Travelling and COVID-19: A Mathematical Model

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Abstract A non-linear mathematical model is proposed to study the impacts of travelling in human-human transmission of COVID- 19.Two different regions are considered and transmission dynamics of COVID-19 dissemination in two regions caused by travelling from one region to other and infection during travel are discussed.Besides contacts between susceptible and infected population of a region off the travel,transmission of disease due to contacts during travel is also considered.The proposed model is analysed using stability theory of ordinary differential equation and feasibility of qualitative results ia checked through numerical simulations.From obtained results,it is shown that travellig and population dispersal can aggravate disease spreading in each region.It is also inferred that rate of travelling and rate of contacts during travel and off the travel can ease the disease to take endemic form and for high rates,it may become pandemic. Further numerical calculations are performed and critical limits of the major factors enhancing spreading of disease.It is revealed that when the rates goes higher than their corresponding critical limits,disease may not be controlled due to high infection.It is also imparted that when the rates are high, disease can only be controlled with high rate of quarantine.Also approximate time or stability is evaluated for maximum as well as minimum rates of key parameters.The results obtained by analysing the model recommends that for early stability of endemic situation,key factors must be kept as minimum as possible within estimated limits and quarantinig infected class to control the transmission of disease.

Keywords Mathematical Model · COVID - 19 · Stability Analysis · Critical limits

Mathematics Subject Classification (2010) 00A71 · 92D30 · 93A30

1 Introduction

Communication system between two regions of a country or between two countries is being developed as time goes by transpiring at the same time with rapid growth in population densities. Besides a blessing to the mankind, this conveyance is figured out as one of the major factors for transmission of various infectious diseases like Influenza, AIDS, SARS, EVD etc between two regions. When a person, infected with communicable diseases, travel from one region to other and make contact with non - infected people, it makes the tranmission and spreading of the diseases easy. Thus travelling and migration of populationr can play a key role in circulation of diseases from one hotspot region to another disease free region. In similar manner, dispersal of population plays a major role in alarming proliferation of Corona Virus Disease 2019(COVID - 19) globally and becomes a threat to the mankind. Having resemblance with SARS coronavirus and MERS coronavirus, it has been classified as zoonotic coronavirus and is highly contagious. 1,696, 588 cases are confirmed so far with fatal cases 105,952 throughout the world [1]. This disease was originated from Wuhan province of China and currently, 210 countries and territories are contaminated by COVID - 19.
To understand the transmission dynamics of infectious diseases analytically, importance of developing mathematical models becomes very much consistent. Many mathematical models have been developed to study the transmission dynamics with its prototype, conditions for stability of various communicable diseases ([2] [3] [4] [5] [6] [7]). Various compartmental models like SI , SIR, SIRS, SEIR etc. have been developed with different compartments and parameters ([2] [7] [8] [9] [10] [11] [12] [13] [14] [15]). Researchers

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have studied impacts of migration in spreading of diseases ([16] [17] [18] [19]). Also multi - city mathematical models have been incorporated with patchy environments to study dynamics of transport related infections ([3] [20] [21] [22] [23] [24] [25] [26]).
In a like manner, a number of models have been studied to understand the epidemiological dynamics and key parameters of COVID - 19. A deterministic compartmental model has been developed on the basis of clinical progression of the disease to study the reproductive number and transmission risk and they have found that in Wuhan, reproductive number may be 6.47[27]. Predicting the epidemiological parameters, epidemic predictions ahve been made by researchers and it has been inferred that 58–76 percent of transmissions must be prevented to stop increasing [28]. A mathematical SEIR model has been proposed to study the outbreak in Wuhan under the consideration of multiple pathways in infection dynamics and the role of environmental reservoir in transmission [29]. Using a mathematical model based on the informations the time-dependent spreading rate of the number of individuals who have caught a contagious disease is proportional to the multiplication of the numbers of those who have caught the disease and those who have not, a study has been made to investigate the pandemic situation and it has been shown that pandemic situation may change ery first in adverse direction [30]. But in these studies, critical limits of key parameters for stability and for eradication of disease are unfathomable. Also the impact of travelling between two regions in transmission of disease has not been studied yet.
Therefore, understanding importance of the above points, we develop a non - linear model. In this model, we assume that two regions H and A are well connected by transportation and infected people travel between two regions. Besides transmission of disease from infected of region H (or A) to susceptible of the same region, it is also considered that during travel, when susceptibles regions H and A travel with infected individuals of region H (or A), disease is transmitted also during that time. We analyse the proposed model for two different cases viz. when migration rates of susceptible and infected individuals are equal and when the rates are unequal. Contact rate between susceptible and infected people of same region and contact rates between susceptible of region H (or A) and infected of region A (or H) are considered different. Critical limits of major parameters playing key role in transmission of disease is calculated and for these critical values, approximate time required to attain stability is also evaluated. To the best of our knowledge, this study is clear enough to recognize from previous works related to COVID - 19.

2 FORMULATION OF MATHEMATICAL MODEL

In order to develop a mathematical model to study the effects of migration and travelling on spreading of Corona Virus Disease-19, we define two different regions:- i. Region where the disease has initially been broken out. This region is referred to as Disease Hotspot Region and for future reference, this region is denoted as region H. ii. Region where disease has been spread due to travelling and immigration of population from region H. This region is referred to as Affected Region and for future reference, this region is denoted as region A. Let, total population of region H be N_h which s divided into two compartments, namely, susceptible class S_h and infected class I_h. We consider total population of region A be N_a which is divided into three compartments, namely, susceptible population S_a, infected population I_a and quarantined population Q_a. Therefore,

$$N_h = S_h + I_h \tag{1.1}$$
$$N_a = S_a + I_a + Q_a \tag{1.2}$$

We also consider the following basic assumptions:- i.Disease is transmitted o a non – infected person only by making contact with an infected individual i.e. only human – to – human transmission is being considered.
ii.Recruitment rate of new susceptible individuals in the class S_h and S_a is considered to be fixed per unit time.
iii.There is no natural death in infected class.
iv.Individuals don't give birth or die during travelling.
v.We further assume that infected individuals don't recover from the disease during travelling.
vi.Two regions are well – connected by transportations like aeroplanes, roads or railways.
vii.When infected individuals travel from region H to region A, they immediately don't mix homogeneously with the population of region A. Therefore, disease can be transmitted to the susceptible population of region A when they make contact with infected individuals of region H in the time between reaching in region A and mixing with population. Same consideration is taken when infected individuals travel from region A to region H.
viii.It is considered there is natural death as well as death due to disease in class Q_a.
In region H, suppose the recruitment rate of new susceptible in class S_h be λ_1 per unit time and per capita natural death rate in this region be μ_1. Susceptible people travel from region H to region A with

a rate of migration α_{ha} and the rate of migration of infected individuals from region H to region A is m_{ha}. Rate at which susceptible individuals move to class I_h by making contact with individuals of class I_h is β_h. Per capita death rate due to disease is δ_h and the rate at which infected individuals are being quarantined is γ_h. In region A, new susceptible joins into class S_a at rate $\lambda_2$and μ_2 be the per capita natural death rate in this region. Susceptible and infected individuals migrate from region A to region H at the rates α_{ah} and m_{ah} respectively. Susceptible individuals move to class I_a at rate β_a when they make contact with infected individuals of class I_a. Per capita death rate due to disease is δ_a and infected individuals move to quarantined classat rate γ_a. When infected individuals from region H travel to region A, at the time of travelling, disease can be transmitted to the susceptible individuals of region H as well as of region A who are travelling companions. As the infected individuals travel, disease is transmitted to the individuals of class S_h travelling with those infected ones at the incidence rate $\eta(m_{ha}I_h)(\alpha_{ha}S_h)$ with transmission rate $\eta m_{ha}\alpha_{ha}$ and to the individuals of class S_a at incidence rate $rS_a(m_{ha}I_h)$ with transmission rate rm_{ha}. In similar manner, When infected individuals from region A travel to region H, at the time of travelling, disease can be transmitted to the susceptible individuals of region A and region H. When they travel, disease is transmitted to the individuals of class S_a travelling with those infected individuals at the incidence rate $\eta(m_{ah}I_a)(\alpha_{ah}S_a)$ with transmission rate $\eta m_{ah}\alpha_{ah}$ and to the individuals of classat incidence rate $rS_h(m_{ah}I_a)$ with transmission rate rm_{ah}. On the basis, of the above assumptions made, proposed mathematical model is:-

$$\frac{dS_h}{dt} = \lambda_1 - \mu_1 S_h - \alpha_{ha}S_h + \alpha_{ah}S_a - \beta_h S_h I_h - r_1 m_a h S_h I_a - \eta_1 \alpha_{ah} m_{ah} S_a I_a \tag{2.1}$$

$$\frac{dI_h}{dt} = \beta_h S_h I_h + r_1 m_{ah} S_h I_a + \eta_1 \alpha_{ah} m_{ah} S_a I_a - m_{ha} I_h + m_{ah} I_a - (\delta_h + \gamma_h) I_h \tag{2.2}$$

$$\frac{dS_a}{dt} = \lambda_2 - \mu_2 S_a - \alpha_{ah}S_a + \alpha_{ha}S_h - \beta_a S_a I_a - r_2 m_{ha} S_a I_h - \eta_2 \alpha_{ha} m_{ha} S_h I_h \tag{2.3}$$

$$\frac{dI_a}{dt} = \beta_a S_a I_a + r_2 m_{ha} S_a I_h + \eta_2 \alpha_{ha} m_{ha} S_h I_h - m_{ah} I_a + m_{ha} I_h - (\delta_a + \gamma_a) I_a \tag{2.4}$$

$$\frac{dQ_a}{dt} = \gamma_a I_a - (\delta_a + \mu_a) Q_a \tag{2.5}$$

$S_h(0) > 0, I_h(0) \geq 0, S_a(0) > 0, I_a(0) \geq 0, Q_a(0) \geq 0$ and all parameters are taken positive with $0 \leq \eta < 1$ and $0 < r \leq 1$. Also $(\alpha_{ah}S_a - \eta_1 \alpha_{ah} m_{ah} S_a I_a) \geq 0$ as $\alpha_{ha}S_a$ is the number of susceptible population migrated from region A to region H which is, to maintain biological relevancy, is larger than the number of susceptible individuals becoming infected while travelling with infected individuals.

2.1 Positivity and Boundedness of Solutions

Theorem 1 *The set* $\Gamma = \{(S_h, I_h, S_a, I_a, Q_a) \in R_+^5 : 0 < (S_h + I_h + S_a + I_a + Q_a) \leq \frac{\lambda_1 + \lambda_2}{\epsilon}\}$ *is positively invariant for the model (2) where* $\epsilon_h = min(\mu_h, \delta_h, \gamma_h), \epsilon_a = min(\mu_a, \delta_a, \gamma_a), \epsilon = min(\epsilon_h, \epsilon_a)$

Proof From equation (2.2), it can be seen that $\frac{dI_h}{dt} \geq -(\alpha_{ha} + \delta_h + \gamma_h) I_h$. Using given initial condition, it results

$$I_h(t) \geq I_h(0) e^{-\int_0^t (\alpha_{ha} + \delta_h + \gamma_h) dz} \geq 0$$

In similar manner, using initial conditions, positivity of solutions can be established from the remaining equations. Now, on adding the equations of the model (2), we obtain,

$$\frac{d}{dt}(S_h + I_h + S_a + I_a + Q_a) = \lambda_1 + \lambda_2 - \{\mu_h S_h + (\delta_h + \gamma_h) I_h\} - \{\mu_a S_a + \delta_a I_a + \delta_a Q_a + \mu_a Q_a\} \tag{3}$$

Now let $\epsilon_h = min(\mu_h, \delta_h, \gamma_h), \epsilon_a = min(\mu_a, \delta_a, \gamma_a), \epsilon = min(\epsilon_h, \epsilon_a)$. On using (1.1) and (1.2), equation (3) results

$$\frac{d}{dt}(N_h + N_a) \leq (\lambda_1 + \lambda_2) - \epsilon(N_h + N_a)$$

which, by comparison theorem, gives $(N_h + N_a)(t) \leq \frac{\lambda_1 + \lambda_2}{\epsilon}$ for $t > 0$.
Let us consider a closed set $\Gamma = \{(S_h, I_h, S_a, I_a, Q_a) \in R_+^5 : 0 < (S_h + I_h + S_a + I_a + Q_a) \leq \frac{\lambda_1 + \lambda_2}{\epsilon}\}$. Then the set Γ is positively invariant for the model (2) and this region becomes feasible when solutions enter in this region. We will study the model in this region

