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A Deterministic Mathematical Model and Analysis of Transmission Dynamics of Covid-19 from Reservoir-to-Human

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ABSTRACT. This article presents a deterministic mathematical model for the transmission dynamics of Covid-19 from the reservoir to the people. The model system properties were analyzed, such as the feasibility of the solutions, positivity of the state variables, and stability of the model equilibria—both local and global equilibrium points. Also, the basic reproduction number, R_0, was computed along with its sensitivity to model parameters to identify the most persuading parameter, and the results proved that high values of the parameters associated with the rate of controlling the infection out of human life and back to the reservoir will drastically minimize the spread rate of Covid-19 among people.
The local stability of disease-free equilibrium was determined through the trace and determinant of matrix method. The disease-free equilibrium will be asymptotically stable if the $tr(J_{\mathbb{E}^0}) < 0$ and $det(J_{\mathbb{E}^0}) > 0$. The disease-free and endemic equilibria were found to be globally stable when the $R_0 < 1$ and $R_0 > 1$ respectively. The analysis of the numerical simulation for the model on various sets of parameters displayed that, there is a strong noteworthy effects on the virulent if the effort of controlling the inffection is at the rate not less than 50% to pull back the infection out of people to reservoir or vanishing.

Keywords: Asymptotic Stability, Covid-19, Deterministic, Dynamics, Reservoir-to-Human.

1 INTRODUCTION

Corona virus is caused by a mild severe respiratory illness which encompasses viruses alongside non-segment, single-stranded and positive sense ribonucleic acid (RNA) genomes which are transmitted when getting in contact with infected materials, for example, through respiratory droplets. Symptoms of Coronavirus are fever, cough, the commonest one is low breathing (which can lead to pneumonic and respiratory flop). There are some recent symptoms associated with the present outbreak like headache, runny nose, body aches, fatigue, nausea, vomiting or diarrhea.

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Covid-19 was discovered in China (Wuhan city) on 31st December, 2019 [27, 28]. The genomic shows that SAR-COV-2 is phylogenetically related to severe acute respiratory syndrome like (SARS-like) bat viruses [6].

The epidemiological characteristics of an outbreak of 2019 Novel Corona Virus Disease (Covid-19) China 2020 stated that those who contacted Covid-19 have been traced to an animal and seafood. Then, it was discovered that they might have probably got the virus transmitted from those sources. In December 2019, new cases of pneumonic was noticed and from research, it was discovered that the source is from Huanan Sea Food market [18, 26]. Also, in January 22, 2020, the source/link of the virus was also traced to group 2 of Beta-Corona virus known as wild bats, and their life cycle step invoices; attachment and entry, replicate protein, transcription, assembly and release. Due to the fast spreading of the Covid-19, 2,394,278 cases were announced as confirmed cases as at April 19, 2020 and people were dying daily due to the disease (Covid-19) [20].

In Africa as a whole, Covid-19 was first noticed on 25th Feb., 2020 through those who tested positive for the disease and its importation was identified on 13th March, 2020 through Kenyan who arrived from the USA. consequently, the death rate increased to 1100 and confirmed cases of about 22,000 [28]. As for the first face of coronavirus outbreak the data gathered from about 1099 patient within 99 laboratory with Covid-19 from 552 hospital in 30 provinces of china on Jan., 29,2020 shows that only 2% of the confirmed cases have link with animals while others residing on visiting wuhan city [23].

The current Covid-19 pandemic which is caused by the highly contagious respiratory pathogen SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) has already claimed close to three million lives. SARS-CoV-2 is a zoonotic disease, which emerged from a bat reservoir and it can infect a number of agricultural and companion animal species [10]. Some of commonest and deadliest human diseases are caused by bacteria or viruses of animal origin. But understanding how an epidemic began is essential to preventing further introductions to the human population. The researchers [16, 25], stated that Coronaviridae is the family name which Covid-19 belong and they usually split into alpha (α-cov), beta (β-cov), gamma (γ-cov) and delta (δ). Alpha and beta coronaviruses can easily infect humans and the one located in human is almost the same as β-cov genius Beta-cov **and** SAR-cov-2 while MERS-COV is from lineage. How an infectious disease crosses the animal-human barrier is a riddle that can take years to solve.

Mathematical models are very essential in order to have knowledge about the behaviour of the disease and how to curtail it. Many researchers have worked in this area such as ([7,11,12,13,14,21,24,29,32]). Ming et al [29] investing a novel Susceptible-Infected-Recovered (SIR) epidemic model to present number of infected cases burdens and those on isolation cases with those in Intensive care Unit (ICU). Tuan et al [32] studied a mathematical model, offered Covid-19 transmission with caputo fractional-order derivative using Adam-Bashforth-moulton apparel. Amirudh [11] investigated the transmission dynamics in predicting the Covid-19 and described the outcome and difficulties of SIR (Susceptible-Infected-Recovered), SEIR (Susceptible-Exposed-Infected-Recovered), etc. Likewise, Akhil et al [7] developed a mathe-

matical model for Covid-19 dynamics where the population was divided into two groups, older and younger which is applicable to the Covid-19 outbreaks in Spain and Italy. The disease-free equilibrium and the basic reproductive number for each case was obtained. Hernandez-Vargas and Velasco-Hernandez [24] considered different starting times of infection by proposed mathematical models to represent SARS-CoV-2 dynamics in infected patients. Based on the target cell limited model, the within-host reproductive number for SARS-CoV-2 which is consistent with the broad values of human influenza infection. To this end, we have countless impetus to apprehend the history, spread and means of controlling infection of Covid-19 and its transmission characteristics from reservoir. This work is arranged as follows. Section 2 is about model formulation and description of Corona virus existing from reservoir. In section 3, qualitative analysis, sensitivity analysis and numerical simulation of the model was discussed. Finally, conclusion and recommendations are given in the last section.

The tables below are the states variables and parameter employed in this article.

Table 1: State variables of the model

Variables	Description
$S(t)$	Number of susceptible human
$E_p(t)$	Exposed human
$I_p(t)$	Symptomatic infected human
$T_P(t)$	Testing those people that are exposed to the virus
$H_h(t)$	Symptomatic people through human to human transmission
$F_m(t)$	Symptomatic infected people to family member
$C_c(t)$	Symptomatic infected patient to care centre (clinic centre)
$A_p(t)$	Asymptomatic infected people
$R_p(t)$	Removed/recovered people
$W(t)$	Infection reservoir
$N(t)$	Total number of human

2 MODEL FORMULATION

The transmission dynamics of Covid-19 infection, from reservoir to human population and back to reservoir, are described in this section using a mathematical model

2.1 Model Description and Formulation

The model was prepared to portray the Covid-19 widespread interaction between reservoir and human population, with the total population denoted by $N(t)$, respectively. The total population at time $t > 0$ was sub-divided into ten sub-population compartments. susceptible $S(t)$, exposed $E_p(t)$; tested people $T_p(t)$; infected $I_p(t)$,human individuals $H_h(t)$; family individual $F_m(t)$, clinic individual $C_c(t)$ recovered individuals $R(t)$, asymptomatic individuals $A_p(t)$, reservoir $W(t)$, so that

$$N(t) = S + E_p + T_p + I_p + H_h + F_m + C_c + R_p + A_p + W.$$

Table 2: Parameter symbols of the model

Parameter	Description
$\wedge_p$	Human recruitment rate
β_2	Transmission rate from I_p and A_p to S
β_1	Transmission rate from W to S
δ_p	Proportion of asymptomatic
γ_p	Rate of spreading the infection within the human
γ_h	Human transmission rate
γ_m	Infection transmission rate within family
γ_c	Rate of symptomatic individuals recovery due to caring
γ'_p	Asymptomatic recovery rate
μ_A	Rate at which asymptomatic infectious transfering infection from A_p to W
μ_p	Rate at which symptomatic infectious transfering infection from I_p to W
ω'_p	Rate of progression from E_p to A_p ($\frac{1}{\omega'_p}$: the latent period of people)
μ	Natural death rate
θ	Infection death rate
α	Rate of testing the symptomatic infectious individuals
ε	Rate at which virus leave the reservoir ($\frac{1}{\varepsilon}$ is the lifetime of the virus)
ω_p	Rate of progression from E_p to I_p ($\frac{1}{\omega_p}$: the incubation period of people)
k	The transmissibility multiple from A_p to that of I_p

Recruitment into the model is being considered in an open population with the idea of basic $S-I-R$ model in [3], then applying ordinary differential equations (ODE) system with bilinear incidence. Note that, when an individual is in contact with any infected entity, the virus begins to multiply within the cells. In the model, compartment of susceptible (S) build up by the quantity $\wedge_p$, where $\wedge_p$ is the recruitment rate into S. The compartment decreases due to infection forces denoted by the quantities $\beta_2 S(I_p + kA_p)$, $\beta_1 SW$, and μS, where β_1 is the infection contact rate from reservoir to susceptible and β_2 is the infection contact rate from infectious compartment to susceptible. Hence, rate of change of the susceptible compartment is given by

$$\frac{dS}{dt} = \wedge_p - \beta_2 S(I_p + kA_p) - \beta_1 SW - \mu S. \tag{2.1}$$

Sub-population of exposed individuals increased by the quantities $\beta_2 S(I_p + kA_p)$ and $\beta_1 SW$, while it is further decreased by the quantities μE_p, $(1-\delta_p)\omega_p E_p$, and $\delta_p \omega' E_p$, where δ_p is asymptomatic progression rate from exposed compartment. Hence, rate of change of sub-population of exposed individuals is given by

$$\frac{dE_p}{dt} = \beta_2 S(I_p + kA_p) + \beta_1 SW - \mu E_p - (1-\delta_p)\omega_p E_p - \delta_p \omega'_p E_p. \tag{2.2}$$

