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Mathematical Analysis of a Swine flu Model with Incident Rate

Dr. Nidhi Vaishnaw
Associate Professor (Mathematics)
MVJ College of Engineering,
Bangalore - 560067

Abstract: In the present paper, we proposed and analyzed an SEIR compartment model of Swine flu with mixing transmission. Determine the steady state of the model and Stability analysis is carried out. Equilibrium analysis is presented and it is found that in each case the equilibrium points are locally asymptotically stable under certain conditions The stability of the equilibriums are studied by using the Routh-Hurwitz criteria.

Index Terms - Epidemic model, Swine flu, Compartment model, Stability.

1. INTRODUCTION

Swine flu is a respiratory virus of pigs that was first identified in 1918 and although historic diffusion to human beings has been sporadic, the infection rate in humans is intensifying at present. Chills, dyspnea, headache, vomiting, diarrhea, myalgia, and fatigue are most common symptoms of swine flu. The virus has not previously circulated in human the virus is entirely new [1].

Many mathematical model have been analyzed to understand the spread of swine flu within human and also in pig populations like in [5,10,11]. Kermack and McKendrick[9] were the first people that's describe an influenza epidemic early in the 20th century. Their model is known as the SIR, which has been used as a basis for all subsequent influenza models. By modifying, the basic SIR model in a variety of ways by including seasonality influenza epidemics can be shown to have sustained cycles [7,13]. The SIR model has also been extended so that it can be used to represent and/or predict the spatial dynamics of an influenza epidemic.
Most recently several investigation have concern themselves with modelling of dynamics of influenza virus [3, 4, 5, 8, 12].

In this paper, we have modified the model of Das, et al. [6] with recovery class. In the first section we present the model in which c is the contact rate at which the susceptible population is converted into the exposed population., S (t), E (t) I (t) and R (t) represent the number of susceptible, exposed, infectious, and recovered Population at the time t respectively, A is the requirement rate of the population, $\mu$is the natural death rate of the population, $\gamma$is thenatural recovery rate of the infective individuals. In the next section, we obtained the disease free and the endemic equilibrium and analyzed the stability conditions for both. In the last section, numerical results are also provided.

The transfer diagram depicted in the following figure: **Figure.1**

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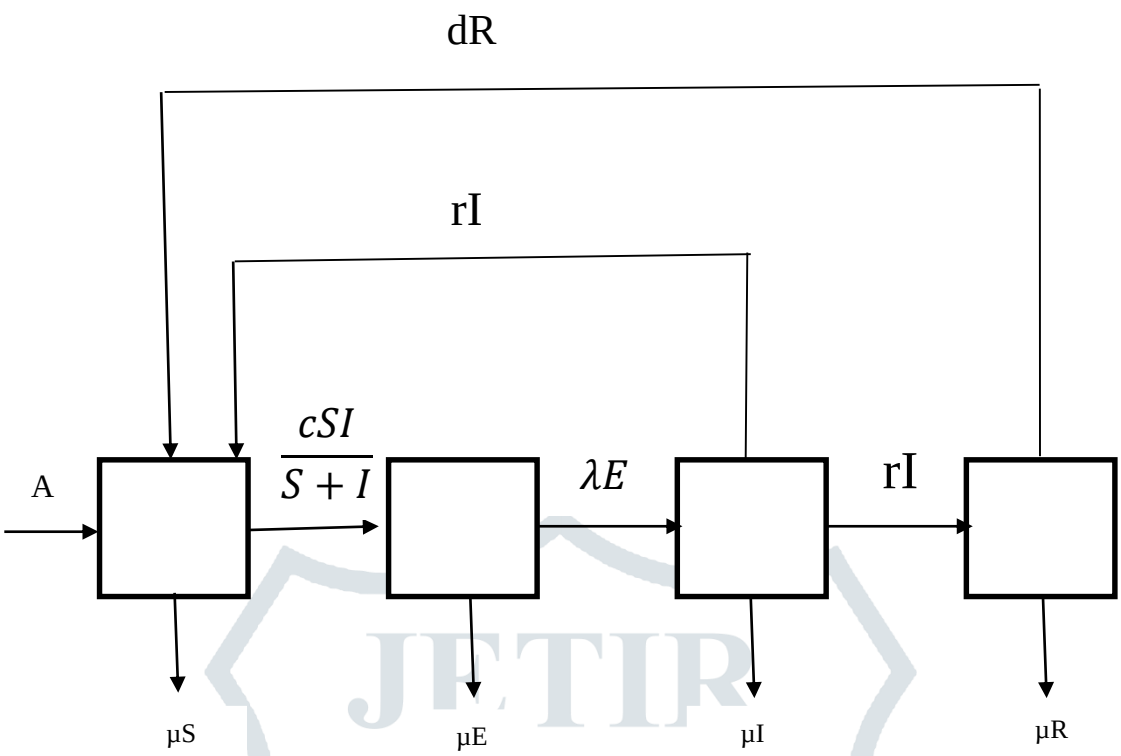