3 Qualitative Analysis

In this section, we study the model (2) qualitatively. We will carry out the qualitative analysis of the model (2) under the assumption that in both the region recruitment rates of new susceptible, per capita natural death rate and per capita diseased death rate are considered to be equal *i.e.* $\lambda_1 = \lambda_2 = \lambda$, $\mu_1 = \mu_2 = \mu$ and $\delta_h = \delta_a = \delta$. The implication of this condition is that demographic parameters are identical in two regions. Also, our aim of this work is to study how migration and travelling speed up the spreading of disease, therefore for simplicity of model as well as calculation, we consider that transmission rates and rate at which infected people are quarantined are equal *i.e* $\beta_h = \beta_a = \beta$, $\eta_1 = \eta_2 = \eta$, $r_1 = r_2 = r$ and $\gamma_h = \gamma_a = \gamma$. Under this assumption, we will study the model (2) for the following cases:-
i. Migration rates of susceptible and infected individuals of region H and migration rates of susceptible and infected individuals in region A are equal *i.e.* $\alpha_{ha} = \alpha_{ah} = m_{ha} = m_{ah} = \alpha$
ii. Migration rates of susceptible individuals of region H and that of region A are equal *i.e.* $\alpha_{ha} = \alpha_{ah} = \alpha$. Also migration rate of infected individuals of region H and region A are equal *i.e* $m_{ha} = m_{ah} = m$ with $\alpha \neq m$.
When there is no immigration between two regions, model (2) becomes simple SI model with two equilibrium points, namely *Disease Free Equilibrium Point* $E_0 \equiv (\frac{\lambda}{\mu}, 0, \frac{\lambda}{\mu}, 0, 0)$ and *Endemic Equilibrium Point* $E^* \equiv (S_h^*, I_h^*, S_a^*, I_a^*, Q_a^*)$ where $S_h^* = \frac{\delta+\gamma}{\beta}, I_h^* = \frac{\mu}{\beta}(R_0 - 1), S_a^* = \frac{\delta+\gamma}{\beta}, I_a^* = \frac{\mu}{\beta}(R_0 - 1), Q_a^* = \frac{\gamma}{\delta+\mu}\frac{\mu}{\beta}(R_0 - 1)$ and $R_0 = \frac{\lambda\beta}{\mu(\delta+\gamma)}$ is the *Basic Reproductive Number*. It can be checked that E_0 is locally asymptotically stable if and only if $R_0 < 1$ and endemic equilibrium point E^* is stable if and only if $R_0 > 1$. There are two more equilibrium points, namely *Disease Free Equilibrium Point in region H* ($I_h = 0$) and *Disease Free Equilibrium Point in region A* ($I_a = 0$) which are unstable whenever exist. Since, this model has widely been studied, we do not analyse this model and we proceed for analysing based upon our assumptions.

A. Migration rates of susceptible and infected individuals of region H and migration rates of susceptible and infected individuals in region A are equal i.e $\alpha_{ha} = \alpha_{ah} = m_{ha} = m_{ah} = \alpha$

under the consideration model (2) is reduced to:

$$\frac{dS_h}{dt} = \lambda - \mu S_h - \alpha S_h + \alpha S_a - \beta S_h I_h - \eta\alpha S_a I_a - r\alpha S_h I_a \tag{4.1}$$
$$\frac{dI_h}{dt} = \beta S_h I_h + \eta\alpha S_a I_a + r\alpha S_h I_a - \alpha I_h + \alpha I_a - (\delta + \gamma) I_h \tag{4.2}$$
$$\frac{dS_a}{dt} = \lambda - \mu S_a - \alpha S_a + \alpha S_h - \beta S_a I_a - \eta\alpha S_h I_h - r\alpha S_a I_h \tag{4.3}$$
$$\frac{dI_a}{dt} = \beta S_a I_a + \eta\alpha S_h I_h + r\alpha S_a I_h + \alpha I_h - \alpha I_a - (\delta + \gamma) I_a \tag{4.4}$$
$$\frac{dQ_A}{dt} = \gamma I_a - (\delta + \mu) Q_a \tag{4.5}$$

The initial conditions and region of attraction remain same for this model.

3.1 Model Analysis

In this section, we study the existence of equilibrium points and stability analysis of the proposed model (4) for the following cases:-
i. Only susceptible individuals are permitted to travel between region H and region A
ii. All individuals travel from region H to A and vice versa
Case I: Only susceptible individuals are permitted to travel between region H and region A
Since there is no migration of infected individuals from region H to region A and vice versa, model (4) can be written as:-

$$\frac{dS_h}{dt} = \lambda - \mu S_h - \alpha S_h + \alpha S_a - \beta S_h I_h \tag{5.1}$$
$$\frac{dI_h}{dt} = \beta S_h I_h - (\delta + \gamma) I_h \tag{5.2}$$
$$\frac{dS_a}{dt} = \lambda - \mu S_a - \alpha S_a + \alpha S_h - \beta S_a I_a \tag{5.3}$$
$$\frac{dI_a}{dt} = \beta S_a I_a - (\delta + \gamma) I_a \tag{5.4}$$
$$\frac{dQ_A}{dt} = \gamma I_a - (\delta + \mu) Q_a \tag{5.5}$$

There is no change in given initial conditions and it can be checked that the set Γ remains unchanged for this reduced model

3.1.1 Existence of Equilibrium Points

The equilibrium points can be evaluated by solving the following system of algebraic equations:-

$$\lambda - \mu S_h - \alpha S_h + \alpha S_a - \beta S_h I_h = 0 \tag{6.1}$$
$$\beta S_h I_h - (\delta + \gamma) I_h = 0 \tag{6.2}$$
$$\lambda - \mu S_a - \alpha S_a + \alpha S_h - \beta S_a I_a = 0 \tag{6.3}$$
$$\beta S_a I_a - (\delta + \gamma) I_a = 0 \tag{6.4}$$
$$\gamma I_a - (\delta + \mu) Q_a = 0 \tag{6.5}$$

From (6.2) and (6.3), we have $I_h = 0, I_h \neq 0$ and $I_a = 0, I_a \neq 0$. Therefore, we study the existence of unique positive equilibrium points for the cases $I_h = 0, I_a = 0; I_h \neq 0, I_a = 0; I_h = 0, I_a \neq 0; I_h \neq 0, I_a \neq 0$. When $I_h = 0, I_a = 0$, we get an equilibrium point $E_0 \equiv (S_{h_0}, 0, S_{a_0}, 0, 0)$ where $S_{h_0} = \frac{\lambda}{\mu}, S_{a_0} = \frac{\lambda}{\mu}$. This equilibrium point exists uniquely and positively for all positive parameters considered. Now, using theory of next generation matrix, Basic Reproductive Number for model (6) can be computed. The required basic reproductive number R_0 defined by $R_0 = \rho(FV^{-1}) = \frac{\lambda\beta}{\mu(\delta+\gamma)}$ where F and V are the next generation matrices [32] given by $F = \begin{pmatrix} \frac{\lambda\beta}{\mu} & 0 \\ 0 & \frac{\lambda\beta}{\mu} \end{pmatrix}$ and $V = \begin{pmatrix} \delta+\gamma & 0 \\ 0 & \delta+\gamma \end{pmatrix}$ and $\rho(FV^{-1})$ is the spectral radius of the matrix FV^{-1}.
When $I_h \neq 0, I_a = 0,$, there exists an equilibrium point $\bar{E} \equiv (\bar{S_h}, \bar{I_h}, \bar{S_a}, 0, 0)$ where

$$\bar{S_h} = \frac{\delta+\gamma}{\beta}, \bar{S_a} = \frac{\lambda + \alpha\bar{S_h}}{\alpha+\mu}, \bar{I_h} = \frac{1}{\beta}[\{\mu R_0 - (\alpha+\mu)\} + \frac{\alpha\beta}{(\delta+\gamma)}\bar{S_a}] \tag{7}$$

Where R_0 is the Basic Reproductive Number. It is clear from (7) that $\bar{I_h}$ is positive when $R_0 > 1 + \frac{\alpha}{\mu}$ which is consequently greater than 1. Therefore, the equilibrium point $\bar{E}$ exists positively and uniquely under the condition $R_0 > 1$. This equilibrium point is called *Disease Free Equilibrium Point of Region A*
When $I_h = 0, I_a \neq 0$, there exists an equilibrium point $\hat{E} \equiv (\hat{S_h}, 0, \hat{S_a}, \hat{I_a}, \hat{Q_a})$ where

$$\hat{S_a} = \frac{\delta+\gamma}{\beta}, \hat{S_h} = \frac{\lambda + \alpha\hat{S_a}}{\alpha+\mu}, \hat{I_a} = \frac{1}{\beta}[\{\mu R_0 - (\alpha+\mu)\} + \frac{\alpha\beta}{(\delta+\gamma)}\bar{S_h}], \hat{Q_a} = \frac{\gamma\hat{I_a}}{(\delta+\mu)} \tag{8}$$

Where R_0 is the Basic Reproductive Number. It is clear from (8) that $\hat{I_a}$ is positive when $R_0 > 1 + \frac{\alpha}{\mu}$ which is consequently greater than 1. Therefore, the equilibrium point $\hat{E}$ exists positively and uniquely under the condition $R_0 > 1$. This equilibrium point is called *Disease Free Equilibrium Point of Region H*
When $I_h \neq 0, I_a \neq 0$, there is an equilibrium point $E^* \equiv (S_h^*, I_h^*, S_a^*, I_a^*, Q_a^*)$ where

$$S_h^* = \frac{\lambda}{\mu}\frac{1}{R_0}, I_h^* = \frac{\lambda}{\delta+\gamma}(1 - \frac{1}{R_0}), S_a^* = \frac{\lambda}{\mu}\frac{1}{R_0}, I_a^* = \frac{\lambda}{\delta+\gamma}(1 - \frac{1}{R_0}), Q_a^* = \frac{\gamma I_a^*}{(\delta+\mu)} \tag{9}$$

This equilibrium point is called *Endemic Equilibrium Point*. It can be observed that unique and positive Endemic equilibrium point E^* exists if and only if $R_0 > 1$.

3.1.2 Stability Analysis

Theorem 2 *The Disease Free Equilibrium point of model (5) is locally asymptotically stable if and only if $R_0 < 1$ and the Endemic Equilibrium Point is locally asymptotically stable if and only if $R_0 > 1$. Whenever endemic equilibrium point exists, disease free equilibrium point becomes unstable. Moreover, the other two equilibrium points become unstable whenever they exist.*

Proof At the equilibrium point E_0, the variational matrix of the model (5) is

$$M_0 = \begin{pmatrix} -(\alpha+\mu) & -\beta\frac{\lambda}{\mu} & \alpha & 0 & 0 \\ 0 & \beta\frac{\lambda}{\mu} - (\delta+\gamma) & 0 & 0 & 0 \\ \alpha & 0 & -(\alpha+\mu) & -\beta\frac{\lambda}{\mu} & 0 \\ 0 & 0 & 0 & \beta\frac{\lambda}{\mu} - (\delta+\gamma) & 0 \\ 0 & 0 & 0 & q & -(\delta+\mu) \end{pmatrix} \tag{10}$$