Sub-population of tested individuals increased by the quantity $(1-\delta_p)\omega_p E_p$ and decreases by the quantities μT_p and αT_p, where α denote the testing rate of individuals. Rate of change of sub-population of tested individuals is generated as

$$\frac{dT_p}{dt} = (1-\delta_p)\omega_p E_p - \mu T_p - \alpha T_p. \tag{2.3}$$

The sub-population of infectious individuals is increased by the quantity αT_p and decreased by the quantities $\gamma_p I_p$, μI_p, $\mu_p I_p$ and θI_p, where γ_p denote natural recovery rate of infected human, μ_p denote the rate at which symptomatic infectious individuals transfer infection from the infectious to the reservoir, θ denote the death through the infection. Hence, rate of change of Infectious class is given by

$$\frac{dI_p}{dt} = \alpha T_p - (\gamma_p + \mu + \mu_p + \theta) I_p. \tag{2.4}$$

The sub-population of human - human symptomatic transmission is increased by the quantity $\gamma_p I_p$ and reduces through the quantities μH_h and $\gamma_h H_h$, where γ_h denote the rate of transmission from human to human. Hence, rate of change of symptomatic human-human transmission compartment is given by

$$\frac{dH_h}{dt} = \gamma_p I_p - (\gamma_h + \mu) H_h. \tag{2.5}$$

The sub-population of symptomatic infected people to family member increased by the quantity $\gamma_h H_h$ and reduces through the quantities μF_m and $\gamma_m F_m$, where γ_m denote the transmission rate within the family member . Thus, the rate of change of Symptomatic infected people within family is given by

$$\frac{dF_m}{dt} = \gamma_h H_h - (\mu + \gamma_m) F_m. \tag{2.6}$$

Sub-population of symptomatic infected patient to care centre increased by the quantity $\gamma_m F_m$ and μC_c and $\gamma_c C_c$, where γ_c denote the rate of caring for the infected individuals. So, the rate of change of clinic care compartment is given by

$$\frac{dC_c}{dt} = \gamma_m F_m - (\mu + \gamma_c) C_c. \tag{2.7}$$

The sub-population of asymptomatic infected people is intensify by the quantity $\delta_p \omega_p' E_p$ and reduces through the quantities μA_p, $\gamma_p' A_p$, $\mu_A A_p$, where γ_p' denote the recovery rate of asymptomatic infectious people and μ_A denote rate of transferring infection from asymptomatic to reservoir. Therefore, the rate of change of the asymptomatic infected people compartment is given by

$$\frac{dA_p}{dt} = \delta_p \omega_p' E_p - (\mu + \gamma_p' + \mu_A) A_p. \tag{2.8}$$

The sub-population of recovered individuals increased by quantities $\gamma_p' A_p$ and $\gamma_c C_c$ and reduces through the quantity μR_p. Thus, the rate of change of recovery compartment is given by

$$\frac{dR_p}{dt} = \gamma_c C_c + \gamma_p' A_p - \mu R_p. \tag{2.9}$$

The sub-population of infection reservoir is increased by the quantities $\mu_p I_p$ and $\mu_A A_p$ and reduces through the quantity μW, εW, where ε denote the rate at which virus leave reservoir and μ denote natural mortality rate. Hence, the rate of change of the reservoir compartment is given by

$$\frac{dW}{dt} = \mu_p I_p + \mu_A A_p - (\mu + \varepsilon) W. \tag{2.10}$$

2.2 Model Assumption

The following assumptions are applied on the model

(i) The population entry is open and exit is through mortality.

(ii) The population is heterogeneous.

(iii) The model assumed that infection started spreading from the reservoir.

(iv) The Covid-19 infected person can either be symptomatic or asymptomatic.

(v) Covid-19 confers temporary immunity. That is individuals in this category become susceptible after recovery from infection.

(vi) The people in each compartment have equal natural death rate.

(vii) The model assumed that symptomatic and asymptomatic infection returned back to the reservoir.

From the description and assumptions above, the flow chart for the $S-E_p-T_p-I_p-H_h-F_m-C_c-A_p-R_p-W$ compartmental dynamics for the Covid-19 spread rate is shown in Figure 1 below.

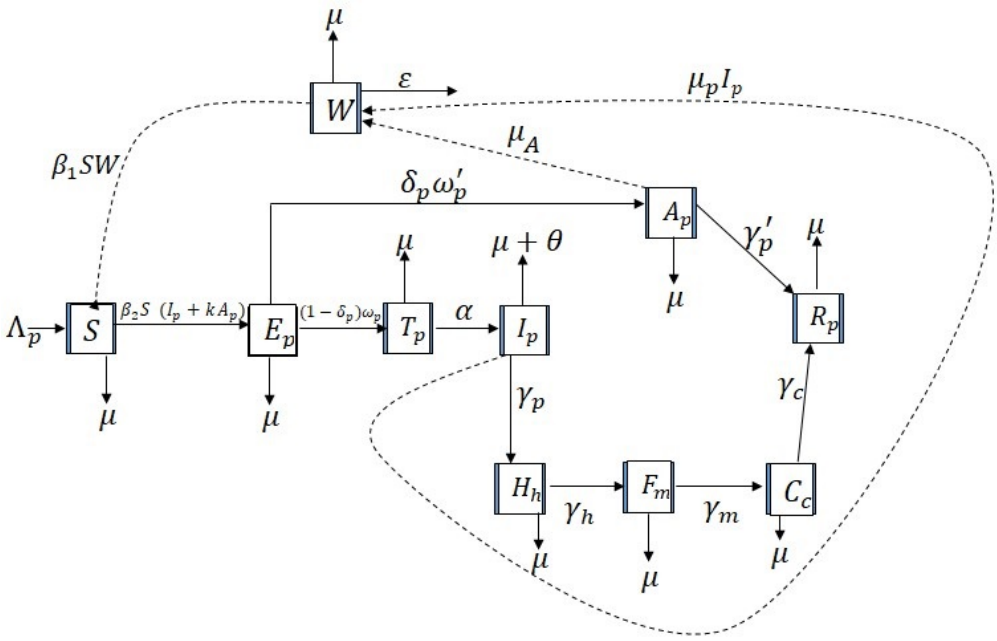


Figure 1: Flow chart of Covid infection transmission from Reservoir-Human.

2.3 Mathematical Formulation of the Model

The state variables and parameters listed in Table 1 and 2 satisfies Eq. (2.11). Thus, the model will be analysed in a suitable region. The ordinary differential equations obtained from the assumptions and descriptions of the flow chart are as follows:

$$\begin{aligned}
\frac{dS}{dt} &= \wedge_p - \beta_2 S(I_p + kA_p) - \beta_1 SW - \mu S,\\
\frac{dE_p}{dt} &= \beta_2 S(I_p + kA_p) + \beta_1 SW - \mu E_p - (1-\delta_p)\omega_p E_p - \delta_p \omega_p' E_p,\\
\frac{dT}{dt} &= (1-\delta_p)\omega_p E_p - \mu T_p - \alpha T_p,\\
\frac{dI_p}{dt} &= \alpha T_p - \gamma_p I_p - (\mu + \mu_p + \theta) I_p,\\
\frac{dH_h}{dt} &= \gamma_p I_p - (\gamma_h + \mu) H_h,\\
\frac{dF_m}{dt} &= \gamma_h H_h - (\mu + \gamma_m) F_m,\\
\frac{dC_c}{dt} &= \gamma_m F_m - (\mu + \gamma_c) C_c,\\
\frac{dA_p}{dt} &= \delta_p \omega_p' E_p - (\mu + \gamma_p' + \mu_A) A_p,\\
\frac{dR_p}{dt} &= \gamma_c C - \mu R_p + \gamma_p' A_p,\\
\frac{dW}{dt} &= \mu_p I_p - (\mu + \varepsilon) W + \mu_A A_p.
\end{aligned} \tag{2.11}$$

With initial condition $S(0) = S_0, E_p(0) = E_{p0}, T_p(0) = T_{p0}, I_p(0) = I_{p0}, H_h(0) = H_{h0}, F_m(0) = F_{m0}, C_c(0) = C_{c0}, A_p(0) = A_{p0}, R_p(0) = R_{p0} = W(0) = W_0$.

3 QUALITATIVE ANALYSIS OF THE MODEL ANALYSIS

In this section, the dynamics of the model and basic properties of model system in Eq. (2.11) such as feasibility and positivity are studied.

3.1 Dynamics of Populations N(t)

Population $N(t)$ is defined by

$$N(t) = S + E_p + T_p + I_p + H_h + F_m + C_c + A_p + R_p + W \tag{3.1}$$

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE_p}{dt} + \frac{dT_p}{dt} + \frac{dI_p}{dt} + \frac{dH_h}{dt} + \frac{dF_m}{dt} + \frac{dC_c}{dt} + \frac{dA_p}{dt} + \frac{dR_p}{dt} + \frac{dW}{dt}, \tag{3.2}$$

$$\frac{dN}{dt} = \wedge_p - \mu(S + E_p + T_p + I_p + H_h + F_m + C_c + A_p + R_p + W) - \theta I_p - \varepsilon W. \tag{3.3}$$

Finally, Eq. (3.3) can be expressed respectively in the form of population dynamic:

$$\frac{dN}{dt} = \wedge_p - \mu N(t) - \theta I_p - \varepsilon W. \tag{3.4}$$

Hence, Eq. (3.4) is showing the changes in the population known as population dynamics.

3.2 Model Feasibility

The feasibility of the model describes the region in which the solution of the system in Eq. (2.11) is biologically meaningful. Since the Covid-19 model displays human populations, it is assumed that all the state variables are non-negative for all time $t \geq 0$ and that the solutions of the model in Eq. (2.11) with positive initial data remain positive for all time $t \geq 0$. The associated parameters are assumed as positive for all time $t \geq 0$. The model Eq. (2.11) will therefore be analyzed in a suitable feasible region, obtained as follows.

