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SIR Epidemic Model with total Population size

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Abstract

We study SIR epidemic model with varying total population size and constant immigration rate. We derive the sufficient conditions on parameters of the system to guarantee that the equilibrium point of the system are locally asymptotically stable or globally asymptotically stable. If the disease free equilibrium point is stable then the disease will not affect the population in the system suppose if the endemic equilibrium point is stable the number of infective will not change which means the infective rate equals to the recovery rate.

Introduction

Mathematical modeling of infectious disease has a long theory. The Starting point is Generally taken to be a paper by Daniel Bernoelli (Bernolli 1760) on the prevention of smallpox by inculcation; an account of Bernulli's model based analysis of the data

can be found in Daley and Gani (1999) However as Bailey (1975)points at it was another hundred years or so before the physical basis for the case of infectious diseases become well – established. thus the pace of progress only really picked up early in the 20th centaury with the work of people such as Hamer (1906); Ross (Ross 1911, 1916) and K eramack and Mckendrick(1927) which established the principle of mass action or homogenous mixing – by which the rate of new infection is proportion to the current numbers of susceptible and infective in the population; and the new – familiar deterministic equations for the general epidemic model. Homogenously mixing models are also referred to as mean field models. Many of the epidemic models in use today have this general epidemic (SIR) model or its stochastic counter part, as their basis and thus it can be used to illustrate many of the main issues

In the SIR mode if x(t), y(t) and z(t) represent respectively the number of susceptible, infective and removed individuals in the population at time t, then

$$dx(t)/dt = -\alpha x(t) y(t)/n$$
$$dy(t)/dt = \{\alpha x(t)/n - \gamma\} y(t)$$
$$dz(t)/dt = \gamma y(t)$$

The variables x, y and z are not restricted to integer values and thus it is only approximate to use this deterministic model for large populations. In some version of the model the parameter α above is replaced by nβ, but the formulation given here is more appropriate when n infection is spread by direct contact and the individual makes potentially infectious contacts at a fixed rate α regardless of the population size. when n is fixed the distinction is not important but confusion may arise if β is regarded as fixed if the limiting situation when nα is considered . The latter parameter is appropriate if the variable x, y and z represent population proportions. The parameter γ can be interpreted as the reciprocal of the mean infection partied. In the natural stochastic formulation of this model infectious periods are independently and exponentially with distributed with Parameter γ.

In the deterministic SIR model the number of infective grows as long as the proportion of susceptible in the population exceeds $\gamma/\alpha = 1/R_0$ where the reproduction ratio $R_0 = \gamma/\alpha$ represents the mean number of effective contacts made by an infective during an infectious period.

In this work we assume that the new number of immigration population may be susceptible and infective. Moreover we will use the standard incidence rate instead of the similar incidence rate to be more realistic when the total population size is quite

large. The disease related death rate is also incorporated in this model. Then our model has the following form.

$$dS(t)/dt = (1-p)A - \lambda\left(S(t)/N(t)\right)I(t) - \sigma S(t)$$

$$dI(t)/dt = PA + \lambda(S(t)/N(t))I(t) - \gamma I(t) - \sigma I(t) - \alpha I(t) \qquad \rightarrow (1)$$

$$dR(t)/dt = \gamma I(t) - \sigma R(t)$$

where $S(t), I(t), R(t)$ is the density of susceptible, infective and recovered population at time t respectively $N(t)$ is the density of total population size at time t where $N(t) = S(t) + I(t) + R(t)$, P is the fraction of infective $0 < P < 1$. A is a constant flow of new members into the whole population per unit time which can be susceptible or infective, λ is the adequate contact rate σ is the natural death rate, γ is the recovery rate, α is the disease related death rate and all parameters are positive.

From system(1) since $N(t) = S(t) + I(t) + R(t)$, we get the equation for the total population size $N(t) = A - \alpha\, I(t) - \sigma N(t)$. If the numbers of the new members entering the system per unit time is equal to the number of the population dying both from the disease and natural causes per unit time, then $N(t) = 0$, this implies that the total population size $N(t)$ is a constant.