The equilibrium point E_0 is locally asymptotically stable if all the eigenvalues of corresponding to the matrix M_0 has negative real parts. From the characteristic equation $|M_0 - \nu I| = 0$ corresponding to the matrix M_0, we obtain, $\nu_5 = -(\delta + \mu) < 0$, $\nu_2 = \nu_4 = \beta\frac{\lambda}{\mu} - (\delta + \gamma)$ which is negative if $\beta\lambda < \mu(\delta + \gamma)$ implying $R_0 < 1$. The other two eigenvalues are $\nu_1 = -\mu, \nu_3 = -(2\alpha + \mu)$ which are negative for all positive values of the parameters considered. Therefore, the disease free equilibrium point E_0 is locally asymptotically stable if and only if $R_0 < 1$. It can be checked that the equilibrium points $\bar{E}$ and $\hat{E}$ are locally asymptotically unstable whenever they exist as the conditions for stability of these two equilibrium points are $R_0 < 1$ which contradict the necessary condition for existence of these two equilibrium points. At the equilibrium point E^*, the variational matrix (10) is,

$$M^* = \begin{pmatrix} a_{11} & a_{12} & a_{13} & 0 & 0 \\ a_{21} & a_{22} & 0 & 0 & 0 \\ a_{31} & 0 & a_{33} & a_{34} & 0 \\ 0 & 0 & a_{43} & a_{44} & 0 \\ 0 & 0 & 0 & a_{54} & a_{55} \end{pmatrix} \tag{11}$$

where $a_{11} = -(\mu R_0 + \alpha), a_{12} = -(\delta + \gamma), a_{13} = \alpha$ $a_{21} = \mu(R_0 - 1), a_{22} = 0, a_{31} = \alpha,$
$a_{33} = -(\mu R_0 + \alpha), a_{34} = -(\delta + \gamma), a_{43} = \mu(R_0 - 1)$, $a_{44} = 0, a_{54} = \gamma, a_{55} = -(\delta + \mu)$
Now, from the charecteristic equation $|M_0 - \nu I| = 0$ corresponding to the matrix M^*, we obtain $\nu_5 = -(\delta + \mu) < 0$.
Other eigenvalues are the root of the equation $A_0\nu^4 + A_1\nu^3 + A_2\nu^2 + A_3\nu + A_4 = 0$ where $A_0 = 1 > 0$
$A_1 = -(a_{11} + a_{33}) = 2(\mu R_0 + \alpha)$
$A_2 = a_{11}a_{33} - (a_{12}a_{21} + a_{13}a_{31} + a_{34}a_{43}) = (\mu R_0 + \alpha)^2 + [2\mu(\delta + \gamma)(R_0 - 1) - \alpha^2]$
$A_3 = a_{12}a_{21}a_{33} + a_{11}a_{34}a_{43} = 2\mu(\delta + \gamma)(R_0 - 1)(\mu R_0 + \alpha)$
$A_4 = a_{12}a_{21}a_{34}a_{43} = \mu^2(\delta + \gamma)^2(R_0 - 1)^2$
By Routh – Hurwitz stability criterion, $A_0\nu^4 + A_1\nu^3 + A_2\nu^2 + A_3\nu + A_4 = 0$ has roots with negative real parts if the following inequalities hold:-
i. $A_i > 0$ for $i = 1, 2, 3, 4$
ii. $A_3(A_1A_2 - A_0A_3) - A_1^2A_4 > 0$
iii. $A_1A_2 - A_0A_3 > 0$ These conditions hold if and only if $R_0 > 1$. Hence, by Routh – Hurwitz stability criteria, endemic equilibrium point E^* is stable if and only if $R_0 > 1$ and whenever E^* is stable, disease free equilibrium point E_0 is unstable.

Remark 1 From (9), it can be observed that $\frac{\partial}{\partial\gamma}(S_h^* + S_a^*) = -\frac{2\lambda}{\mu {R_0}^2}\frac{\partial R_0}{\partial\gamma} > 0$ and $\frac{\partial}{\partial\gamma}(I_h^* + I_a^*) = \frac{2\mu}{\beta}\frac{\partial R_0}{\partial\gamma} < 0$ as $\frac{\partial R_0}{\partial\gamma} < 0$. As γ goes high *i.e.* more infected individuals are quarantined, it prevents the disease from spreading and therefore, total number of susceptible individuals in both region increases. When γ goes very low *i.e.* when individuals are quarantined at very low rate, total infected population of region H and region R goes very high due to increasing in R_0. In that case, instead of disease free equilibrium point, endemic equilibrium point arises and as this rate goes lower, disease can be transmitted through contact with infected population in a high scale which causes enormous outbreak of the disease.

Case II: All individuals are permitted to travel from region H to region A and vice versa
For this case, we study existence of equilibrium points and their stability analysis of the model (5). Initial conditions and region of attraction have already been discussed before.

3.1.3 Existence of Equilibrim Points

The equilibrium points of model (4) can be obtained by solving following system of algebraic equations:-

$$\lambda - \mu S_h - \alpha S_h + \alpha S_a - \beta S_h I_h - \eta\alpha S_a I_a - r\alpha S_h I_a = 0 \tag{12.1}$$
$$\beta S_h I_h + \eta\alpha S_a I_a + r\alpha S_h I_a - \alpha I_h + \alpha I_a - (\delta + \gamma) I_h = 0 \tag{12.2}$$
$$\lambda - \mu S_a - \alpha S_a + \alpha S_h - \beta S_a I_a - \eta\alpha S_h I_h - r\alpha S_a I_h = 0 \tag{12.3}$$
$$\beta S_a I_a + \eta\alpha S_h I_h + r\alpha S_a I_h + \alpha I_h - \alpha I_a - (\delta + \gamma) I_a = 0 \tag{12.4}$$
$$\gamma I_a - (\delta + \mu) Q_a = 0 \tag{12.5}$$

this system has unique positive equilibrium point $E_0 \equiv (S_{h_0}, 0, S_{a_0}, 0, 0)$ where $S_{h_0} = \frac{\lambda}{\mu}, S_{a_0} = \frac{\lambda}{\mu}$ when $I_h = 0, I_a = 0$. It is known as *Disease Free Equilibrium Point*. This equilibrium point exists without any conditions and for all positive values of parameters considered. The Basic Reproductive Number R_{0_m} for this case is evaluated by using next generation matrices $F = \begin{pmatrix} \frac{\lambda\beta}{\mu} & \frac{\alpha\lambda}{\mu}(\eta + r) \\ \frac{\alpha\lambda}{\mu}(\eta + r) & \frac{\lambda\beta}{\mu} \end{pmatrix}$ and $V = \begin{pmatrix} \alpha + \delta + \gamma & -\alpha \\ -\alpha & \alpha + \delta + \gamma \end{pmatrix}$.
which is

$$R_{0_m} = \rho(FV^{-1}) = \frac{\lambda\beta + \alpha\lambda(\eta + r)}{\mu(\delta + \gamma)} = R_0 + \frac{\alpha\lambda(\eta + r)}{\mu(\delta + \gamma)} \tag{13}$$

When $I_h \neq 0, I_a \neq 0$, *Endemic Equilibrium Point* $E^* \equiv (S_h^*, I_h^*, S_a^*, I_a^*, Q_a^*)$ is obtained where

$$S_h^* = \frac{\lambda}{\mu}\frac{1}{R_{0_m}}, I_h^* = \frac{\lambda}{\delta+\gamma}(1-\frac{1}{R_{0_m}}), S_a^* = \frac{\lambda}{\mu}\frac{1}{R_{0_m}} I_a^* = \frac{\lambda}{\delta+\gamma}(1-\frac{1}{R_{0_m}}), Q_a^* = \frac{\gamma I_a^*}{(\delta+\mu)} \tag{14}$$

From (14), it can be noticed that the endemic equilibrium point E^* exists uniquely and positively if and only if $R_{0_m} > 1$. There are also two possibilities $I_h = 0, I_a \neq 0$ and $I_h \neq 0, I_a = 0$. For $I_h = 0, I_a \neq 0$, (13.4) results $S_a = \frac{\alpha+\delta+\gamma}{\beta}$ using this result and $I_h = 0$, we obtain $\eta\alpha S_a I_a + r\alpha S_h I_a + \alpha I_a = 0$ from which we reach to a contradiction to the fact $I_a \neq 0$ as $\eta\alpha S_a + r\alpha S_h + \alpha \neq 0$. Therefore, If region H is disease free, there is no possibilities to spread the disease in region A. Again for $I_h \neq 0, I_a = 0$, we have $S_h = \frac{\alpha+\delta+\gamma}{\beta}$ for which we can't find any positive value of S_a. Therefore, under this condition also, there is no equilibrium point. This leads to the fact that when one region is disease free, then there is no possibility for spreading of disease caused by travelling and migration.

Remark 2 When susceptible as well as infected individuals travel between two regions, basic reproductive number becomes higher than that in the case of only travelling of susceptible individuals.

Remark 3 Clearly $\lim_{\alpha\to 0} R_{0_m} = R_0$. When migration rate is very low, then basic reproductive number in this case tends to R_0. A little increase in α can result outbreak of disease which may be unbearable for the regions.

Remark 4 When, during travelling, susceptible people of region H and region A come to contact with infected ones of that region in high rate, it makes R_{0_m} higher. Then, disease can spread in an alarming scale. Also, in this case, total susceptible population decreases with increasing infected population because as $\frac{\partial R_{0_m}}{\partial \eta} > 0, \frac{\partial R_{0_m}}{\partial r} > 0$,

$$\frac{\partial}{\partial \eta}(S_h^* + S_a^*) = -2\frac{\lambda}{\mu}\frac{1}{{R_{0_m}}^2}\frac{\partial R_{0_m}}{\partial \eta} < 0, \frac{\partial}{\partial \eta}(I_h^* + I_a^*) = 2\frac{\lambda}{(\delta+\gamma)}\frac{1}{{R_{0_m}}^2}\frac{\partial R_{0_m}}{\partial \eta} > 0 \tag{15.1}$$

$$\frac{\partial}{\partial r}(S_h^* + S_a^*) = -2\frac{\lambda}{\mu}\frac{1}{{R_{0_m}}^2}\frac{\partial R_{0_m}}{\partial r} < 0, \frac{\partial}{\partial r}(I_h^* + I_a^*) = 2\frac{\lambda}{(\delta+\gamma)}\frac{1}{{R_{0_m}}^2}\frac{\partial R_{0_m}}{\partial r} > 0 \tag{15.2}$$

Remark 5 From (14), it can be noted that on choosing $\lambda = 1$, $R_{0_m} > 1$ when $\beta + \alpha(\eta + r) > \mu(\delta + \gamma)$ and $R_{0_m} < 1$ when $\beta + \alpha(\eta + r) < \mu(\delta + \gamma)$. It is clear that higher rate of contacts, migration can cause severe outbreak of disease.

3.1.4 Stability Analysis

Theorem 3 *The Disease Free Equilibrium point of model (4) is locally asymptotically stable if and only if* $2R_0 < R_{0_m} < 1$ *and the Endemic Equilibrium Point is locally asymptotically stable if and only if* $1 < R_{0_m} < 2R_0$. *Whenever endemic equilibrium point exists, disease free equilibrium point becomes unstable.*

Proof At the equilibrium point E_0, the jacobian matrix corresponding to model (4) becomes,

$$M_0 = \begin{pmatrix} a_{11} & a_{12} & a_{13} & a_{14} & 0 \\ 0 & a_{22} & 0 & a_{24} & 0 \\ a_{31} & a_{32} & a_{33} & a_{34} & 0 \\ 0 & a_{42} & 0 & a_{44} & 0 \\ 0 & 0 & 0 & a_{54} & a_{55} \end{pmatrix} \tag{16}$$

where $a_{11} = -(\alpha+\mu), a_{12} = -\frac{\beta\lambda}{\mu}, a_{13} = \alpha, a_{14} = -\frac{\alpha\lambda}{\mu}(\eta + r)$
$a_{22} = \frac{\beta\lambda}{\mu} - (\alpha + \delta + \gamma), a_{24} = \frac{\alpha\lambda}{\mu}(\eta + r) + \alpha$
$a_{31} = \alpha, a_{32} = -\frac{\alpha\lambda}{\mu}(\eta + r), a_{33} = -(\alpha + \mu), a_{34} = -\frac{\beta\lambda}{\mu}$
$a_{42} = \frac{\alpha\lambda}{\mu}(\eta + r) + \alpha, a_{44} = \frac{\beta\lambda}{\mu} - (\alpha + \delta + \gamma)$
$a_{54} = \gamma, a_{55} = -(\delta + \mu)$
The necessary condition for the stability of E_0 is that all the eigenvalues corresponding to the matrix M_0 have negative real parts and these can be calculated from the charecteristic equation $|M_0 - \nu I| = 0$ corresponding to the matrix M_0. One eigenvalue is clearly $\nu_5 = -(\delta + \mu) < 0$. Other eigenvalues can be evaluated by solving charecteristic equation corresponding to the matrix

$$P_0 = \begin{pmatrix} a_{11} & a_{12} & a_{13} & a_{14} \\ 0 & a_{22} & 0 & a_{24} \\ a_{31} & a_{32} & a_{33} & a_{34} \\ 0 & a_{42} & 0 & a_{44} \end{pmatrix} \tag{17}$$

It can be checked that $a_{11} = a_{33}, a_{12} = a_{34}, a_{22} = a_{44}, a_{13} = a_{31}, a_{14} = a_{32}, a_{24} = a_{42}$. Therefore, matrix P_o can be represented as,

$$P_0 = \begin{pmatrix} U & V \\ V & U \end{pmatrix}, U = \begin{pmatrix} a_{11} & a_{12} \\ 0 & a_{22} \end{pmatrix}, V = \begin{pmatrix} a_{13} & a_{14} \\ 0 & a_{24} \end{pmatrix} \tag{18}$$