Theorem 3.1. *The solution of the model in Eq. (3.4) with initial condition in $\mathbb{R}_+^{10}$ for which Eq. (3.4) hold, approaches and stays in compact set (Ω) as $t \to \infty$. Then, the model feasible solution is given by*

$$\Gamma = \left\{ (S, E_p, T_p, I_p, H_h, F_m, C_c, A_p, R_p, W) \in \mathbb{R}_+^{10} : N(t) \leq \frac{\wedge_p}{\mu} \right\}.$$

Proof. From Eq. (3.4) changes in N leads to

$$\frac{dN}{dt} = \wedge_p - \mu N(t) - \theta I_p - \varepsilon W, \tag{3.5}$$

In the absence of disease ($\theta = \varepsilon = 0$), Eq. (3.5) reduces to

$$\frac{dN}{dt} = \wedge_p - \mu N(t). \tag{3.6}$$

Applying theorem on differential inequalities in [22] and method of separation of variables on inequality in Eq. (3.6) gives

$$\frac{dN}{dt} = \wedge_p - \mu N(t) - \theta I_p - \varepsilon W \leq \wedge_p - \mu N(t). \tag{3.7}$$

Hence,

$$\frac{dN}{dt} \leq \wedge_p - \mu N(t), \tag{3.8}$$

this implies

$$\frac{dN(t)}{\wedge_p - \mu N(t)} \leq dt. \tag{3.9}$$

After solving Eq. (3.9) with $t \to \infty$, N approaches

$$0 \leq N \leq \frac{\wedge_p}{\mu} \implies N(t) \leq \frac{\wedge_p}{\mu}, \tag{3.10}$$

This implies that $0 \leq N \leq \frac{\wedge_p}{\mu}$, then paths of the model Eq. (2.11) are bounded.

Hence, the solution set for the system (2.11) is obtained as

$$\Gamma = \left\{ (S, E_p, T_p, I_p, H_h, F_m, C_c, A_p, R_p, W) \in \Re_+^{10} : N(t) \leq \frac{\wedge_p}{\mu} \right\},$$

is a subset of the system's state space which is bounded and closed, so it contains all its limit points, if the system starts within this set at an initial time, it will remain within the set for all future times. Hence the system (2.11) is epidemiologically important and well-posed mathematically in the interior of domain Γ. □

3.3 Positivity of Solutions of State Variables

If all of the state variables in the model assume non-negative values, the solution to model Eq. (2.11) is said to be positive. The model in Eq. (2.11) must be shown to have non-negative state variables for all time t in order for it to be epidemiologically significance. It must be shown that model Eq. (2.11) solutions with positive beginning data continue to be positive for all times $t > 0$. The result is displayed below.

Theorem 3.2. *If the initial value of the system in Eq.* (2.11) *be* $\{(S(0),E_p(0),T_p(0),I_p(0),H_h(0),F_m(0),C_c(0),A_p(0),R_p(0),W(0)) \geq 0\} \in \Gamma$. *Then, the solution set* $\{S(t),E_p(t),T_p(t),I_p(t),H_h(t),F_m(t),C_c(t),A_p(t),R_p(t),W(t)\}$ *of Eq.* (2.11) *is non-negative for all* $t > 0$.

Proof. According to Theorem 3.2, we obtain following results.

First equation from system Eq. (2.11),

$$\frac{dS}{dt} = \wedge_p - \beta_2 S(I_p + kA_p) - \beta_1 SW - \mu S$$

$$\frac{dS}{dt} \geq -\mu S. \tag{3.11}$$

$$\int \frac{1}{S} dS \geq -\mu \int dt, \tag{3.12}$$

$$\ln S(t) \geq -\mu t + C. \tag{3.13}$$

$$S(t) \geq A\mathrm{e}^{-\mu t}. \quad \text{where A is a constant} \tag{3.14}$$

Setting t = 0 and substituting the initial conditions, yields

$$S(t) \geq S(0)\mathrm{e}^{-\mu t} \geq 0, \quad \text{since} \quad \mu > 0. \tag{3.15}$$

Hence S is positive for $t > 0$.

Similarly, the remaining state variables in Eq. (2.11) are obtained in the same manner, gives:

$$E_p(t) \geq 0, T_p \geq 0, I_p \geq 0, H_h \geq 0, F_m \geq 0, C_c \geq 0, R_p \geq 0, W(t) \geq 0. \tag{3.16}$$

The inequalities in Eqs. (3.15) and (3.16) shows that the variables $S(t),E_p(t),T_p(t),I_p(t),H_h(t),F_m(t),C_c,R_p$ and W(t) are positive for all $t > 0$.
Therefore we have shown that all state variables are non-negative for all $t > 0$. □

3.4 Existence of Equilibrium Points

If $\mathbb{E}(S+E_p+T_p+I_p+H_h+F_m+C_c+A_p+R_p+W) \in \Gamma$ are the equilibrium points of the system in Eq. (2.11).
Then setting the condition below, equilibrium states are obtained.

$$\frac{dS}{dt} = \frac{dE_p}{dt} = \frac{dT_p}{dt} = \frac{dI_p}{dt} = \frac{dH_h}{dt} = \frac{dF_m}{dt} = \frac{dC_c}{dt} = \frac{dA_p}{dt} = \frac{dR_p}{dt} = \frac{dW}{dt} = 0.$$

The equilibrium states give the following equations:

$$\begin{aligned}
\wedge_p - \beta_2 S(I_p + kA_p) - \beta_1 SW - \mu S &= 0 \\
\beta_2 S(I_p + kA_p) + \beta_1 SW - \mu E_p - (1-\delta_p)\omega_p E_p - \delta_p \omega_p' E_p &= 0 \\
(1-\delta_p)\omega_p E_p - \mu T_p - \alpha T_p &= 0 \\
\alpha T_p - \gamma_p I_p - (\mu + \mu_p + \theta) I_p &= 0 \\
\gamma_p I_p - (\gamma_h + \mu) H_h = &\ 0 \\
\gamma_h H_h - (\mu + \gamma_m) F_m = &\ 0 \\
\gamma_m F_m - (\mu + \gamma_c) C_c = &\ 0 \\
\delta_p \omega_p' E_p - (\mu + \gamma_p' + \mu_A) A_p &= 0 \\
\gamma_c C - \mu R_p + \gamma_p' A_p &= 0 \\
\mu_p I_p - (\mu + \varepsilon) W + \mu_A A_p &= 0
\end{aligned} \tag{3.17}$$

System (2.11) yield $\Re_+^{10}$: the disease-free equilibrium is $\mathbb{E}^0(S^0 + E_p^0 + T_p^0 + I_p^0 + H_h^0 + F_m^0 + C_c^0 + A_p^0 + R_p^0 + W^0) \in \Gamma^0$ and endemic equilibrium is $\mathbb{E}^*(S^* + E_p^* + T_p^* + I_p^* + H_h^* + F_m^* + C_c^* + A_p^* + R_p^* + W^*) \in \Gamma^*$

3.5 Disease - free equilibrium (DFE) Point

When there is no infection or the illness has been completely eradicated, the situation is known as the disease-free equilibrium point. $\mathbb{E}^0 = (S^0, E_p^0, T_p^0, I_p^0, H_h^0, F_m^0, C_c^0, A_p^0, R_p^0, W^0)$ is the disease-free equilibrium points.
Solving model Eq. (2.11) simultaneously to obtain disease - free equilibrium, becomes

$$\mathbb{E}^0 = (S^0, E_p^0, T_p^0, I_p^0, H_h^0, F_m^0, C_c^0, A_p^0, R_p^0, W^0) = \left(\frac{\wedge_p}{\mu}, 0, 0, 0, 0, 0, 0, 0, 0, 0\right). \tag{3.18}$$

3.6 Basic Reproductive Number of the Model

The differential equations related to the compartments $E_p, T_p, I_p, H_h, F_m, C_c$ and A_p are used to derive the R_0. The next generation matrix method in [19, 33] was employed to determine the rate of emergence of a new infection in compartment E, in which the rate of appearance of new infection is $\mathscr{F}_i$ and the transfer of individuals out of the classes of system Eq. (2.11) by other means is $\mathscr{V}_i$. Where i is represented with the following compartments $E_p, T_p, I_p, H_h, F_m, C_c, A_p$. Also $V_i = V_i^- - V_i^+$, with $V_i^+(x)$ be the rate of transfer of individuals into compartment i by all other means and $V_i^-(x)$ be the rate of transfer of individuals out of compartment i.

$$\mathscr{F} = \begin{bmatrix} \beta_2 S(I_p + kA_p) + \beta_1 SW \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \mathscr{V} = \begin{bmatrix} (\mu + \omega_p - \delta_p \omega_p + \delta_p \omega_p') E_p \\ -(1-\delta_p)\omega_p E_p + \mu T_p + \alpha T_p \\ -\alpha T_p + \gamma_p I_p + (\mu + \mu_p + \theta) I_p \\ -\gamma_p I_p + (\gamma_h + \mu) H_h \\ -\gamma_h H_h + (\mu + \gamma_m) F_m \\ -\gamma_m F_m + (\mu + \gamma_c) C_c \\ -\delta_p \omega_p' E_p + (\mu + \gamma_p' + \mu_A) A_p \end{bmatrix} \tag{3.19}$$

