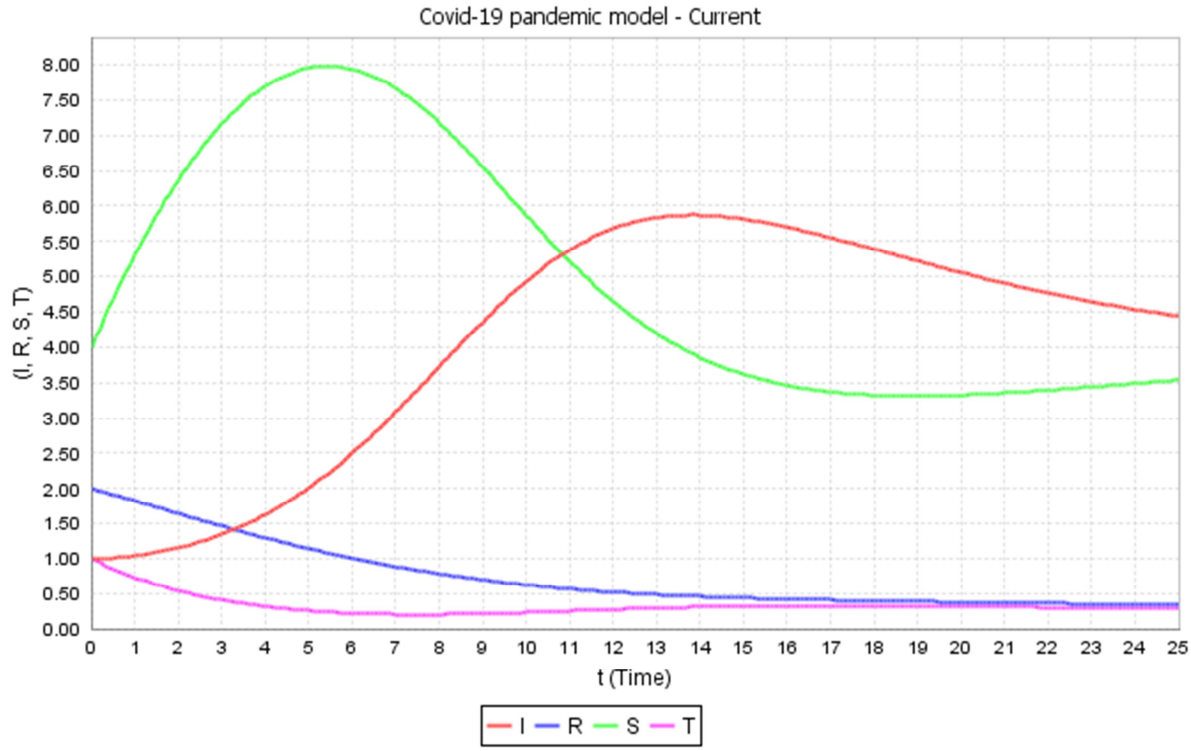

Figure 4. *Time series plot for COVID-19 pandemic at* $\alpha = 0.02$ *with* $R_o = 0.465$.

From Figure 3 and Figure 4, one can observe that the number of infected individual look like logistic curve, meaning the disease continue to spread in the community for some period of time. These phenomenon stable or die out in some time in the future which is supplemented by the basic reproduction number $R_o = 1$ in figure 3 From the time series plot in figure 4, $R_o = 0.465$ that shows the disease dies out or under control.

8. Conclusion and Recommendation

In this paper, a mathematical model of COVID-19 pandemic with treatment given to the infected individuals has been developed based on reasonable assumptions. Moreover, positivity, boundedness, and existence of solution of the model is verified or proved to clarify the model is meaningful and mathematically well posed. Existence of equilibrium points of the model were identified. Local Stability analysis of disease-free equilibrium point (DFEP) is proved with the concept of next generation matrix and global stability analysis of endemic equilibrium point is done by taking appropriate liapunove function. In this study, the basic reproduction numbers were computed as$R_0 = 3.93, 1, 0.469$for different infection rate$\alpha = 0.169, 0.043, 0.02$ respectively with constant treatment. For those basic reproduction numbers $R_0 > 1$, the numbers of cases of COVID-19 pandemic increase rapidly and will persist in the community. For those basic reproduction numbers $R_0 < 1$, COVID-19 pandemic become slow or weak in spreading and gradually the disease may dies out. The smaller infection rate leads to smaller reproduction number. Hence it is recommend to reduce infection rates by Masks, gloves, wash or sanitize hands. Moreover, both Health and government officials have to create awareness and apply proper interventions about COVID-19 pandemic and its transmission so as to reduce COVID-19 pandemic in the community.