The characteristic polynomial corresponding to the matrix P_0 can be incorporated as

$$|P_0 - \nu I| = |U + V - \nu I||U - V - \nu I| \tag{19}$$

ν_1, ν_2 are eigenvalues of $|U + V - \nu I| = 0$ and ν_3, ν_4 are the eigenvalues of $|U - V - \nu I| = 0$. These eigenvalues have negative real parts if the following conditions hold:-
i. $tr(U + V) < 0, tr(U - V) < 0$
ii. $|U + V| > 0, |U - V| > 0$.
Now,
i. $tr(U + V) = -\mu + (\delta + \gamma)(R_{0_m} - 1) < 0$ when $R_{0_m} < 1$, $tr(U - V) = -(4\alpha + \mu) - (\delta + \gamma)\{1 + (R_{0_m} - 2R_0)\}$ < 0 if $R_{0_m} > 2R_0$
ii. $|U + V| = \mu(\delta + \gamma)(1 - R_{0_m}) > 0$ if $R_{0_m} < 1$, $|U - V| = (2\alpha + \mu)\{2\alpha + (\delta + \gamma)(1 + R_{0_m} - 2R_0)\}$ under the codition $R_{0_m} > 2R_0$
Hence, the disease free equilibrium point E_0 is locally asymptotically stable if and only if $2R_0 < R_{0_m} < 1$
At the equilibrium point E^* , Jacobian of (4) becomes

$$M^* = \begin{pmatrix} a_{11} & a_{12} & a_{13} & a_{14} & 0 \\ a_{21} & a_{22} & a_{23} & a_{24} & 0 \\ a_{31} & a_{32} & a_{33} & a_{34} & 0 \\ a_{41} & a_{42} & a_{43} & a_{44} & 0 \\ 0 & 0 & 0 & a_{54} & a_{55} \end{pmatrix} \tag{20}$$

where $a_{11} = -(\alpha + \beta I_h^* + r\alpha I_a^* + \mu), a_{12} = -\beta S_h^*, a_{13} = \alpha - \eta\alpha I_a^*, a_{14} = -(r\alpha S_h^* + \eta\alpha S_a^*)$
$a_{21} = \beta I_h^* + r\alpha I_a^*, a_{22} = \beta S_h^* - (\alpha + \delta + \gamma), a_{23} = \eta\alpha I_a^*, a_{24} = r\alpha S_h^* + \eta\alpha S_a^* + \alpha$
$a_{31} = \alpha - \eta\alpha I_h^*, a_{32} = -(r\alpha S_h^* + \eta\alpha S_a^*), a_{33} = -(\alpha + r\alpha I_h^* + \beta I_a^* + \mu), a_{34} = -\beta S_a^*$
$a_{41} = \eta\alpha I_h^*, a_{42} = r\alpha S_h^* + \eta\alpha S_a^* + \alpha, a_{43} = \beta I_a^* + r\alpha I_h^*, a_{44} = \beta S_a^* - (\alpha + \delta + \gamma)$
$a_{54} = \gamma, a_{55} = -(\delta + \mu)$
From the charecteristic equation $|M^* - nuI| = 0$ corresponding to the matrix M^*, one eigenvalue is $\nu_5 = -(\delta + \mu) < 0$. Other eigenvalues can be evaluated from

$$P^* = \begin{pmatrix} a_{11} & a_{12} & a_{13} & a_{14} \\ a_{21} & a_{22} & a_{23} & a_{24} \\ a_{31} & a_{32} & a_{33} & a_{34} \\ a_{41} & a_{42} & a_{43} & a_{44} \end{pmatrix} \tag{21}$$

It can be observed that ‘$a_{11} = a_{33}, a_{12} = a_{34}, a_{22} = a_{44}, a_{13} = a_{31}, a_{14} = a_{32}, a_{24} = a_{42}$. Therefore, P^* can be written as

$$P^* = \begin{pmatrix} U^* & V^* \\ V^* & U^* \end{pmatrix}, U^* = \begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix}, V = \begin{pmatrix} a_{13} & a_{14} \\ a_{23} & a_{24} \end{pmatrix} \tag{22}$$

The characteristic polynomial corresponding to the matrix P^* can be incorporated as

$$|P^* - \nu I| = |U^* + V^* - \nu I||U^* - V^* - \nu I| \tag{23}$$

ν_1, ν_2 are eigenvalues of $|U^* + V^* - \nu I| = 0$ and ν_3, ν_4 are the eigenvalues of $|U^* - V^* - \nu I| = 0$. These eigenvalues have negative real parts if the following conditions hold:-
i. $tr(U^* + V^*) < 0, tr(U^* - V^*) < 0$
ii. $|U^* + V^*| > 0, |U^* - V^*| > 0$.

$$U^* + V^* = \begin{pmatrix} -\mu R_{0_m}(1 - \frac{1}{R_{0_m}}) + \mu & -(\delta + \mu) \\ \mu R_{0_m}(1 - \frac{1}{R_{0_m}}) & 0 \end{pmatrix} \tag{24.1}$$

$$U^* - V^* = \begin{pmatrix} -\{\alpha + \mu + \beta I_h^* + r\alpha I_a^* + (\alpha - \eta\alpha I_a^*)\} & \frac{\lambda}{\mu R_{0_m}}\{\alpha(\eta + r) - \beta\} \\ \frac{\mu R_0}{\beta}(\beta + \alpha r - \eta\alpha)(1 - \frac{1}{R_{0_m}}) & -2\frac{\alpha(\delta+\gamma)(\eta+r+1)}{\beta+\alpha(\eta+r)} \end{pmatrix} \tag{24.2}$$

Now, it is very clear from (24.1) and (24.2)that $tr(U^* + V^*)$ is always negative provided $R_{0_m} > 1$. Since $(\alpha - \eta\alpha I_a^*)$ is always positive, $tr(U^* - V^*)$ is negative under the condition $R_{0_m} > 1$. Again
$|(U^* + V^*)| = (\delta + \mu)\mu R_{0_m}(1 - \frac{1}{R_{0_m}}) > 0$ if $R_{0_m} > 1$. $|U^* - V^*| > 0$ if $\frac{\lambda}{\beta}\frac{R_0}{R_{0_m}}(1 - \frac{1}{R_{0_m}})\{(\alpha r)^2 - (\beta - \alpha\eta)^2\} < 0$ which implies the condition $R_{0_m} < 2R_0$.

Remark 6 When α, β, η and r become high such that $\beta + \alpha(\eta + r) > \mu(\delta + \gamma)$ holds, endemic equilibrium point E^* becomes stable with $R_{0_m} > 1$. When α, β, η and r become low and γ becomes high so that $\beta + \alpha(\eta + r) < \mu(\delta + \gamma)$ holds, then endemic equilibrium point ceases to be stable and disease free equilibrium point becomes stable.

Remark 7 When $0 < R_0 < \frac{1}{2}$, it implies $R_{0_m} < 1$. Therefore, instead of endemic equilibrium point, disease free equilibrium point gets stability in that case.

Remark 8 It can be observed that $\alpha(\eta + r) = \beta$ rises the case $R_{0_m} = 2R_0$. In that case, stability of disease free equilibrium point or endemic equilibrium point depend on the value of the incidence rates $\eta\alpha, r\alpha$ and β.

B. Migration rates of susceptible individuals of region H and that of region A are equal *i.e.* $\alpha_{ha} = \alpha_{ah} = \alpha$**. Also migration rate of infected individuals of region H and region A are equal** *i.e* $m_{ha} = m_{ah} = m$ **with** $\alpha \neq m$

3.2 Model Analysis

This consideration reduces the model (2) to the following form:

$$\frac{dS_h}{dt} = \lambda - \mu S_h - \alpha S_h + \alpha S_a - \beta S_h I_h - rmS_h I_a - \eta\alpha m S_a I_a \tag{25.1}$$

$$\frac{dI_h}{dt} = \beta S_h I_h + rmS_h I_a + \eta\alpha m S_a I_a - mI_h + mI_a - (\delta + \gamma)I_h \tag{25.2}$$

$$\frac{dS_a}{dt} = \lambda - \mu S_a - \alpha S_a + \alpha S_h - \beta S_a I_a - rmS_a I_h - \eta\alpha m S_h I_h \tag{25.3}$$

$$\frac{dI_a}{dt} = \beta S_a I_a + rmS_a I_h + \eta\alpha m S_h I_h - mI_a + mI_h - (\delta + \gamma)I_a \tag{25.4}$$

$$\frac{dQ_a}{dt} = \gamma I_a - (\delta + \mu)Q_a \tag{25.5}$$

3.2.1 Existence of Equilibrium Points

The equilibrium points of model (27) can be obtained by solving following system of algebraic equations:-

$$\lambda - \mu S_h - \alpha S_h + \alpha S_a - \beta S_h I_h - rmS_h I_a - \eta\alpha m S_a I_a = 0 \tag{26.1}$$

$$\beta S_h I_h + rmS_h I_a + \eta\alpha m S_a I_a - mI_h + mI_a - (\delta + \gamma)I_h = 0 \tag{26.2}$$

$$\lambda - \mu S_a - \alpha S_a + \alpha S_h - \beta S_a I_a - rmS_a I_h - \eta\alpha m S_h I_h = 0 \tag{26.3}$$

$$\beta S_a I_a + rmS_a I_h + \eta\alpha m S_h I_h - mI_a + mI_h - (\delta + \gamma)I_a = 0 \tag{26.4}$$

$$\gamma I_a - (\delta + \mu)Q_a = 0 \tag{26.5}$$

There exists a unique positive equilibrium point $E_0 \equiv (S_{h_0}, 0, S_{a_0}, 0, 0)$ where $S_{h_0} = \frac{\lambda}{\mu}, S_{a_0} = \frac{\lambda}{\mu}$ when $I_h = 0, I_a = 0$ known as *Disease Free Equilibrium Point*. This equilibrium point exists without any conditions and for all positive values of parameters considered. The Basic Reproductive Number R_{0_m} for this case is evaluated by using next generation matrices $F = \begin{pmatrix} \frac{\lambda\beta}{\mu} & \frac{m\lambda}{\mu}(\eta\alpha + r) \\ \frac{m\lambda}{\mu}(\eta\alpha + r) & \frac{\lambda\beta}{\mu} \end{pmatrix}$ and $V = \begin{pmatrix} m + \delta + \gamma & -m \\ -m & m + \delta + \gamma \end{pmatrix}$. which is

$$\overline{R}_{0_m} = \rho(FV^{-1}) = \frac{\lambda\beta + m\lambda(\eta\alpha + r)}{\mu(\delta + \gamma)} = R_0 + \frac{m\lambda(\eta\alpha + r)}{\mu(\delta + \gamma)} \tag{27}$$

When $I_h \neq 0, I_a \neq 0$, *Endemic Equilibrium Point* $E^* \equiv (S_h^*, I_h^*, S_a^*, I_a^*, Q_a^*)$ is acquired where

$$S_h^* = \frac{\lambda}{\mu}\frac{1}{\overline{R}_{0_m}}, I_h^* = \frac{\lambda}{\delta + \gamma}(1 - \frac{1}{\overline{R}_{0_m}}), S_a^* = \frac{\lambda}{\mu}\frac{1}{\overline{R}_{0_m}}, I_a^* = \frac{\lambda}{\delta + \gamma}(1 - \frac{1}{\overline{R}_{0_m}}), Q_a^* = \frac{\gamma I_a^*}{(\delta + \mu)} \tag{28}$$

From (28), it can be observed that the endemic equilibrium point E^* exists uniquely and positively if and only if $\overline{R}_{0_m} > 1$. There are also two possibilities $I_h = 0, I_a \neq 0$ and $I_h \neq 0, I_a = 0$. For $I_h = 0, I_a \neq 0$, $S_a = \frac{m+\delta+\gamma}{\beta}$ which gives $\eta\alpha m S_a I_a + rmS_h I_a + mI_a = 0$ from which we reach to a contradiction to the fact $I_a \neq 0$ as $\eta\alpha m S_a + rmS_h + m \neq 0$. Therefore, If region H is disease free, there is no possibilities to spread the disease in region A. Again for $I_h \neq 0, I_a = 0$, $S_h = \frac{m+\delta+\gamma}{\beta}$ for which we can't find any positive value of S_a. Therefore, under this condition also, there is no equilibrium point. This leads to the fact that when one region is disease free, then there is no possibility for spreading of disease caused by travelling and migration.