Obtaining the partial derivatives (i.e Jacobian matrix) of $\mathscr{F}$ and $\mathscr{V}$ in (3.19) with respect to $E_p, T_p, I_p, H_h, F_m, C_c, A_p$ at the disease-free equilibrium state gives

$$F = \begin{bmatrix} 0 & 0 & \beta_2 S^0 & 0 & 0 & 0 & \beta_2 k S^0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}, V = \begin{bmatrix} B_1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -B_2 & B_3 & 0 & 0 & 0 & 0 & 0 \\ 0 & -B_4 & B_5 & 0 & 0 & 0 & 0 \\ 0 & 0 & -B_6 & B_7 & 0 & 0 & 0 \\ 0 & 0 & 0 & -B_8 & B_9 & 0 & 0 \\ 0 & 0 & 0 & 0 & -B_{10} & B_{11} & 0 \\ -B_{12} & 0 & 0 & 0 & 0 & 0 & B_{13} \end{bmatrix} \tag{3.20}$$

$$\mathscr{V}^{-1} = \begin{bmatrix} \frac{1}{B_1} & 0 & 0 & 0 & 0 & 0 & 0 \\ \frac{B_2}{B_3 B_1} & \frac{1}{B_3} & 0 & 0 & 0 & 0 & 0 \\ \frac{B_4 B_2}{B_5 B_3 B_1} & \frac{B_4}{B_5 B_3} & \frac{1}{B_5} & 0 & 0 & 0 & 0 \\ \frac{B_6 B_4 B_2}{B_7 B_5 B_3 B_1} & \frac{B_6 B_4}{B_7 B_5 B_3} & \frac{B_6}{B_7 B_5} & \frac{1}{B_7} & 0 & 0 & 0 \\ \frac{B_8 B_6 B_4 B_2}{B_9 B_7 B_5 B_3 B_1} & \frac{B_8 B_6 B_4}{B_9 B_7 B_5 B_3} & \frac{B_8 B_6}{B_9 B_7 B_5} & \frac{B_8}{B_9 B_7} & \frac{1}{B_9} & 0 & 0 \\ \frac{B_{10} B_8 B_6 B_4 B_2}{B_9 B_7 B_5 B_3 B_1 B_{11}} & \frac{B_{10} B_8 B_6 B_4}{B_9 B_7 B_5 B_3 B_{11}} & \frac{B_{10} B_8 B_6}{B_9 B_7 B_5 B_{11}} & \frac{B_{10} B_8}{B_9 B_7 B_{11}} & \frac{B_{10}}{B_9 B_{11}} & \frac{1}{B_{11}} & 0 \\ \frac{B_{12}}{B_1 B_{13}} & 0 & 0 & 0 & 0 & 0 & \frac{1}{B_{13}} \end{bmatrix} \tag{3.21}$$

$$\mathscr{F}\mathscr{V}^{-1} = \begin{bmatrix} \frac{\beta_2 S^0 B_4 B_2}{B_5 B_3 B_1} + \frac{\beta_2 k S^0 B_{12}}{B_1 B_{13}} & \frac{\beta_2 S^0 B_4}{B_5 B_3} & \frac{\beta_2 S^0}{B_5} & 0 & 0 & 0 & \frac{\beta_2 k S^0}{B_{13}} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \tag{3.22}$$

Then the eigenvalues of the matrix (3.22) are obtained as

$$\left.\begin{aligned} \lambda_1 &= 0 \\ \lambda_2 &= 0 \\ \lambda_3 &= 0 \\ \lambda_4 &= 0 \\ \lambda_5 &= 0 \\ \lambda_6 &= 0 \\ \lambda_7 &= \frac{\beta_2 S^0 (B_4 B_2 B_{13} + k B_{12} B_5 B_3)}{B_5 B_3 B_1 B_{13}} \end{aligned}\right\}$$

From the eigenvalues $\lambda_1 - \lambda_7$ above, the dominant largest eigenvalues is λ_7. Therefore, the basic reproduction number which is given by the largest eigenvalue for the model denoted by R_0 is given by

$$R_0 = \frac{\beta_2 S^0 (B_4 B_2 B_{13} + k B_{12} B_5 B_3)}{B_5 B_3 B_1 B_{13}}$$

where,
$S^0 = \frac{\wedge_p}{\mu}$, $B_1 = \mu + \omega_p - \delta_p \omega_p + \delta_p \omega_p'$, $B_2 = (1-\delta_p)\omega_p$, $B_3 = \mu + \alpha$, $B_4 = \alpha$, $B_5 = \gamma_p + \mu + \mu_p + \theta$, $B_6 = \gamma_p$, $B_7 = \gamma_h + \mu$, $B_8 = \gamma_h$, $B_9 = \mu + \gamma_m$, $B_{10} = \gamma_m$, $B_{11} = \gamma_c + \mu$, $B_{12} = \delta_p \omega_p'$, $B_{13} = \mu + \gamma_p' + \mu_A$
i.e.,

$$R_0 = \frac{\beta_2 \Lambda_p \left(\alpha \omega_p (1-\delta_p)\left(\mu + \gamma_p' + \mu_A\right) + k \delta_p \omega_p' \left(\gamma_p + \mu + \mu_p + \theta\right)(\alpha + \mu)\right)}{\mu \left(\gamma_p + \mu + \mu_p + \theta\right)(\alpha + \mu)\left(\mu + \omega_p - \delta_p \omega_p + \delta_p \omega_p'\right)\left(\mu + \gamma_p' + \mu_A\right)} \tag{3.23}$$

Remark 1: Epidemiologically

(i) if $R_0 = 1$, Covid-19 infection persist in the populace.

(ii) if $R_0 < 1$, Covid-19 infection prevalence will wane and ultimately wiped out.

(iii) if $R_0 > 1$, The Covid-19 infection will continue to spread frequently.

3.7 Local Stability Analysis of the DFE Point

To determine the stability or otherwise of the disease - free equilibrium point $\mathbb{E}^0$, we examine the behaviour of the model population near the equilibrium solution. The conditions for DFE to be stable and asymptotically stable will be discussed here.

Definition 3.1. Jacobian Matrix

The Jacobian matrix is a matrix containing the first-order partial derivatives of a vector-valued function with respect to its input variables. It provides the linear approximation of the function near a given point.
Let $\mathbf{F}(\mathbf{x}) = [f_1(\mathbf{x}), f_2(\mathbf{x}), \ldots, f_m(\mathbf{x})]^T$ be a vector-valued function, where each f_i is a scalar function, and $\mathbf{x} = [x_1, x_2, \ldots, x_n]^T$ is a vector of variables. The Jacobian matrix $J(\mathbf{x})$ is defined as follows:

$$J(\mathbf{x}) = \begin{pmatrix} \frac{\partial f_1}{\partial x_1} & \frac{\partial f_1}{\partial x_2} & \cdots & \frac{\partial f_1}{\partial x_n} \\ \frac{\partial f_2}{\partial x_1} & \frac{\partial f_2}{\partial x_2} & \cdots & \frac{\partial f_2}{\partial x_n} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\partial f_m}{\partial x_1} & \frac{\partial f_m}{\partial x_2} & \cdots & \frac{\partial f_m}{\partial x_n} \end{pmatrix}$$

Each element of the Jacobian matrix represents the rate of change of one component of the output with respect to one of the input variables.

Theorem 3.3. *The disease-free equilibrium point $\mathbb{E}^0$ is locally asymptotically stable if $R_0 < 1$ for $tr(J_{\mathbb{E}^0}) < 0$ and $det(J_{\mathbb{E}^0}) > 0$, and unstable if $R_0 > 1$ for $tr(J_{\mathbb{E}^0}) > 0$ and $det(J_{\mathbb{E}^0}) < 0$.*

Proof. The proof of the Theorem 3.3 can be established by constructing a Jacobian matrix for the model system Eq. (2.11) evaluated at the DFE ($\mathbb{E}^0$). At disease-free equilibrium, $I_p^0 = A_p^0 = W = 0$ and $S^0 = \dfrac{\wedge_p}{\mu}$ the Jacobian matrix is

$$J_{\mathbb{E}^0} = \begin{bmatrix} -\mu & 0 & 0 & -G_1 & 0 & 0 & 0 & -kG_1 & 0 & -G_2 \\ 0 & -G_3 & 0 & G_1 & 0 & 0 & 0 & kG_1 & 0 & G_2 \\ 0 & G_4 & -G_5 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha & -G_6 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \gamma_p & -G_7 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma_h & -G_8 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \gamma_m & -G_9 & 0 & 0 & 0 \\ 0 & G_{10} & 0 & 0 & 0 & 0 & 0 & -G_{11} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \gamma_c & \gamma_p' & -\mu & 0 \\ 0 & 0 & 0 & \mu_p & 0 & 0 & 0 & \mu_A & 0 & -(\mu+\varepsilon) \end{bmatrix} \tag{3.24}$$

Where, $G_1 = \frac{\beta_2 \wedge_p}{\mu}, G_2 = \frac{(\beta_1 \wedge_p)}{\mu}, G_3 = (\mu + (1-\delta_p)\omega_p + \delta_p \omega_p'), G_4 = (1-\delta_p)\omega_p, G_5 = (\mu + \alpha), G_6 = (\gamma_p + \mu + \mu_p + \theta), G_7 = (\mu + \gamma_h), G_8 = (\mu + \gamma_m), G_9 = (\gamma_c + \mu), G_{10} = \delta_p \omega_p', G_{11} = (\mu + \gamma_p' + \mu_A)$

The method of trace and determinant was applied to evaluate our system of equations without explicitly calculating eigenvalues.

The matrix $J_{\mathbb{E}^0}$ in Eq. (3.24) of dimension 10 is stable if its trace is negative i.e $tr(J_{\mathbb{E}^0}) < 0$ and its determinant is positive i.e $det(J^0) \geq 0$.