Fig 1: Swine Flu Model with Incident Rate

2. The Mathematical Model:
Using the symbols, notations and basic assumptions of [11,2], the model we consider for reinvestigation can be expressed as:

$$\frac{dS}{dt} = A - \frac{cSI}{S+I} + rI + dR - \mu S$$
$$\frac{dE}{dt} = \frac{cSI}{S+I} - (\lambda + \mu)E$$
$$\frac{dI}{dt} = \lambda E - (r + \gamma + \mu)I$$
$$\frac{dR}{dt} = \gamma I - (\mu + d)R$$

3. Stability Analysis.
For the equilibrium points, the above differential equation should be equated to zero.
$$i.e.\ \frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$$

We have two equilibrium points are given by $P_0 = (A/\mu, 0,0,0)$is the disease free equilibrium points of the system (1.1) and the unique endemic equilibrium point $P^* = (S^*, E^*, I^*, R^*)$, where

$$S^* = \frac{p}{c-p} I^*,$$
$$E^* = \frac{(r+\gamma+\mu)}{\lambda} I^*,$$
$$I^* = \frac{A}{\left[\frac{\mu p}{c-p} + p - r - \frac{dr}{d+\mu}\right]}$$
$$R^* = \frac{\gamma}{d+\mu} I^*$$
$$where\ p = \frac{(\lambda+\mu)(r+\gamma+\mu)}{\lambda}$$
The basic reproduction number defined as
$$R_0 = \frac{c\lambda}{(\lambda+\mu)(r+\gamma+\mu)}$$

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3.1 Theorem. The disease free equilibrium of the system is locally asymptotically stable if $R_0 < 1$and unstable if $R_0 > 1$.

Proof: We consider equations

$F_1 = A - \frac{cSI}{S+I} + rI + dR - \mu S$

$F_2 = \frac{cSI}{S+I} - (\lambda + \mu)E$

$F_3 = \lambda E - (r + \gamma + \mu)I$

$F_4 = \gamma I - (\mu + d)R$

The Jacobian matrix

$$J_0 = \begin{bmatrix} \frac{-cI^2}{(S+I)} - \mu & 0 & \frac{-cS^2}{(S+I)^2} + r & d \\ \frac{cI^2}{(S+I)} & -(\lambda+\mu) & \frac{cS^2}{(S+I)^2} & 0 \\ 0 & \lambda & -(r+\gamma+\mu) & 0 \\ 0 & 0 & \gamma & -(\mu+d) \end{bmatrix}$$

At equilibrium point $P_0 = (A/d\,, 0,0,0)$ the jacobian matrix becomes

$$J_0 = \begin{bmatrix} -\mu & 0 & -c+r & d \\ 0 & -(\lambda+\mu) & c & 0 \\ 0 & \lambda & -(r+\gamma+\mu) & 0 \\ 0 & 0 & \gamma & -(\mu+d) \end{bmatrix}$$

The characteristics equation $|J_0 - \varphi I| = 0$ is given as

$$\begin{vmatrix} -(\mu+\varphi) & 0 & -c+r & d \\ 0 & -(\lambda+\mu+\varphi) & c & 0 \\ 0 & \lambda & -(r+\gamma+\mu+\varphi) & 0 \\ 0 & 0 & \gamma & -(\mu+d+\varphi) \end{vmatrix} = 0$$

$\Rightarrow (\mu + d + \varphi)^2[(\lambda+\mu+\varphi)(r+\gamma+\mu+\varphi) - c\lambda] = 0$

Clearly two Eigen values $\varphi = -\mu - d, -\mu - d$ are negative, other Eigen values are given by the quadratic equation $\varphi^2 + a_1\varphi + a_2 = 0$

Therefore, by Routh-Hurwitz criteria the disease-free equilibrium stable if $a_1 > 0$ and $a_2 > 0$
If $(\lambda+\mu)(r+\gamma+\mu) > c\lambda$, i.e $R_0 < 1$.