Remark 9 $\overline{R}_{0_m} - R_{0_m} = \frac{1}{(\delta+\mu)}\{\lambda\alpha\eta(m-1) + \lambda r(m-\alpha)\}$. If $m = \alpha = 1$, then $\overline{R_{0_m}} = R_{0_m}$. For $m > 1$, $m > \alpha$, $\overline{R_{0_m}} > R_{0_m}$. Now there two possibilities: $\alpha < 1 < m$ and $1 < \alpha < m$. It can be checked in both cases that $\overline{R}_{0_m} > R_{0_m}$ hold good. It shows that when there is an increasing of value of m from α, even this increasing is very small, it can result spreading of disease more seriously than the case when the values of two parameters are equal.

Remark 10 Clearly $\frac{\partial\overline{R}_{0_m}}{\partial\alpha} > 0$ implying $\overline{R}_{0_m}$ increases with increasing α. From (13), we can notice that

$$\frac{\partial R_{0_m}}{\partial\alpha} = \frac{\lambda(\eta+r)}{\mu(\delta+\gamma)}, \frac{\partial\overline{R}_{0_m}}{\partial\alpha} = \frac{m\lambda\eta}{\mu(\delta+\gamma)}$$

When $m > 1$, clearly $\frac{\partial\overline{R}_{0_m}}{\partial\alpha} > \frac{\partial R_{0_m}}{\partial\alpha}$ which implies when m considers a value greater than 1, then rate of increasing of $\overline{R}_{0_m}$ w.r.t α is higher than that of R_{0_m} w.r.t α.

3.2.2 Stability Analysis

Theorem 4 *The Disease Free Equilibrium point of model (27) is locally asymptotically stable if and only if* $2R_0 < \overline{R}_{0_m} < 1$ *and the Endemic Equilibrium Point is locally asymptotically stable if and only if* $1 < \overline{R}_{0_m} < 2R_0$. *When endemic equilibrium point exists, it makes disease free equilibrium point unstable.*

Proof At the equilibrium point E_0, the variational matrix corresponding to the model (25) becomes,

$$M_0 = \begin{pmatrix} a_{11} & a_{12} & a_{13} & a_{14} & 0 \\ 0 & a_{22} & 0 & a_{24} & 0 \\ a_{31} & a_{32} & a_{33} & a_{34} & 0 \\ 0 & a_{42} & 0 & a_{44} & 0 \\ 0 & 0 & 0 & a_{54} & a_{55} \end{pmatrix} \tag{29}$$

where $a_{11} = -(\alpha+\mu), a_{12} = -\frac{\beta\lambda}{\mu}, a_{13} = \alpha, a_{14} = -\frac{m\lambda}{\mu}(\eta\alpha + r)$
$a_{22} = \frac{\beta\lambda}{\mu} - (m+\delta+\gamma), a_{24} = \frac{m\lambda}{\mu}(\eta\alpha+r) + m$
$a_{31} = \alpha, a_{32} = -\frac{m\lambda}{\mu}(\eta\alpha+r), a_{33} = -(\alpha+\mu), a_{34} = -\frac{\beta\lambda}{\mu}$
$a_{42} = \frac{m\lambda}{\mu}(\eta\alpha+r) + m, a_{44} = \frac{\beta\lambda}{\mu} - (m+\delta+\gamma)$
$a_{54} = \gamma, a_{55} = -(\delta+\mu)$
The disease free equilibrium point E_0 is locally asymptotically stable if and only if all the eigenvalues corresponding to the variational matrix M_0 have negative real parts. From the charecteristic equation $|M_0 - \nu I| = 0$ corresponding to the matrix M_0. One eigenvalue is clearly $\nu_5 = -(\delta+\mu) < 0$. Other eigenvalues can be evaluated by solving charecteristic equation corresponding to the matrix

$$P_0 = \begin{pmatrix} a_{11} & a_{12} & a_{13} & a_{14} \\ 0 & a_{22} & 0 & a_{24} \\ a_{31} & a_{32} & a_{33} & a_{34} \\ 0 & a_{42} & 0 & a_{44} \end{pmatrix} \tag{30}$$

It can be checked that $a_{11} = a_{33}, a_{12} = a_{34}, a_{22} = a_{44}, a_{13} = a_{31}, a_{14} = a_{32}, a_{24} = a_{42}$. Therefore, matrix P_o can be represented as,

$$P_0 = \begin{pmatrix} U & V \\ V & U \end{pmatrix}, U = \begin{pmatrix} a_{11} & a_{12} \\ 0 & a_{22} \end{pmatrix}, V = \begin{pmatrix} a_{13} & a_{14} \\ 0 & a_{24} \end{pmatrix} \tag{31}$$

The characteristic polynomial corresponding to the matrix P_0 can be incorporated as

$$|P_0 - \nu I| = |U + V - \nu I||U - V - \nu I| \tag{32}$$

ν_1, ν_2 are eigenvalues of $|U+V-\nu I| = 0$ and ν_3, ν_4 are the eigenvalues of $|U-V-\nu I| = 0$. These eigenvalues have negative real parts if the following conditions hold:-
i. $tr(U+V) < 0, tr(U-V) < 0$
ii. $|U+V| > 0, |U-V| > 0$.
Now,
i. $tr(U+V) = -\mu + (\delta+\gamma)(\overline{R}_{0_m} - 1) < 0$ when $\overline{R}_{0_m} < 1$,
$tr(U-V) = -(2\alpha + 2m + +\mu) - (\delta+\gamma)\{1 + (\overline{R}_{0_m} - 2R_0)\} < 0$ if $\overline{R}_{0_m} > 2R_0$
ii. $|U+V| = \mu(\delta+\gamma)(1-\overline{R}_{0_m}) > 0$ if $\overline{R}_{0_m} < 1$, $|U-V| = (2\alpha+\mu)\{2m + (\delta+\gamma)(1+\overline{R}_{0_m} - 2R_0)\}$ under the codition $\overline{R}_{0_m} > 2R_0$

Hence, the disease free equilibrium point E_0 is locally asymptotically stable if and only if $2R_0 < \overline{R}_{0_m} < 1$
At the equilibrium point E^*, (31) becomes

$$M^* = \begin{pmatrix} a_{11} & a_{12} & a_{13} & a_{14} & 0 \\ a_{21} & a_{22} & a_{23} & a_{24} & 0 \\ a_{31} & a_{32} & a_{33} & a_{34} & 0 \\ a_{41} & a_{42} & a_{43} & a_{44} & 0 \\ 0 & 0 & 0 & a_{54} & a_{55} \end{pmatrix} \tag{33}$$

where $a_{11} = -(\alpha + \beta I_h^* + rmI_a^* + \mu), a_{12} = -\beta S_h^*, a_{13} = \alpha - \eta\alpha m I_a^*, a_{14} = -(rmS_h^* + \eta\alpha m S_a^*)$
$a_{21} = \beta I_h^* + rmI_a^*, a_{22} = \beta S_h^* - (m + \delta + \gamma), a_{23} = \eta\alpha m I_a^*, a_{24} = rmS_h^* + \eta\alpha m S_a^* + m$
$a_{31} = \alpha - \eta\alpha m I_h^*, a_{32} = -(rmS_h^* + \eta\alpha m S_a^*), a_{33} = -(\alpha + rmI_h^* + \beta I_a^* + \mu), a_{34} = -\beta S_a^*$
$a_{41} = \eta\alpha m I_h^*, a_{42} = rmS_h^* + \eta\alpha m S_a^* + m, a_{43} = \beta I_a^* + rmI_h^*, a_{44} = \beta S_a^* - (m + \delta + \gamma)$
$a_{54} = \gamma, a_{55} = -(\delta + \mu)$
From the charecteristic equation $|M^* - nuI| = 0$ corresponding to the matrix M^*, one eigenvalue is $\nu_5 = -(\delta + \mu)$ which is always negative. Other eigenvalues can be evaluated from

$$P^* = \begin{pmatrix} a_{11} & a_{12} & a_{13} & a_{14} \\ a_{21} & a_{22} & a_{23} & a_{24} \\ a_{31} & a_{32} & a_{33} & a_{34} \\ a_{41} & a_{42} & a_{43} & a_{44} \end{pmatrix} \tag{34}$$

It can be observed that ‘$a_{11} = a_{33}, a_{12} = a_{34}, a_{22} = a_{44}, a_{13} = a_{31}, a_{14} = a_{32}, a_{24} = a_{42}$. Therefore, P^* can be written as

$$P^* = \begin{pmatrix} U^* & V^* \\ V^* & U^* \end{pmatrix}, U^* = \begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix}, V^* = \begin{pmatrix} a_{13} & a_{14} \\ a_{23} & a_{24} \end{pmatrix} \tag{35}$$

The characteristic polynomial corresponding to the matrix P^* can be incorporated as

$$|P^* - \nu I| = |U^* + V^* - \nu I||U^* - V^* - \nu I| \tag{36}$$

ν_1, ν_2 are eigenvalues of $|U^* + V^* - \nu I| = 0$ and ν_3, ν_4 are the eigenvalues of $|U^* - V^* - \nu I| = 0$. These eigenvalues have negative real parts if the following conditions hold:-
i. $tr(U^* + V^*) < 0, tr(U^* - V^*) < 0$
ii. $|U^* + V^*| > 0, |U^* - V^*| > 0$.

$$U^* + V^* = \begin{pmatrix} -\mu\overline{R}_{0_m}(1 - \frac{1}{\overline{R}_{0_m}}) + \mu & -(\delta + \mu) \\ \mu\overline{R}_{0_m}(1 - \frac{1}{\overline{R}_{0_m}}) & 0 \end{pmatrix} \tag{37.1}$$

$$U^* - V^* = \begin{pmatrix} -\{\alpha + \mu + \beta I_h^* + rmI_a^* + (\alpha - m\eta\alpha I_a^*)\} & \frac{\lambda}{\mu\overline{R}_{0_m}}\{m(\eta\alpha + r) - \beta\} \\ \frac{\mu R_0}{\beta}(\beta + mr - \eta\alpha m)(1 - \frac{1}{\overline{R}_{0_m}}) & -2\frac{m(\delta+\gamma)(\eta\alpha+r+1)}{\beta+m(\eta\alpha+r)} \end{pmatrix} \tag{37.2}$$

Now, it is very clear from (40.1) and (40.2)that $tr(U^* + V^*)$ is always negative provided $\overline{R}_{0_m} > 1$. Since $(\alpha - \eta\alpha m I_a^*)$ is always positive, $tr(U^* - V^*)$ is negative under the condition $\overline{R}_{0_m} > 1$. Again
$|(U^* + V^*)| = (\delta + \mu)\mu\overline{R}_{0_m}(1 - \frac{1}{\overline{R}_{0_m}}) > 0$ if $\overline{R}_{0_m} > 1$.
$|U^* - V^*| > 0$ if $\frac{\lambda}{\beta}\frac{R_0}{\overline{R}_{0_m}}(1 - \frac{1}{\overline{R}_{0_m}})\{(mr)^2 - (\beta - \alpha\eta m)^2\} < 0$ which implies the condition $\overline{R}_{0_m} < 2R_0$.

Remark 11 Endemic equilibrium point is stable under the condition $1 < \overline{R}_{0_m} < 2R_0$ and unstable whenever $\overline{R}_{0_m} > 2R_0$. The inequality $\overline{R}_{0_m} > 2R_0$ has a very important significance. Performing a simple calculation, it can be established that $\overline{R}_{0_m} > 2R_0$ only when $m(\eta\alpha + r) > \beta$ holds. Now, left hand side of $m(\eta\alpha + r) > \beta$ contains the rates related to transportation and right hand side contains contact rate of susceptible class of a region with infected class of that very region and $m(\eta\alpha + r)$ is greater than β under two circumstances:- a. When β is very low compared to $m(\eta\alpha + r) > \beta$ (it is considered that $m(\eta\alpha + r) > \beta$ also low), R_0 becomes low (less than 1) which, eventually, makes $\overline{R}_{0_m} < 1$. This is the condition for stability of disease free equilibrium point which is already stated in theorem 4.2.Therefore when rates concerning travelling and migration are low and contact rate β is also low compared to those rates, disease free equilibrium point becomes stable instead of endemic equilibrium point. b. When the rates related to transportation, specially m and α becomes very much high compared to β, in that case also $m(\eta\alpha + r) > \beta$ holds and $\overline{R}_{0_m}$ acquires higher value than 1. In this case also $\overline{R}_{0_m} > 2R_0$ which violates the condition for stability of endemic equilibrium point. In this case, disease free equilibrium point is also unstable as $\overline{R}_{0_m}$ is greater than 1. Due to high rate of migration of infected population, number of infected individuals become so high that it takes a very long time to get stability implying instability of endemic equilibrium point. Therefore, $\overline{R}_{0_m} > 2R_0$ implies instability of endemic equilibrium point. But whether disease free equilibrium point gets stability or it is also unstable depends on the values of rates related to transportation and migration m, η, α, r and contact rate β. These cases are also shown in section (4).