The trace of matrix $J_{\mathbb{E}^0}$ is obtained as:

$$\begin{aligned} tr(J_{\mathbb{E}^0}) &= -3\mu - G_3 - G_5 - G_6 - G_7 - G_8 - G_9 - G_{11} - \varepsilon \\ &= -(3\mu + G_3 + G_5 + G_6 + G_7 + G_8 + G_9 + G_{11} + \varepsilon) \\ &= -(9\mu + (1-\delta_p)\omega_p + \delta_p \omega_p' + \alpha + \gamma_p + \mu_p + \theta + \gamma_h + \gamma_m + \gamma_c + \gamma_p' + \mu_A + \varepsilon) \\ tr(J_{\mathbb{E}^0}) &< 0 \end{aligned} \tag{3.25}$$

Also, the determinant of matrix $J_{\mathbb{E}^0}$ is generated as

$$det(J_{\mathbb{E}^0}) = \mu^2 G_7 G_8 G_9 \left(G_6 G_5 G_3 G_{11}\varepsilon - G_6 G_5 G_{10}\mu_A G_2 - G_6 G_5 G_{10} k G_1 \varepsilon - G_1 \alpha G_4 G_{11}\varepsilon - \mu_p \alpha G_4 G_{11} G_2\right)$$

$$\det(J_{\mathbb{E}^0}) = \mu^2 G_7 G_8 G_9 \left[\varepsilon(1-R_0) - G_2(G_6 G_5 G_{10}\mu_A + \mu_p \alpha G_4 G_{11})\right] \tag{3.26}$$

$$\begin{aligned} det(J_{\mathbb{E}^0}) > 0 \text{ if and only if } \ & \varepsilon(1-R_0) > G_2(G_6 G_5 G_{10}\mu_A + \mu_p \alpha G_4 G_{11}), \\ & \varepsilon > \tfrac{G_2(G_6 G_5 G_{10}\mu_A + \mu_p \alpha G_4 G_{11})}{(1-R_0)} \ \text{ and } R_0 < 1. \end{aligned} \tag{3.27}$$

From the result of the trace and determinant of the matrix which shows that $tr(J_{\mathbb{E}^0}) < 0$ and $det(J_{\mathbb{E}^0}) > 0$ then $R_0 < 1$.

This proves that the disease-free equilibrium point is locally asymptotically stable. Biologically, this means that the disease dies out.

Conversely if $R_0 > 1$ then $tr(J_{\mathbb{E}^0}) > 0$. This would cause the determinant to be negative (i.e $det(J_{\mathbb{E}^0}) < 0$) and making the disease free-equilibrium point unstable. Biologically, this means that the disease persists. □

3.8 Endemic Equilibrium Point

The condition for endemic equilibrium of model system (2.11) is determined here. Endemic equilibrium state is the state where the disease cannot be totally eradicated but persist in the population. Then, all the state variables in Eq. (2.11) must not be zero at this equilibrium state. i.e.,
$\mathbb{E}^* = (S^*, E_p^*, T_p^*, I_p^*, H_h^*, F_m^*, C_c^*, A_p^*, R_p^*, W^*)\Gamma \neq (0,0,0,0,0,0,0,0,0,0)$:

Solving Eq. (2.11) simultaneously in terms of R_0, the solution obtained is given below.

Let,

$$S^* = \frac{S^0}{R_0},$$

Therefore,

$$\begin{aligned}
S^* &= \frac{\varepsilon\Phi_1\Phi_2\Phi_3(\mu+\alpha)}{\left[(1-\delta_p)\omega_p\alpha\Phi_1\Phi_4+\delta_p\omega_p'(\mu+\alpha)\Phi_3\Phi_5\right]} \\
E_p^* &= \frac{\vartheta_1}{\Phi_2\vartheta_2} \\
T_p^* &= \frac{(1-\delta_p)\omega_p\vartheta_1}{\Phi_2(\mu+\alpha)\vartheta_2} \\
I_p^* &= \frac{(1-\delta_p)\omega_p\alpha\vartheta_1}{\Phi_2\Phi_3(\mu+\alpha)\vartheta_2} \\
H_h^* &= \frac{(1-\delta_p)\omega_p\alpha^2\vartheta_1}{\Phi_2\Phi_3(\mu+\alpha)(\gamma_h+\mu)\vartheta_2} \\
F_m^* &= \frac{\gamma_h(1-\delta_p)\omega_p\alpha^2\vartheta_1}{\Phi_2\Phi_3(\mu+\alpha)^2(\gamma_h+\mu)\vartheta_2} \\
C_c^* &= \frac{\gamma_m\gamma_h(1-\delta_p)\omega_p\alpha^2\vartheta_1}{\Phi_2\Phi_3(\mu+\alpha)^2(\gamma_h+\mu)(\mu+\gamma_c)\vartheta_2} \\
A_p^* &= \frac{\delta_p\omega_p'\left[\wedge_p\left[(1-\delta_p)\omega_p\alpha\Phi_1\Phi_4+\delta_p\omega_p'(\mu+\alpha)\Phi_3\Phi_5\right]-\mu\varepsilon\Phi_1\Phi_2\Phi_3(\mu+\alpha)\right]}{\Phi_2\Phi_1\left[(1-\delta_p)\omega_p\alpha\beta_2\varepsilon\Phi_1+\beta_1[\mu_p(1-\delta_p)\omega_p\alpha\Phi_1+\mu_A\delta_p\omega_p'(\mu+\alpha)\Phi_3]-\beta_2\varepsilon\Phi_3k\delta_p\omega_p'(\mu+\alpha)\right]} \\
R_p^* &= \frac{\vartheta_1\left[\gamma_c\gamma_m\gamma_h(1-\delta_p)\omega_p\alpha^2+\delta_p\alpha'\omega_p'(\mu+\alpha)^2(\gamma_h+\mu)(\mu+\gamma_c)\right]}{\Phi_2\Phi_3\mu(\mu+\alpha)^2(\gamma_h+\mu)(\mu+\gamma_c)\vartheta_2} \\
W^* &= \frac{[\mu_p(1-\delta_p)\omega_p\alpha\Phi_1+\mu_A\delta_p\omega_p'(\mu+\alpha)\Phi_3]\vartheta_1}{\varepsilon\Phi_1\Phi_2\Phi_3(\mu+\alpha)\vartheta_2}
\end{aligned} \tag{3.28}$$

where, $\vartheta_1 = \left[\wedge_p\left[(1-\delta_p)\omega_p\alpha\Phi_1\Phi_4+\delta_p\omega_p'(\mu+\alpha)\Phi_3\Phi_5\right]-\mu\varepsilon\Phi_1\Phi_2\Phi_3(\mu+\alpha)\right]$, $\vartheta_2 = \left[(1-\delta_p)\omega_p\alpha\beta_2\varepsilon\Phi_1+\beta_1[\mu_p(1-\delta_p)\omega_p\alpha\Phi_1+\mu_A\delta_p\omega_p'(\mu+\alpha)\Phi_3]-\beta_2\varepsilon\Phi_3k\delta_p\omega_p'(\mu+\alpha)\right]$, $\Phi_1 = (\mu+\gamma_p'+\mu_A)$, $\Phi_2 = (\mu+\omega_p-\delta_p\omega_p+\delta_p\omega_p')$, $\Phi_3 = (\gamma_p+\mu+\mu_p+\theta)$,$\Phi_4 = (\beta_2\varepsilon+\beta_1\mu_p)$ and $\Phi_5 = (\beta_2\varepsilon k+\beta_1\mu_A)$

3.9 Global Stability of Disease-Free Equilibrium

In this subsection, global stability of the disease-free equilibrium ($\mathbb{E}^0$) will be proved. The result is obtained by means of Lyapunov function constructed of the linear function (see, [8,30,34,35]).

Theorem 3.4. *For $R_0 \leq 1$, the disease-free equilibrium of the system in Eq.* (2.11) *is globally asymptotically stable.*

Proof. Consider the Lyapunov candidate function below

$$\begin{aligned} L(t) &= \left(S - S^0 - S^0 \ln \tfrac{S^0}{S}\right) + d_1 E_P + d_2 T_P + d_3 I_p + d_4 H_h + d_5 F_m + d_6 C_c + d_7 A_P + d_8 R + d_9 W \\ \dot{L}(t) &= \left(1 - \tfrac{S^0}{S}\right)\dot{S} + d_1 \dot{E_P} + d_2 \dot{T_P} + d_3 \dot{I_p} + d_4 \dot{H_h} + d_5 \dot{F_m} + d_6 \dot{C_c} + d_7 \dot{A_P} + d_8 \dot{R} + d_9 \dot{W} \end{aligned} \tag{3.29}$$

$$\begin{gathered} \dot{L}(t) = \left(1 - \tfrac{S^0}{S}\right)[\wedge_p - \beta_2 S(I_p + kA_p) - \beta_1 SW - \mu S] + d_1\beta_2 SI_p + kd_1\beta_2 SA_p + \\ d_1\beta_1 SW - d_1(\mu + (1-\delta_p)\omega_p + \delta_p\omega_p')E_p + d_2(1-\delta_p)\omega_p E_p - d_2(\mu+\alpha)T_p + \\ d_3\alpha T_p - d_3(\gamma_p + \mu + \mu_p + \theta)I_p + d_4\gamma_p I_p - d_4(\gamma_h + \mu)H_h + d_5\gamma_h H_h - \\ d_5(\mu+\gamma_m)F_m + d_6\gamma_m F_m - d_6(\mu+\gamma_c)C_c + d_7\delta_p\omega_p' E_p - d_7(\mu + \gamma_p' + \mu_A)A_p + \\ d_8\gamma_c C - d_8\mu R_p + d_8\gamma_p' A_p + d_9\mu_p I_p - d_9\varepsilon W + d_9\mu_A A_p \end{gathered} \tag{3.30}$$