3.2 Theorem. If $R_0 > 1$ the endemic equilibrium $P^*$is locally asymptotically stable.

Proof: The variation matrix at the endemic point $P^*(S^*, E^*, I^*, R^*)$

$$J_1 = \begin{bmatrix} \frac{-cI^{*2}}{(S^*+I^*)^2} - \mu & 0 & \frac{-cS^{*2}}{(S^*+I^*)^2} + r & d \\ \frac{cI^{*2}}{(S^*+I^*)} & -(\lambda+\mu) & \frac{cS^{*2}}{(S^*+I^*)^2} & 0 \\ 0 & \lambda & -(r+\gamma+\mu) & 0 \\ 0 & 0 & \gamma & -(\mu+d) \end{bmatrix}$$

Consider that

$w_1 = \frac{cI^{*2}}{(S^*+I^*)^2}$ and $w_2 = \frac{cS^{*2}}{(S^*+I^*)^2}$

Then J_1 becomes

$$J_1 = \begin{bmatrix} -w_1 - \mu & 0 & -w_2 + r & d \\ w_1 & -(\lambda+\mu) & w_2 & 0 \\ 0 & \lambda & -(r+\gamma+\mu) & 0 \\ 0 & 0 & \gamma & -(\mu+d) \end{bmatrix}$$

The characteristics equation $|J_1 - \varphi I| = 0$ is given as

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$$\begin{vmatrix} -(w_1+\mu+\varphi) & 0 & -w_2+r & d \\ w_1 & -(\lambda+\mu+\varphi) & w_2 & 0 \\ 0 & \lambda & -(r+\gamma+\mu+\varphi) & 0 \\ 0 & 0 & \gamma & -(\mu+d+\varphi) \end{vmatrix} = 0$$

$$\Rightarrow (\mu+d+\varphi)[(w_1+\mu+\varphi)(\lambda+\mu+\varphi)(r+\gamma+\mu+\varphi)-(w_1+\mu+\varphi)w_2\lambda+(w_2-r)w_1\lambda]=0$$

Clearly one Eigen value is negative $\varphi=-(\mu+d)$ and other Eigen values are given by the cubic equation.
$\varphi^3+a_1\varphi^2+a_2\varphi+a_3$=0
Where
$a_1=3\mu+\lambda+w_1+r+\gamma$
$a_2=[(\lambda+\mu)(w_1+\mu)+(w_1+2\mu+\lambda)(r+\gamma+\mu)-w_2\lambda]$
$a_3=(\lambda+\mu)(w_1+\mu)(r+\gamma+\mu)-(\mu w_2+rw_1)\lambda$
By Routh-Hurwitz criteria, the system (2.1) is locally asymptotically stable if$a_1>0, a_3>0\ and a_1a_2>a_3$. Thus, $P^*$is locally asymptotically stable.

4. Numerical Simulation

4.1 Numerical Simulation for Disease free Equilibrium

From the numerical values of the parameters as$A=1, c=0.003, r=0.1, \mu=0.02, \lambda=0.1 and\ \gamma=0.01$ Then the calculated disease free equilibrium point and basic reproductive number are $P_0(S,0,0,0)=(60,0,0,0)$and $R_0=0.192307<1$. Fig. 2 **shows** that S(t) goes to its steady state, while E(t), I(t) and R(t) goes to zero with respect to time. Hence, the disease dies out.