4 NUMERICAL SIMULATION

Table 1

Parameters	Values (per week)
λ	1
μ	0.48
α	1.88
β	0.36
η	0.052
r	0.065
δ	0.31
γ	0.46

To examine the validity of the results obtained by analysing the model qualitatively, we perform numerical simulation also through MATLAB. First, we have performed quantitative analysis of model (2) by considering the case when rate of migration of susceptible and infected individuals between two regions are equal which is developed in model (5). Values of parameters are given in table 1. For the above values of parameters, evaluated endemic equilibrium point is

$$S_h^* = 1.3278, I_h^* = 0.4710, S_a^* = 1.3275, I_a^* = 0.4711, Q_a^* = 0.2743$$

and corresponding eigenvalues are

$$-4.3826 + 0.1794i, -4.3826 - 0.1794i, -0.7900, -0.3766 + .2618i, -0.3766 - .2618i$$

Clearly all eigenvalues are with negative real parts and basic reproductive number is $R_{0_m} = 1.5692$. Also it has been found that $R_0 = 0.9740 < 1 < R_{0_m} < 2R_0 = 1.9481$. Therefore, E^* is locally asymptotically stable

In fig (1), variation of susceptible class is shown with infected class of region H and A respectively for

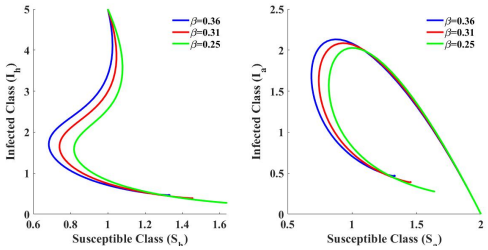


Fig. 1: Variation of I_h with S_h and I_a with S_a for different β

changes in β. It confirms that as β decreases, susceptible population in both region increases with decreasing infected individuals. Further calculation has been made and it has been found that when $\beta = 0.14$, $R_{0_m} = 0.9739 < 1$. Therefore, keeping other parameters fixed as in table 1, when β is less than 0.14, instead of endemic equilibrium point, disease free equilibrium point becomes stable which implies eradication of disease. Fig (2) confirms that decrement of α results decrement in equilibrium level of infected class

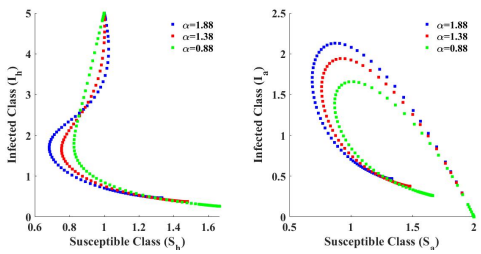
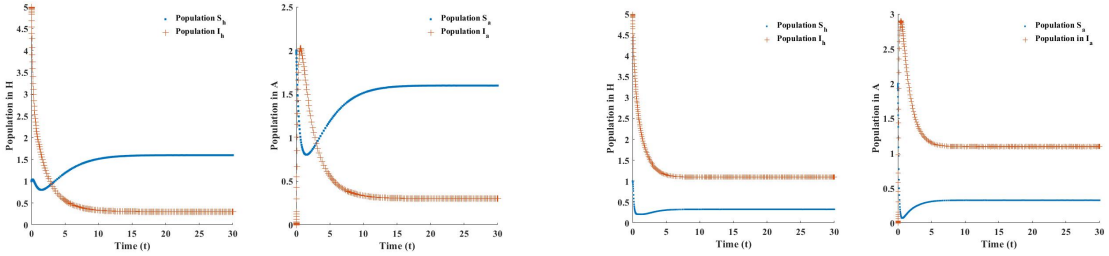


Fig. 2: Variation of I_h with S_h and I_a with S_a for different α

in both regions and increment of equilibrium level of susceptible class. Keeping other parameters fixed as in table 1, it has been calculated by performing further calculation that for $\alpha \leq 0.068$, value of R_{0_m} becomes 0.9956 indicating stability of disease free equilibrium point instead of endemic equilibrium point. Also when $\alpha > 3.15$, number of infected individuals become very high with high R_{0_m}. It makes endemic equilibrium point unstable as it can't be controlled at early stage and it takes much higher time to become stable. Therefore, for stability of endemic equilibrium point $0.068 < \alpha \leq 3.15$ and for $\alpha \leq 0.068$, disease free equilibrium point becomes stable

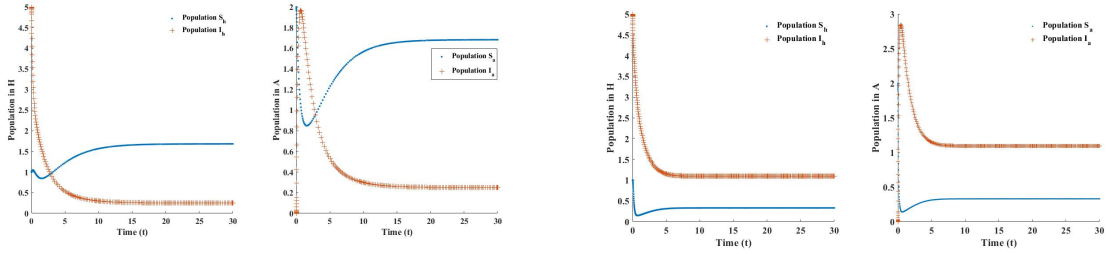
In fig (3a) and (3b), variations of susceptible and infected population in both regions have been shown



(a) (b)

Fig. 3: Variation in Population of region H and A for $\eta = 0, \eta = 1, 0 < r < 1$

with time taking $\eta = 0$ and $\eta = 1$ respectively taking other parameters fixed as in table 1. Fig (4a) and



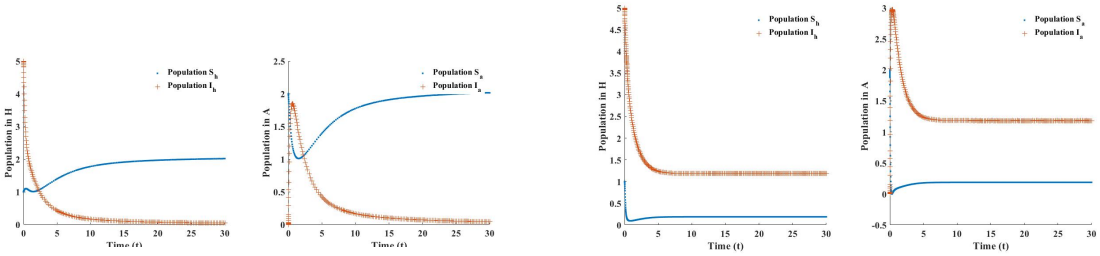
(a) (b)

Fig. 4: Variation in Population of region H and A for $r = 0, r = 1, 0 < \eta < 1$

(4b) have shown the same variations considering $r = 0$ and $r = 1$ respectively. These figures confirms that whenever η or r increase, it increases equilibrium level of infected class in both regions with increment in basic reproductive number. When η and r both are 0, equilibrium levels of susceptible individuals in both regions become high with very low equilibrium levels of infected class. In this case, basic reproductive number R_{0_m} is 0.9740 which is less than 1. It confirms that when η and r both are zero, disease free equilibrium point becomes stable and endemic equilibrium point becomes unstable. This result has been shown in fig (5a). When η and r both acquire the value 1, the basic reproductive number becomes very high and the condition for stability $R_{0_m} < 2R_0$ is also violated which has been shown in fig(5b). Thus, it is confirmed that for stability of endemic equilibrium, $0 < \eta < 1, 0 < r < 1$ must hold. Keeping values of other parameters fixed, we have performed further calculation from which we have revealed that to keep the endemic equilibrium point stable, η must be less than 0.13 as for $\eta \geq 0.13$, basic reproductive number becomes so high that the condition $R_{0_m} < 2R_0$ is violated. Also for $r > 0.143$, endemic equilibrium point becomes unstable also as $R_{0_m} > 2R_0$, R_0 being very high. Therefore, r must be less than 0.143 to maintain stability of endemic equilibrium point.

Fig (6) confirms that when α increases, γ must also be increased to make the equilibrium level of infected class lower. From further calculation, it has been confirmed that that keeping other parameters fixed as described in table 1, if $\gamma < 0.15$, then number of infected individuals become very high. This is due to the fact that for such values of γ, R_{0_m} becomes much higher and also greater than $2R_0$. It makes endemic equilibrium point very unstable. Also, for $\gamma \geq 0.91$, R_{0_m} becomes less than 1 which indicates stability of disease free equilibrium point. Therefore, for endemic equilibrium point to be stable $0.15 \leq \gamma < 0.91$,

Next, the case where migration rates of susceptible individuals of region H and that of region A are equal



(a) (b)

Fig. 5: Variation in Population of region H and A for $r = 0, \eta = 0$ and $r = 1, \eta = 1$

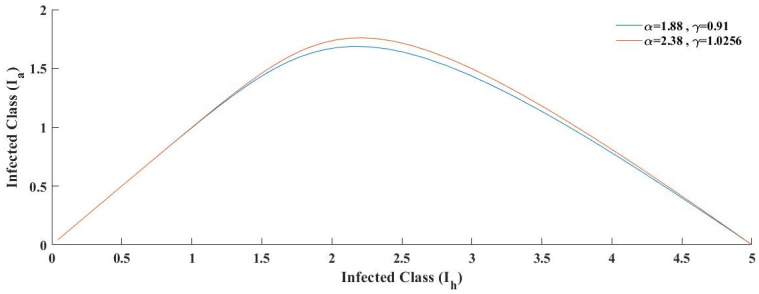


Fig. 6: Variation of I_a with I_h for different α and γ

i.e. $\alpha_{ha} = \alpha_{ah} = \alpha$. Also migration rate of infected individuals of region H and region A are equal *i.e* $m_{ha} = m_{ah} = m$.with $\alpha \neq m$ have been discussed. The values of parameters are given in table 2. In this

Table 2

Parameters	Values (per week)
λ	1
μ	0.48
α	1.2
m	1.7
β	0.36
η	0.052
r	0.065
δ	0.31
γ	0.46

case, evaluated endemic equilibrium point is

$$S_h^* = 1.3112, I_h^* = 0.4891, S_a^* = 1.3110, I_a^* = 0.4926, Q_a^* = 0.2866$$

and corresponding eigenvalues are

$$-3.9440, -3.0969, -0.7900, -0.3885 + 0.2715i, -0.3885 - 0.2715i$$

with negative real parts. Calculated basic reproductive number is $\overline{R}_{0_m} = 1.5600$. Also it has been calculated that $R_0 = 0.9740 < 1 < R_{0_m} < 2R_0 = 1.9481$. It confirms stability of endemic equilibrium point E^*.

In fig (7), variation of infected class of region A has been shown with variation of infected class of region H for different values of m. This figure confirms that when m decreases, number of infected population as well as equilibrium level of infected classes in both regions also decreases and endemic equilibrium point becomes stable earlier. From further calculation, keeping other parameters fixed as in table 2, we have found that if $m \leq 0.05$, $\overline{R}_{0_m} = 0.9913 < 1$ and equilibrium level of infected individuals in both regions lowers to 0. In this case, disease free equilibrium level point becomes stable instead of endemic equilibrium point. Again when $m \geq 2.826$, I_h^* and I_a^* become very high with high basic reproductive number so that endemic equilibrium point becomes unstable and it takes much longer time to control it. Therefore, for stability of endemic equilibrium point, m must lie within 0.05 and 2.826.