Solving the equation involves with the coefficient of $E_P, T_p, I_p, H_h, F_m, C_c, A_P, R_P, W$ simultaneously, yields

$$\begin{gathered} d_1 = \tfrac{d_3(\gamma_p+\mu+\mu_p+\theta)\varepsilon}{(\varepsilon k\beta_2+\mu_p\beta_1)S}, d_2 = \tfrac{d_3\gamma_p}{(\mu+\gamma_p)}, d_7 = \tfrac{d_3(\gamma_p+\mu+\mu_p+\theta)(\varepsilon k\beta_2+\mu_A\beta_1)}{(\varepsilon k\beta_2+\mu_p\beta_1)(\mu+\gamma_p'+\mu_A)}, \\ d_9 = \tfrac{\beta_1 d_3(\gamma_p+\mu+\mu_p+\theta)}{(\varepsilon k\beta_2+\mu_p\beta_1)}, d_4 = d_5 = d_6 = d_8 = 0 \end{gathered} \tag{3.31}$$

On substituting the values of $d_1 \ldots d_9$ into Eq. (3.30) gives

$$\begin{aligned} \dot{L}(t) &= \left(1 - \frac{S^0}{S}\right)[\wedge_p - \beta_2 S(I_p + kA_p) - \beta_1 SW - \mu S] + \frac{d_3(\gamma_p+\mu+\mu_p+\theta)\varepsilon\beta_2 I_p}{(\varepsilon k\beta_2+\mu_p\beta_1)} + \\ &\frac{d_3 k(\gamma_p+\mu+\mu_p+\theta)\varepsilon\beta_2 A_p}{(\varepsilon k\beta_2+\mu_p\beta_1)} + \frac{d_3(\gamma_p+\mu+\mu_p+\theta)\varepsilon\beta_1 W}{(\varepsilon k\beta_2+\mu_p\beta_1)} + \frac{d_3\gamma_p(1-\delta_p)\omega_p E_p}{(\mu+\gamma_p)} \\ &- \frac{d_3(\gamma_p+\mu+\mu_p+\theta)\varepsilon(\mu+(1-\delta_p)\omega_p+\delta_p\omega_p')E_p}{(\varepsilon k\beta_2+\mu_p\beta_1)S} - \frac{d_3\gamma_p(\mu+\alpha)T_p}{(\mu+\gamma_p)} - d_3(\gamma_p+\mu+\mu_p+\theta)I_p \\ &+ d_3\alpha T_p + \frac{d_3(\gamma_p+\mu+\mu_p+\theta)(\varepsilon k\beta_2+\mu_A\beta_1)\delta_p\omega_p' E_p}{(\varepsilon k\beta_2+\mu_p\beta_1)(\mu+\gamma_p'+\mu_A)} + \frac{\beta_1 d_3(\gamma_p+\mu+\mu_p+\theta)\mu_p I_p}{(\varepsilon k\beta_2+\mu_p\beta_1)} \\ &- \frac{d_3(\gamma_p+\mu+\mu_p+\theta)(\varepsilon k\beta_2+\mu_A\beta_1)A_p}{(\varepsilon k\beta_2+\mu_p\beta_1)} - \frac{\beta_1 d_3(\gamma_p+\mu+\mu_p+\theta)\varepsilon W}{(\varepsilon k\beta_2+\mu_p\beta_1)} + \frac{\beta_1 d_3(\gamma_p+\mu+\mu_p+\theta)\mu_A A_p}{(\varepsilon k\beta_2+\mu_p\beta_1)} \end{aligned} \tag{3.32}$$

After Simplification we have,

$$\begin{aligned} \dot{L}(t) \leq -\Bigg[\left(\frac{S^0}{S} - 1\right)[\mu(S-S^0) + \beta_2 S(I_p + kA_p) + \beta_1 SW] + \frac{d_3(\gamma_p-\alpha)\mu T_p}{(\mu+\gamma_p)} \\ + \frac{d_3(\gamma_p+\mu+\mu_p+\theta)(k-1)\varepsilon\beta_2 I_p}{(\varepsilon k\beta_2+\mu_p\beta_1)} + \frac{d_3[\Phi_1 - (\Phi_2+\Phi_3)S]E_p}{(\mu+\gamma_p)(\varepsilon k\beta_2+\mu_p\beta_1)(\mu+\gamma_p'+\mu_A)S}\Bigg] \end{aligned} \tag{3.33}$$

$\Phi_1 = (\mu+\gamma_p)(\mu+\gamma_p'+\mu_A)(\gamma_p+\mu+\mu_p+\theta)\varepsilon(\mu+(1-\delta_p)\omega_p+\delta_p\omega_p')$
$\Phi_2 = \gamma_p(1-\delta_p)\omega_p(\varepsilon k\beta_2+\mu_p\beta_1)(\mu+\gamma_p'+\mu_A)$

$\Phi_3 = (\mu+\gamma_p)(\gamma_p+\mu+\mu_p+\theta)(\varepsilon k\beta_2+\mu_A\beta_1)\delta_p\omega_p'$
Hence, $\dot{L}<0$, if $S>0$, $d_3>0$, $\Phi_1,\Phi_2,\Phi_3>0$, $\gamma_p>\alpha$, and $\Phi_1>(\Phi_2+\Phi_3)S$. Also, $\dot{L}=0$ iff $d_3=0$, $S=S^0$, and $I_p=E_p=T_p=0$.
Thus, every solution that starts in Γ approaches $\mathbb{E}^0$ as $t\to\infty$. This shows that $\mathbb{E}^0$ is globally asymptotically stable in Γ. □

3.10 Global Stability of Endemic Equilibrium

Lyapunov functions used in [1, 2, 3, 4, 8, 15, 31] will be applied here to demonstrate the global stability of the endemic equilibrium of the model in Eq. (2.11). The results follow as.

Theorem 3.5. The endemic equilibrium $\mathbb{E}^*$ is globally asymptotically stable on Γ if and only if $P_1,P_2,P_3,P_4,P_5,P_6,P_7>0$ and $S=S^*$, $E_p=E_p^*$,$T_p=T_p^*$, $I_A=I_A^*$, $H_h=H_h^*$, $F_m=F_m^*$, $C_c=C_c^*$, $A_p=A_p^*$, $R_p=R_p^*$, $W=W^*$ with $R_0>1$.

Proof. Given the Lyapunov candidate function as

$$\begin{gathered}L=S-S^*\ln S+E_p-E_p^*\ln E_p+T_p-T_p^*\ln T_p+P_1(I_p-I_p^*\ln I_p)+\\ P_2(H_h-H_h^*\ln H_h)+P_3(F_m-F^*\ln F_m)+P_4(C_c-C_c^*\ln C_c)+\\ P_5(A_p-A^*\ln A_P)+P_6(R_p-R_p^*\ln R_p)+P_7(W-W^*\ln W)\end{gathered}\tag{3.34}$$

$$\begin{gathered}\dot{L}=\left(1-\tfrac{S^*}{S}\right)\dot{S}+\left(1-\tfrac{E_p^*}{E_p}\right)\dot{E}_p+\left(1-\tfrac{T_p^*}{T_p}\right)\dot{T}_p+P_1\left(1-\tfrac{I_p^*}{I_p}\right)\dot{I}_p+P_2\left(1-\tfrac{H_h^*}{H_h}\right)\dot{H}_h+\\ P_3\left(1-\tfrac{F_m^*}{F_m}\right)\dot{F}_m+P_4\left(1-\tfrac{C_c^*}{C_c}\right)\dot{C}_c+P_5\left(1-\tfrac{A_p^*}{A_p}\right)\dot{A}_p+P_5\left(1-\tfrac{R_p^*}{R_p}\right)\dot{R}_p+P_6\left(1-\tfrac{W^*}{W}\right)\dot{W}.\end{gathered}\tag{3.35}$$

$$\begin{gathered}\dot{L}=\left(1-\tfrac{S^*}{S}\right)[\wedge_p-\beta_2S(I_p+kA_p)-\beta_1SW-\mu S]+\left(1-\tfrac{E_p^*}{E_p}\right)[\beta_2S(I_p+kA_p)+\\ \beta_1SW-\mu E_p-(1-\delta_p)\omega_pE_p-\delta_p\omega_p'E_p]+\left(1-\tfrac{T_p^*}{T_p}\right)[(1-\delta_p)\omega_pE_p-\mu T_p-\alpha T_p]+\\ P_1\left(1-\tfrac{I_p^*}{I_p}\right)[\alpha T_p-\gamma_pI_p-(\mu+\mu_p+\theta)I_p]+P_2\left(1-\tfrac{H_h^*}{H_h}\right)[\gamma_pI_p-(\gamma_h+\mu)H_h]+\\ P_3\left(1-\tfrac{F_m^*}{F_m}\right)[\gamma_hH_h-(\mu+\gamma_m)F_m]+P_4\left(1-\tfrac{C_c^*}{C_c}\right)[\gamma_mF_m-(\mu+\gamma_c)C_c]\\ +P_5\left(1-\tfrac{A_p^*}{A_p}\right)[\delta_p\omega_p'E_p-(\mu+\gamma_p'+\mu_A)A_p]+P_6\left(1-\tfrac{R_p^*}{R_p}\right)[\gamma_cC-\mu R_p+\gamma_p'A_p]+\\ P_7\left(1-\tfrac{W^*}{W}\right)[\mu_pI_p-(\mu+\varepsilon)W+\mu_AA_p].\end{gathered}\tag{3.36}$$