References

[1] Yaqing Fang, Yiting Nie, Marshare Penny. Transmission dynamics of the COVID-19 outbreak and effectiveness of government interventions: A data-driven analysis. Journal of medical virology, Wiley. March 2020.

[2] Chayu, Yang and Jin Wang, March 2020. A mathematical model for the novel corona virus epidemic in Wuhan, China. Mathematical biosciences and engineering 17 (3): March (2020) 2708–2724.

[3] Alexander, Okhuese Victor. mathematical predictions for covid-19 as a global pandemic. Research Gate. march 2020.

[4] Jyoti Bhola, Vandana Revathi Venkateswaran and Monika Koul. Corona Epidemic in Indian context: Predictive Mathematical Modeling, med Rxiv preprint doi: https://doi.org/10.1101/2020.04.03.20047175.

[5] Binti Hamzah FA, Lau C, Nazri H, Ligot DV, Lee G, Tan CL, etal. Corona Tracker: World-wideCOVID-19 Outbreak Data Analysis and Prediction. Bull World Health Organ. E-pub: 19 March 2020. doi: http://dx.doi.org/10.2471/BLT.20.255695.

[6] Website: https://www. who. int› health-topics› corona virus.

[7] Website: https:/www.who.int›docs›default-source›who-china-joint.

[8] P. Zhou, X. L. Yang, X. G. Wang, B. Hu, L. Zhang, W. Zhang, et al., Discovery of a novel corona virus associated with the recent pneumonia outbreak in humans and its potential bat origin, bioRxiv, 2020.

[9] Abayneh Fentie Bezabih, Geremew Kenassa Edessa, Koya Purnachandra Rao "Mathematical Eco-Epidemic Model on Prey-Predator System. IOSR Journal of Mathematics (IOSR-JM), 16 (1), (2020): pp. 22-34.

[10] Alfred Hugo, Estomih S. Massawe, and Oluwole Daniel Makinde. An Eco-Epidemiological Mathematical Model with Treatment and Disease Infection in both Prey and Predator Population. Journal of Ecology and natural environment Vol. 4 (10), July 2012, pp. 266-273.

[11] Tadele Tesfa Tegegne, Purnachandra Rao Koya and Temesgen Tibebu Mekonnen. Impact of Heterosexuality & Homosexuality on the transmission and dynamics of HIV/AIDS, IOSR Journal of Mathematics (IOSR-JM), Volume 12, Issue 6 Ver, 2016, PP 38-49.

[12] P. van den Driessche and James Watmough. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. Mathematical Biosciences 180 (2002) 29–48.

[13] Abayneh Fentie Bezabih, Geremew Kenassa Edessa, Purnachandra Rao Koya. Mathematical Eco-Epidemiological Model on Prey-Predator System. Mathematical Modeling and Applications. Vol. 5, No. 3, 2020, pp. 183-190. doi: http://10.11648/j.mma.20200503.17.

[14] Selam Nigusie Mitku, Purnachandra Rao Koya. Mathematical Modeling and Simulation Study for the Control and Transmission Dynamics of Measles. American Journal of Applied Mathematics. Vol. 5, No. 4, 2017, pp. 99-107. doi: http://10.11648/j.ajam.20170504.

[15] Sachin Kumar and Harsha Kharbanda. Stability Analysis of Prey-Predator Model with Infection, Migration and Vaccination In Prey, arXiv: 1709. 10319vl [math. DS], 29 Sep 2017.

[16] Abayneh Fentie Bezabih, Geremew Kenassa Edessa, Purnachandra Rao Koya. Mathematical Epidemiology Model Analysis on the Dynamics of COVID-19 Pandemic. American Journal of Applied Mathematics. Vol. 8, No. 5, 2020, pp. 247-256. doi: http://10.11648/j.ajam.20200805.12.