In fig (8), infected classes $I_h^*$and I_a^* are plotted respectively against time t for the following cases:- • Values

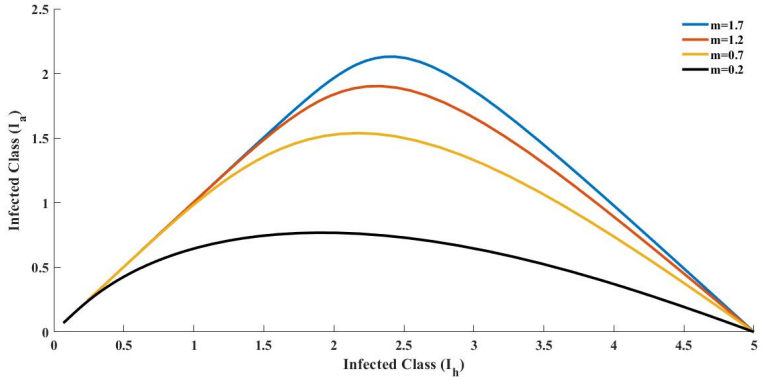


Fig. 7: Variation of I_a with I_h for different m

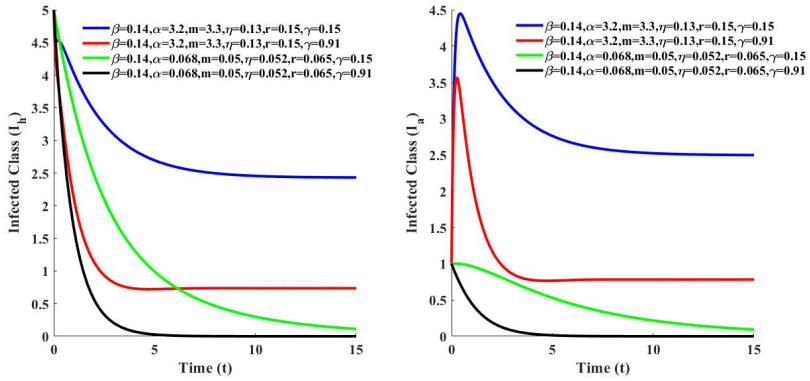


Fig. 8: Variation of I_h and I_a with time for critical limits of parameters

of $\beta, \alpha, m, \eta, r$ are maximum and γ is minimum as calculated above keeping other parameters fixed as in table 2

• Values of $\beta, \alpha, m, \eta, r$ are maximum and γ is maximum as calculated above keeping other parameters fixed as in table 2

• Values of α, m are minimum and γ is minimum as calculated above keeping other parameters fixed as in table 2 (Since there is no lower limits for β, η, r, we consider these values as of table 2)

• Values of α, m are minimum and γ is maximum as calculated above keeping other parameters fixed as in table 2 For the first case, it can be seen that equilibrium level of infected classes in both region is high and it takes a long time for eradication of disease. In second case, when γ becomes maximum, equilibrium level of infected individuals becomes lower but the disease doesn't die out completely. In third cases, when the values of key parameters are taken minimum, then fig (8) shows that the disease may die out completely but the disease free equilibrium point gets stable approximately after 12 – 15 weeks. But, when γ is taken maximum, disease free equilibrium point gets stability within 5 weeks and the disease dies out completely.

5 DISCUSSION

We have proposed a non – linear mathematical model to investigate the effects of travelling and migration on spreading of CoVid 19 severely in two different regions. It has been showed how migration of infected population, susceptible population, contact rates play a key role in proliferation of this disease. We also have discussed that this disease can be controlled by regulating these key factors. The proposed model has been analysed considering two different cases. We have reduced the assumed model in forms suitable for these cases and then the reduced models have been analysed qualitatively using stability theory of ordinary differential equation in disease free equilibrium point as well as endemic equilibrium point. Also numerical simulation has been performed to check the feasibility of obtained results. To keep the endemic equilibrium point stable, following critical limits have been found:-

• Lower limit of contact rate between susceptible and infected class between same region. When the rate is below this critical limit, disease becomes extinct.

• Upper limit of transmission rate of disease from infected individuals of a region to susceptible class of that region during travelling. If the rate is above the limit, there is an instability of the system as number of infected individuals becomes very high.
• Upper limit of transmission rate of disease from infected individuals of a region to susceptible class of the region where the infected ones are travelling to. If this rate crosses the limit, the system becomes unstable due to large number of infected population.
• An upper as well as lower limit for the rate of travelling and migration of susceptible class and also infected class. When this rate is below the lower limit, number of infected individuals becomes very low and the disease is eradicated. When the rate is above the upper limit, it makes a long delay in stabilization of the system as number of infected people becomes very high.
• an upper as well as lower limit of rate of quarantine. When the rate of quarantine becomes higher than the upper limit, the system gets stabilization early with very low number of infected population. When the rate is below the lower limit, there is a delay in stabilization for the system as it results high number of infected individuals.
• We have also found a range for basic reproductive number.
On the basis of the above results, we can conclude in brief that rate of migration and travelling of individuals between two regions, contacts between them during travelling and also apart from travelling, rate of quarantine are the significant parameters in spreading of this disease and controlling them by keeping the values of parameters as mentioned, disease can be made stabilized early. It is, therefore, recommended to stop all the transportations between regions at the first stage of spreading of disease so that no susceptible or infected person can travel from and to the region. A very short delay in locking down of transportation can cause a large break out of disease. Travel of a single infected person may result transmission of disease in a disease free region. Therefore, Screening before travelling is highly recommended. Infected individuals must be quarantined as early as possible so that contacts between susceptible and infected persons remain very low. It has also been shown that when the values of key parameters are minimum, quarantining infected people at maximum rate can eradicate the disease at an early stage. There it is recommended to keep the rates which cause outbreak of disease as minimum as possible and rate of quarantine as high as possible to make the system stable early.

6 Relevance to the current pandamic situation

Corelating the proposed model followed by qualitative and quantitative analysis to the current situation, it can be presumed that the reproductive numbers in the territories where disease has been propagated through travelling are much higher than 2 and therefore, it makes the infection too high to become stable at early stage. So, in those countries and territories, first reproductive numbers must be made lower, precisely less than 2 to make the current situation stable by quarantining infected people, ceasing susceptibles to make contact with infected people by complete lockdown and stopping transportation so that no people can travel from and to. Those countries where disease has been originated originated must make the contact rates lower and high quarantine. Also, those countries must be locked down completely untill the disease is eradicated completely to avoid further spreading. Countries with no infections till now are recommended to stop transportation so that no individuals can travel to or from the countries.