Considering Eq. (2.11) at endemic equilibrium, where first line is

$$\wedge_p=\beta_2S^*(I_p^*+kA_p^*)+\beta_1S^*W^*+\mu S^*.$$

Substituting the values of $\wedge_p$ into Eq. (3.36) we obtained

$$\dot{L} \leq \left(1-\frac{S^*}{S}\right)[\beta_2 S^*(I_p^*+kA_p^*)+\beta_1 S^* W^*+\mu S^*-\beta_2 S(I_p+kA_p)-\beta_1 SW-\mu S]+$$
$$\left(1-\frac{E_p^*}{E_p}\right)[\beta_2 S(I_p+kA_p)+\beta_1 SW-\mu E_p-(1-\delta_p)\omega_p E_p-\delta_p\omega_p' E_p]+$$
$$\left(1-\frac{T_p^*}{T_p}\right)[(1-\delta_p)\omega_p E_p-\mu T_p-\alpha T_p]+P_1\left(1-\frac{I_p^*}{I_p}\right)[\alpha T_p-\gamma_p I_p-(\mu+\mu_p+\theta)I_p]+$$
$$P_2\left(1-\frac{H_h^*}{H_h}\right)[\gamma_p I_p-(\gamma_h+\mu)H_h]+$$
$$P_3\left(1-\frac{F_m^*}{F_m}\right)[\gamma_h H_h-(\mu+\gamma_m)F_m]+P_4\left(1-\frac{C_c^*}{C_c}\right)[\gamma_m F_m-(\mu+\gamma_c)C_c]$$
$$+P_5\left(1-\frac{A_p^*}{A_p}\right)[\delta_p\omega_p' E_p-(\mu+\gamma_p'+\mu_A)A_p]+P_6\left(1-\frac{R_p^*}{R_p}\right)[\gamma_c C-\mu R_p+\gamma_p' A_p]+$$
$$P_7\left(1-\frac{W^*}{W}\right)[\mu_p I_p-(\mu+\varepsilon)W+\mu_A A_p].$$

After simplification,

$$\dot{L} \leq -\left[\left(\frac{S^*}{S}-1\right)[\beta_2[(I_p^*+kA_p^*)S^*-(I_p+kA_p)S]+\beta_1(S^*W^*-SW)+\mu(S^*-S)]+\right.$$
$$\left(\frac{E_p^*}{E_p}-1\right)\beta_2 S(I_p+kA_p)+\left(\frac{E_p^*}{E_p}-1\right)\beta_1 SW+\mu(E_p-E_p^*)+(1-\delta_p)\omega_p(E_p-E_p^*)+$$
$$\delta_p\omega_p'(E_p-E_p^*)+\left(\frac{T_p^*}{T_p}-1\right)(1-\delta_p)\omega_p E_p+\mu(T_p-T_p^*)+\alpha(T_p-T_p^*)+P_1\left(\frac{I_p^*}{I_p}-1\right)\alpha T_p+$$
$$P_1\gamma_p(I_p-I_p^*)+P_1(\mu+\mu_p+\theta)(I_p-I_p^*)+P_2\left(\frac{H_h^*}{H_h}-1\right)\gamma_p I_p+P_2(\gamma_h+\mu)(H_h-H_h^*)+$$
$$P_3\left(\frac{F_m^*}{F_m}-1\right)\gamma_h H_h+P_3(\mu+\gamma_m)(F_m-F_m^*)+P_4\left(\frac{C_c^*}{C_c}-1\right)\gamma_m F_m+P_4(\mu+\gamma_c)(C_c-C_c^*)+$$
$$P_5\left(\frac{A_p^*}{A_p}-1\right)\delta_p\omega_p' E_p+P_5(\mu+\gamma_p'+\mu_A)(A_p-A_p^*)+P_6\left(\frac{R_p^*}{R_p}-1\right)\gamma_c C+P_6\mu(R_p-R_p^*)+$$
$$\left.P_6\left(\frac{R_p^*}{R_p}-1\right)\gamma_p' A_p+P_7\left(\frac{W^*}{W}-1\right)\mu_p I_p+P_7(\mu+\varepsilon)(W-W^*)+P_7\left(\frac{W^*}{W}-1\right)\mu_A A_p\right].$$

Thus, $\dot{L}<0$ if and only if $P_1,P_2,P_3,P_4,P_5,P_6,P_7>0$. Note that, $\dot{L}=0$ if and only if $S=S^*$, $E_p=E_p^*$, $T_p=T_p^*$, $I_A=I_A^*$, $H_h=H_h^*$, $F_m=F_m^*$, $C_c=C_c^*$, $A_p=A_p^*$, $R_p=R_p^*$ and $W=W^*$. Hence, $\mathbb{E}^*$ is globally asymptotically stable in the interior of Γ. □

3.11 Sensitivity Analysis of the Model

The sensitivity analysis is to check the effect of each parameter in order to reduce the transmission of Covid from reservoir to the human then with the family. Comparative contributions of each parameters applied in the model which responsible for the transmission and prevalence of Covid-19 is been discussed here. The Table 3 displayed each parameters used in this section chosen from the realistic ranges for illustrative purpose.

Table 3: Parameter values of the model.

Parameter Symbol	Baseline value
$\wedge_p$	1000
β_2	0.0510
β_1	0.02
δ_p	0.65
α	0.015
γ_p	0.03
γ_h	0.05
γ_m	0.01
γ_c	0.8
γ_p'	0.8
μ_A	0.05
μ	0.013
μ_p	[0.0 - 1.0]
ω_p'	0.001
θ	0.05
ε	0.01
ω_p	0.0058
k	0.001

Definition 3.2. Normalized forward sensitivity index of a variable Q that differentially depends on a parameter m, is defined as: $Z_m^Q = \frac{\partial Q}{\partial m} \times \frac{m}{Q}$ where, $Z_m^{R_0}$ is the sensitivity index of R_0 with respect to parameter, m.

3.11.1 Sensitivity Indices of R_0

Given the explicit form of R_0; analytical expression for its sensitivity to each parameter is obtained by applying the normalized forward sensitivity index in [5, 9, 17] and given as:

$$Z_m^{R_0} = \frac{\partial R_0}{\partial m} \times \frac{m}{R_0} \tag{3.37}$$

Sensitivity indices of R_0 corresponding to these parameters: $\wedge_p, \beta_2, \delta_p, k, \mu_p, \mu, \theta, \mu_A, \omega_p', \omega_p, \gamma_p, \gamma_p', \alpha$ was derived and computed as follows.

$$\left.\begin{aligned} Z_{\wedge_p}^{R_0} &= \frac{\partial R_0}{\partial \wedge_p} \times \frac{\wedge_p}{R_0} = +1.00000 \\ Z_{\beta}^{R_0} &= \frac{\partial R_0}{\partial \beta_2} \times \frac{\beta_2}{R_0} = +1.00000 \\ Z_{\delta_p}^{R_0} &= \frac{\partial R_0}{\partial \delta_p} \times \frac{\delta_p}{R_0} = -1.85925 \end{aligned}\right\} \tag{3.38}$$

The remaining indices are generated following the same method and presented in Table 4.

Table 4: Sensitivity indices of R_0.

Parameters	Sensitivity indices R_0
$\wedge_p$	+1.000000000
β_2	+1.000000000
δ_p	-1.859247020
k	+0.006313642165
μ_p	-0.5489979877
μ	-3.174859406
θ	-0.01372494969
μ_A	-0.002924675064
ω_p'	-0.04164621907
ω_p	+0.9787081234
γ_p	-0.08234969816
γ_p'	-0.002924675064
α	+0.8887194887

From Table 4, the indices with positive signs reveal that the value of R_0, increases when the corresponding parameters increases and indices with negative signs shows that, the value of R_0 reduces with increase in the corresponding parameters. This analysis is done to establish which parameters govern the results of our analysis.
Hence, it is clear from Table 4 that R_0 will be minimized with increases in the values of the relevant parameters, since the sensitivity indices of these parameters are negative.

4 NUMERICAL SIMULATION AND ANALYSIS

In this section, numerical simulations of the model was obtained through the assumed and estimated parameters values shown in Table 3. Moreover, simulations have been obtained with the help of Maple-17 package and MATLAB 2020b software with following initial conditions:$S(0) = 75990; E_p(0) = 3876; T_p(0) = 1000; I_p(0) = 50; H_h(0) = 10; F_m(0) = 6; C_c(0) = 4; A_p(0) = 10; R(0) = 0; W(0) = 100, N = 81046$. The step size during simulations is taken to be $h = 10^{-2}$. Table 5 shows the effect of varying the symptomatic infectious rate (μ_p), asymptomatic (δ_p) and infectious contact rate (β_2) parameters on reproduction number (R_0).

The initial population values above was used for the simulation and the graphical solution obtained is shown in the Figures 2-6.

Figure 4 describes the graph of asymptomatic infectious individuals against time (t) with effect of asymptomatic infectious rate to reservoir μ_A.

Table 5: Effect of varying Symptomatic (μ_p), Asymptomatic (δ_p) and contact (β_2) rates Parameters on Reproduction Number.