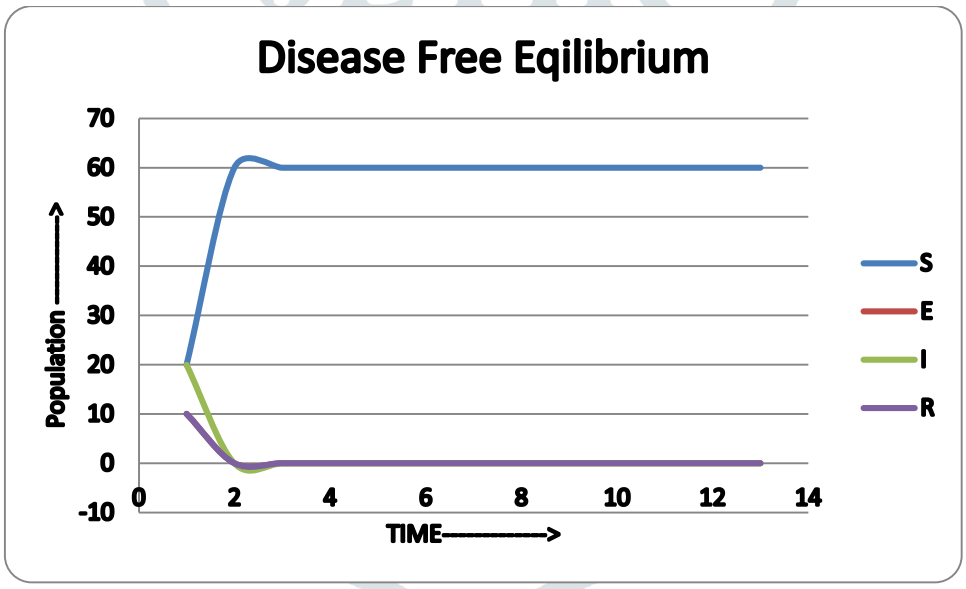

Figure 2: Above figure shows that the disease free equilibrium is locally stable for the choice of parameter values.

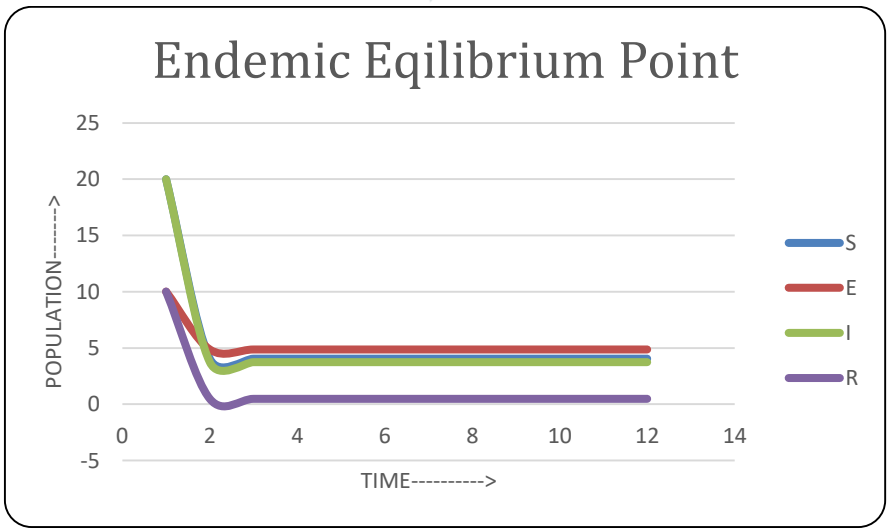

Figure 3: Above figure shows that the endemic equilibrium point is stable for the choice of parameter values.

4.2. Numerical Simulation for Endemic Equilibrium

We change the value of $c = 0.3$ and all other parameters are as above. Then, we obtain $P^*(S^*, E^*, I^*, R^*) = (4.053324, 4.863989, 3.74153, 0.47619)$ and $R_0 = 1.92307 > 1$. Therefore, the endemic equilibrium P^* is locally asymptotically stable. Fig. 3 shows that S, E,I and R goes to their steady state values. Hence, the disease becomes endemic

5. Conclusion:

In this paper, we analyzed an SEIR compartment model of Swine flu, the results are helpful to predict the developing tendency of disease and recovery. We analyzed the Steady state and stability of the equilibrium points. The model equations were solved analytically. We can conclude that the basic reproduction number $R_0 < 1$ then the disease free equilibrium P_0 is locally asymptotically stable and if $R_0 > 1$ the endemic equilibrium P^* is locally asymptotically stable.

Numerical simulations were presented graphically. We have also observed that contact rate c plays an important role in stability; the basic reproduction number R_0 will be decrease if the contact rate c decreases when disease is endemic.

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