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Declarations

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Figures

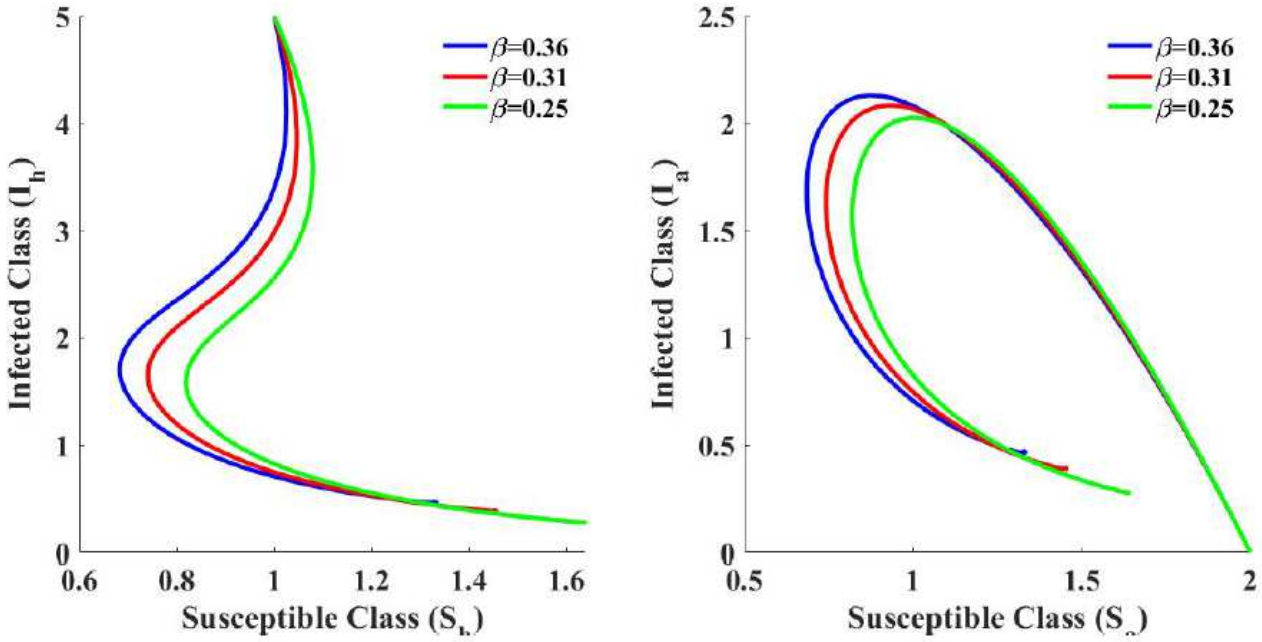

Figure 1

Variation of Ih with Sh and Ia with Sa for different β

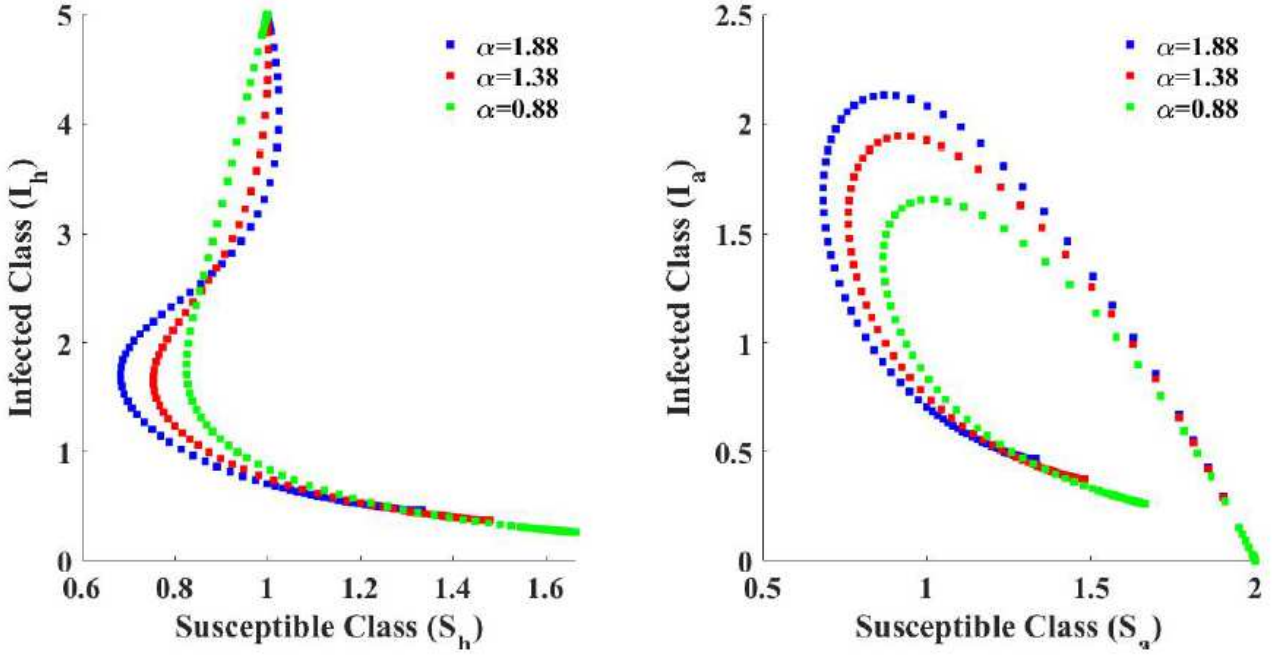

Figure 2

Variation of Ih with Sh and Ia with Sa for different α

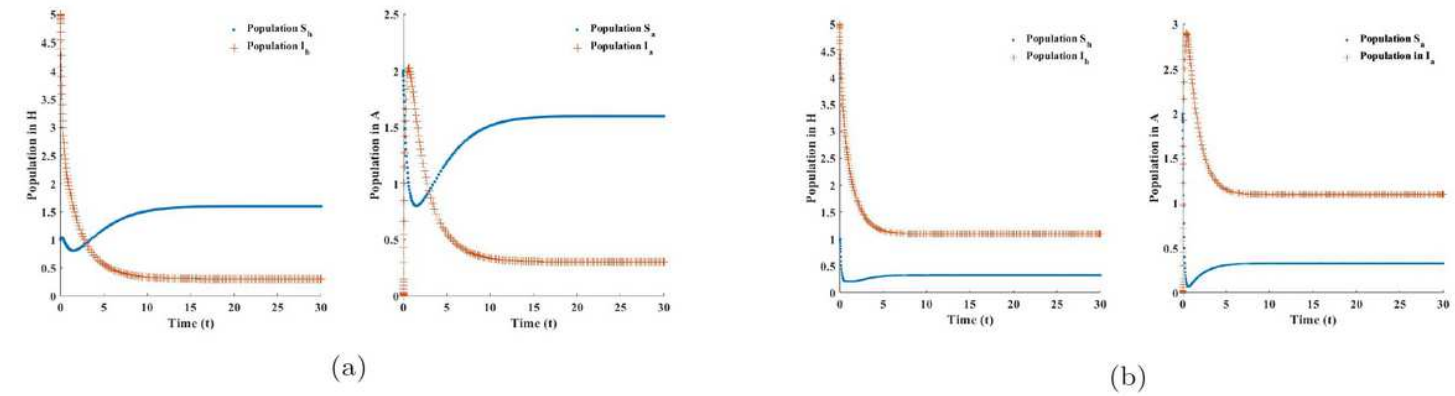

Figure 3

Variation in Population of region H and A for n = 0; n = 1; 0 < r < 1

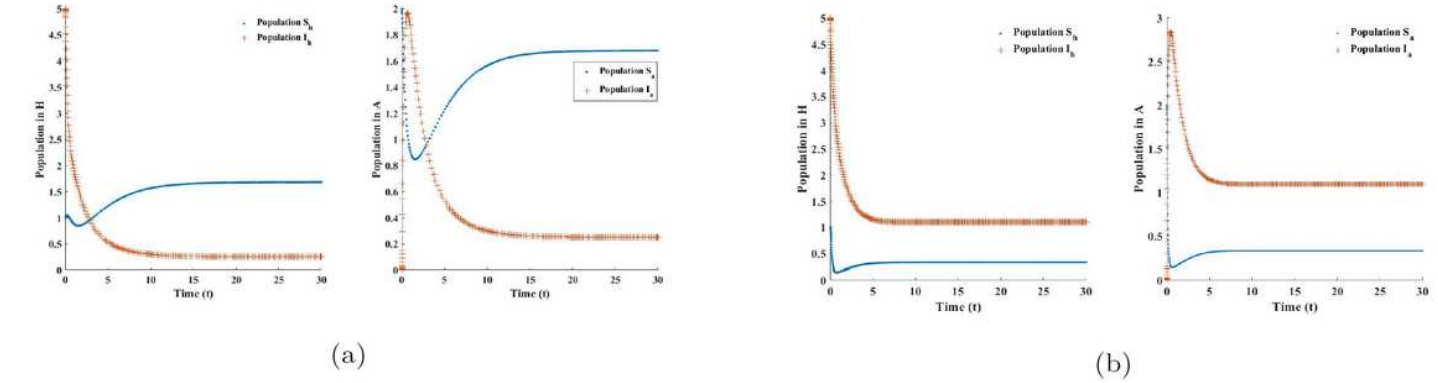

Figure 4

Variation in Population of region H and A for r = 0; r = 1; 0 < n < 1

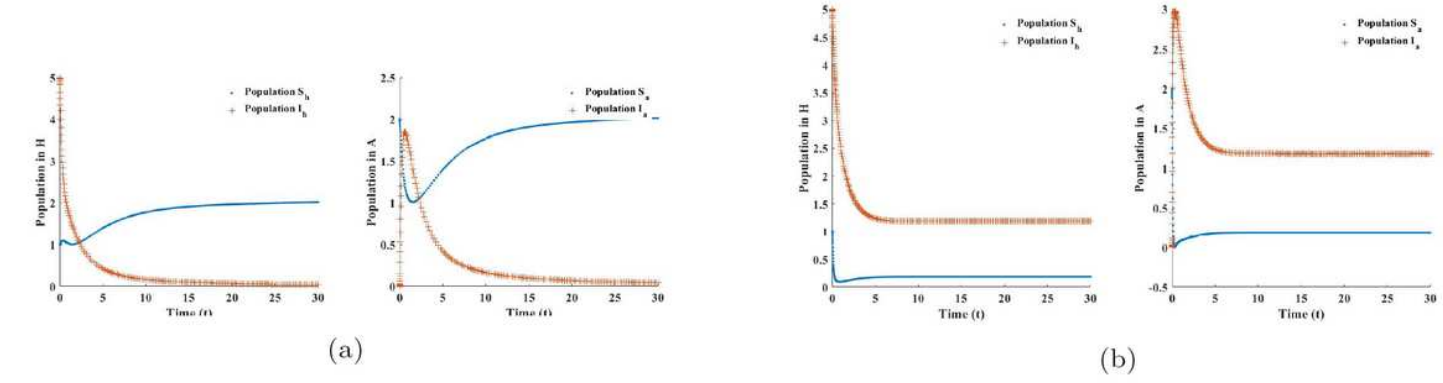

Figure 5

Variation in Population of region H and A for r = 0; n = 0 and r = 1; n = 1

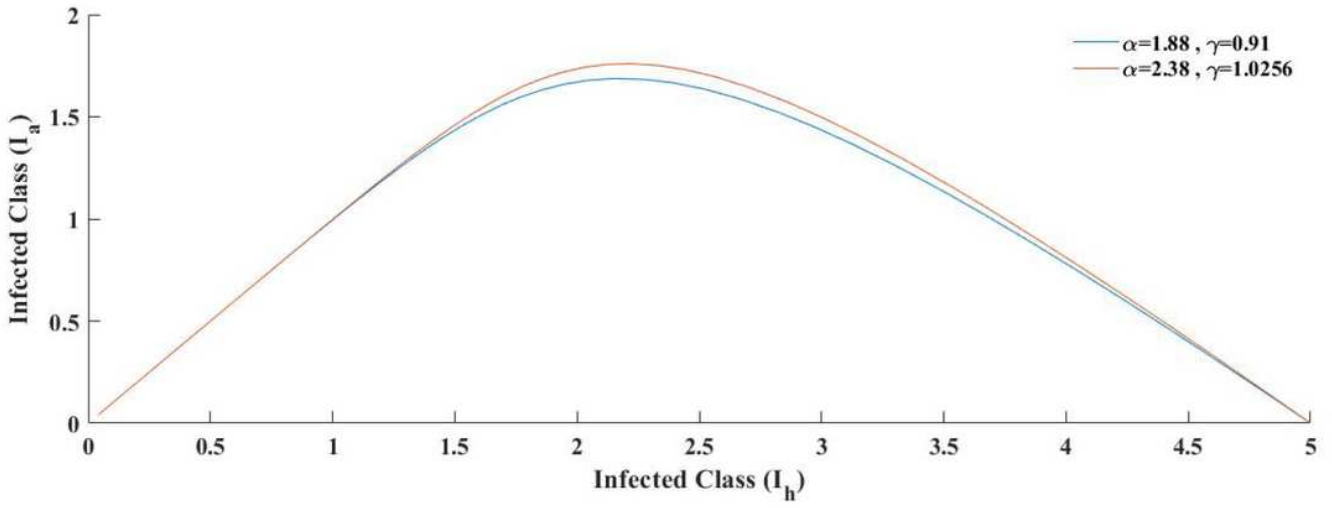

Figure 6

Variation of Ia with Ih for different α and γ

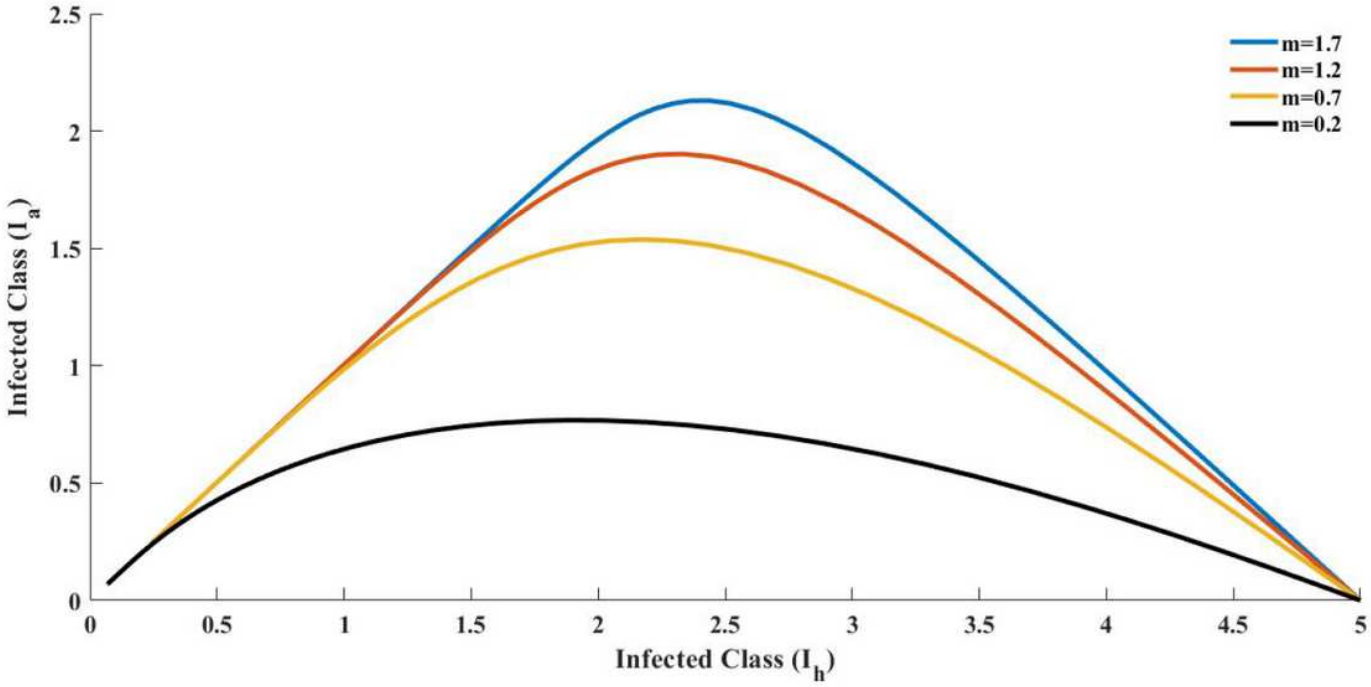

Figure 7

Variation of Ia with Ih for different m

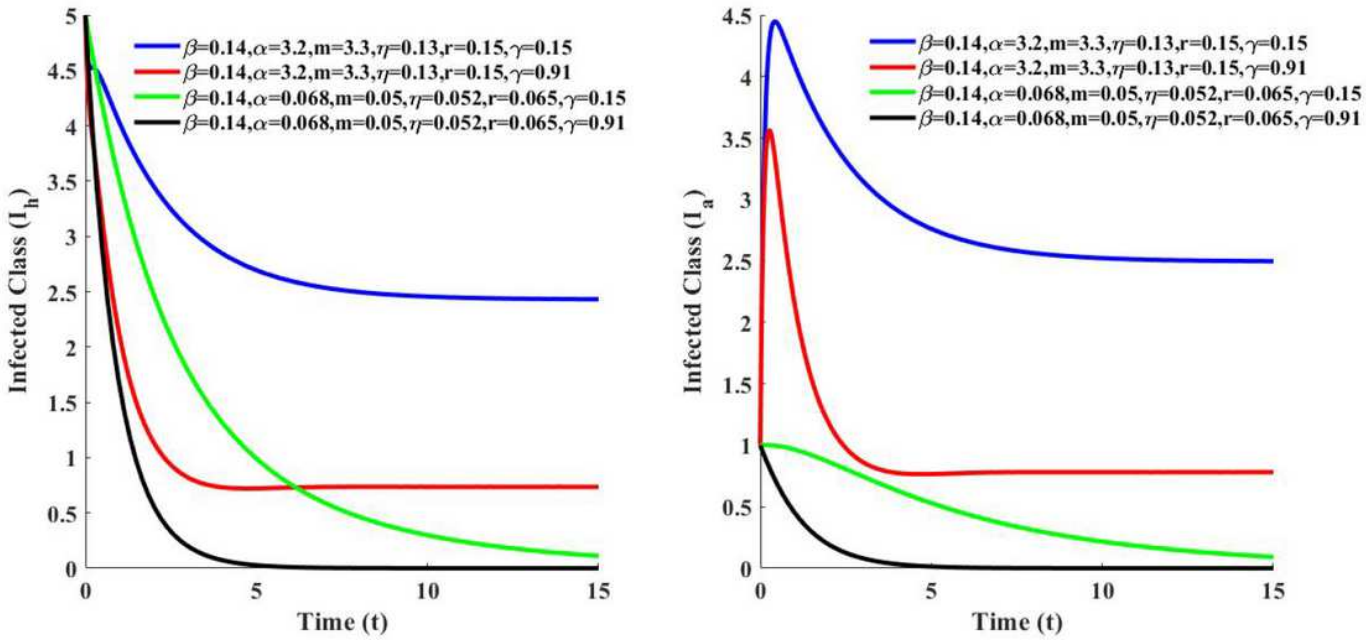

Figure 8

Variation of Ih and Ia with time for critical limits of parameters