	Parameters	**Case 1**	**Case 2**	**Case 3**	**Case 4**	**Case 5**	**Case 6**
1.	μ_p	0.0	0.2	0.4	0.6	0.8	1.0
	R_0	3.9332	1.7663	1.1417	0.8450	0.6716	0.5579
2.	δ_p	0.0	0.2	0.4	0.6	0.8	1.0
	R_0	3.2966	2.6242	1.9602	1.3044	0.6567	0.0190
3.	β_2	0.0810	0.0710	0.0610	0.0510	0.0410	0.0310
	R_0	1.5421	1.3517	1.1613	0.9709	0.7806	0.5902

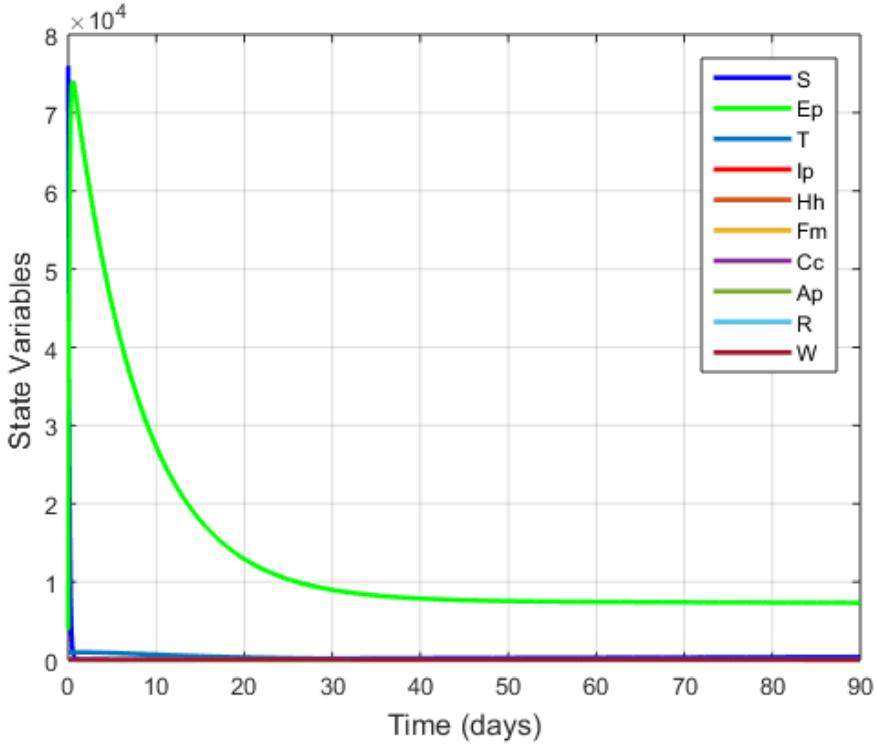


Figure 2: Graph of the state variables with time using $\beta_1 > 0, \mu_p = \mu_A = \gamma_c = 0$.

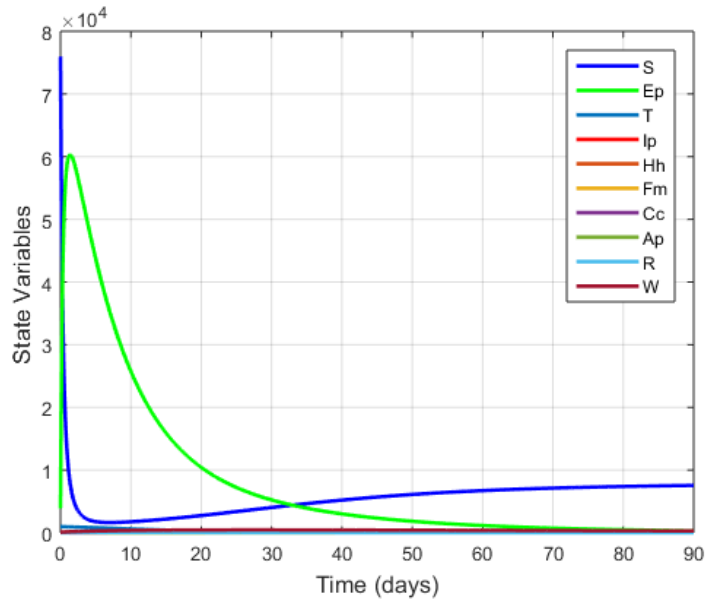


Figure 3: Graph of the state variables with time using controls $\mu_p, \mu_A, \gamma_c > 0$ and $\beta_1 = 0$.

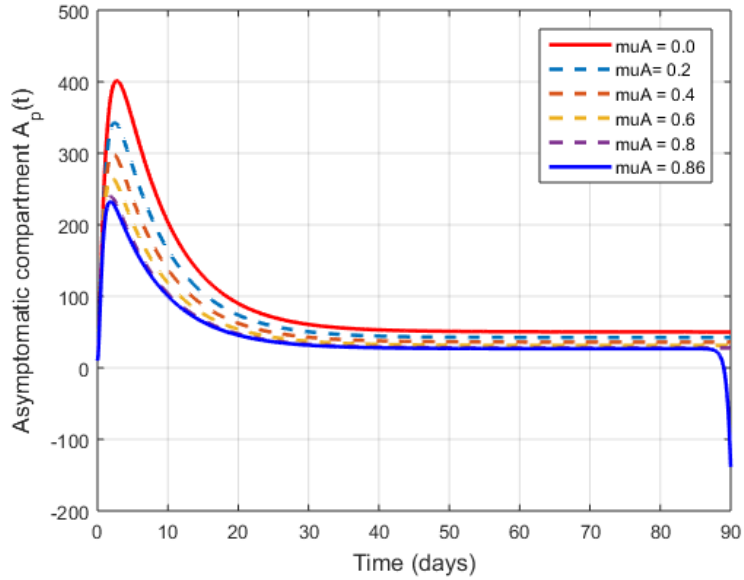


Figure 4: Simulations of the model with varying effect values of μ_A for asymptomatic individuals.

It is seen that the asymptomatic infected class will reduce significantly with time when at most 80% of people that are having infection without symptoms recovered and make sure the infection returned back to reservoir.

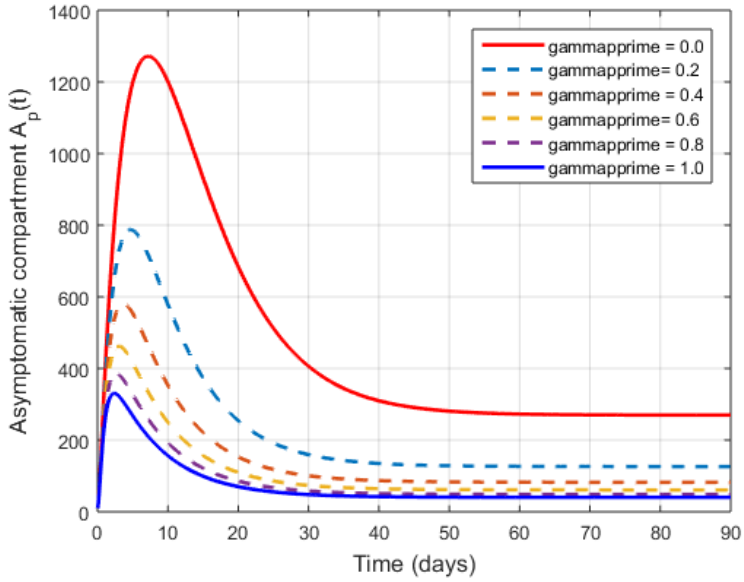
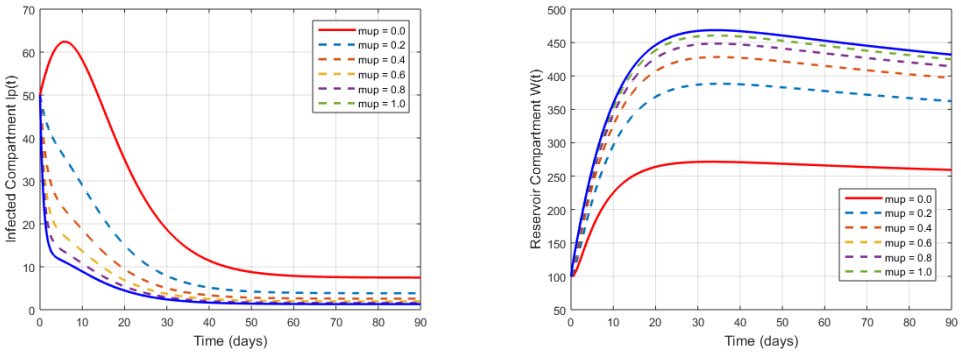


Figure 5: Model simulations with varying effect values of γ_p' for asymptomatic individuals.

Shown in Fig. 5, as the recovery rate of asymptomatic increases the number of asymptomatic infected become low and as the value of γ_p' decreases the number of asymptomatic infected population increases. This shows that the infected people without symptoms are significantly supporting the disease burden in the society.

Figures 6 (a) & (b) shows that if μ_p is applied at the rate of 50% to 100%, the disease spread rate will be reduced from infected compartment and returned to reservoir or totally eradicated.



(a) Symptomatic-infected-compartment (b) Resevoir-comp

Figure 6: Plots of I_P(t) and W(t) for different values of μ_p = 0.0, 0.2, 0.4, 0.6, 0.8,1.0.

5 CONCLUSION AND RECOMMENDATION

5.1 Conclusion

A deterministic mathematical model was formulated and analysed in this work to investigate the transmission dynamics of Covid-19 existence from reservoir to the society. The feasible region and positivity solution of the model were obtained. Then, the next-generation matrix method was applied to compute the basic reproductive number, R_0. Local and global stability of disease-free and endemic equilibra were analysed. The result shows that the Covid-19-free equilibrium point is locally and as well globally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$. The global stability of the disease-free and endemic equilibrium point were determined by using the Lyapunov method. Besides, the equilibrium point is locally asymptotically stable if $R_0 > 1$. From the epidemiological point of view, the disease can be controlled if R_0 is less than unity. Otherwise, the disease can live on in the community. In 'Parameter estimation', the model parameters were projected and followed from the existing literature.
In 'analysis of sensitivity', the normalized sensitivity indices of R_0 show that the most sensitivity parameters are μ, δ_p, μ_p and μ_A with negative sign, which shows that increasing the rate of controlling symptomatic infected individuals reduces R_0 while the least sensitive parameters are $\wedge_p$, β_1 and β_2. This indicates that reducing the contact rate of exposed individuals reduces R_0.

The model was numerically simulated to display the graphical solution of the model through MATLAB computer programming. The results show that, if the contact rate between infected and susceptible human is very low, the disease will be minimal in the society and remain in the reservoir. Also, if the rate of caring for the symptomatic patient is not less than 50%, the disease will vanish and can only occur in the reservoir.

5.2 Recommendation

The future work will immensely focus on ways to control and eradicate the infection from the reservoir in order to save the society completely from Covid-19 disease by applying optimal control method.

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