Here we study and investigate the equilibrium solutions and stability behavior of system (1).

Main Result

Here we study an SIR epidemic model to obtain properties of the equilibrium points and analyze sufficient conditions under which the equilibrium points are locally stable or globally stable.

We rewrite the system (1) into the form

$$\dot{S} = (1-P)A - \frac{\lambda}{N} SI - \sigma S$$

$$\dot{I} - PA + \frac{\lambda}{N} SI - (\gamma + \sigma \propto) I \qquad \rightarrow (2)$$

$$\dot{R} = \gamma I - \sigma R$$

and from biological consideration we focus our attention on the closed set

$$\Gamma = \left\{(S, I, R) \in R_+^3; 0 < S + I + R = N \leq (A/\sigma)\right\}$$

So, that the solution of the system can be realistically interpreted for clear understanding of the SIR epidemic model.

First we study the steady states of the system (2), These x steady states (S^*, I^*, R^*) are determined analytically by setting $S = I = R = 0$. Then we obtain

$$S^* = \frac{\alpha(I-P)A}{\frac{\lambda}{N^*}(A-\sigma N^*)+\alpha\sigma} \quad \rightarrow (3)$$

$$I^* = \frac{1}{\propto}(A - \sigma N^*) \quad \rightarrow (4)$$

$$R^* = (\gamma / \sigma\alpha)\left(A-\sigma N^*\right) \quad \rightarrow (5)$$

$Since\ N^* = S^*+I^* + R^*$, by substituting S^*, I^* and R^* we obtain

$$0 = (1/\alpha)\left[\lambda-(\lambda/\alpha N^*)(A-\sigma N^*)-(\lambda\gamma/\alpha\sigma N^*)-(\gamma+\sigma+\alpha)\right](A-\sigma N^*)+PA \quad \rightarrow (6)$$

Letting

$$F(N) = \lambda-(\lambda/\alpha N)(A-\sigma N)-(\lambda\gamma/\alpha\sigma N)(A-\sigma N)-(\gamma+\sigma+\alpha)$$

We have

$$0 = (F(N^*)/\alpha)(A-\sigma N^*)+PA \quad \rightarrow (7)$$

If (7) has a solution where $N^* \in (0, A/\sigma]$ then S^*, I^*, and R^* also can be calculated.

The system (2) will have a solution; it means the equilibrium point will exist.

Stability of the disease – free equilibrium point.

Proposition

The system (2) has a disease free equilibrium point if and only if $P = O$ and $N = \frac{A}{\sigma}$.

Theorem

Let $R_0 = (\lambda/(\alpha+\sigma+\gamma))$,if $R_0 < 1$

Then the disease – free equilibrium point E_O whenever it exists, is locally asymptotically stable and E_O is unstable of $R_O > 1$.

Proof:

The characteristic equation of (2) where $P = 0$ at E_O is

$(\lambda^* + \sigma)[\lambda^* - \lambda + (\gamma + \sigma + \alpha)](\lambda^* + \sigma) = 0.$

Thus the disease – free equilibrium point E_O is locally asymptotically stable if $R_O < 1$ and unstable if $R_O > 1$.

Theorem

If $R_O \leq 1$, then the disease – free equilibrium point E_O is globally asymptotically stable, wherever it exists.

Proof

Constructing a suitable Lyapunov function $V_1(S, I, R) = I$, we then have $\frac{dv_1}{dt} = \dot{V}_1 = \dot{I}, if\ R_O < 1$, we have $\dot{V}_1 \leq 0$. It is easy to see that $\dot{V}_1 \leq 0$ if and only if $I = 0$. Then the largest compact variant set of (2) where $P = 0$ in the set $\{(S, I, R \in \Gamma, \dot{V}_1 \leq 0\}$. is the singleton set $\{E_0\}$. Therefore the Lassalle's Invariance principle implies that the endemic equilibrium points It is easy to see that E_0 is globally asymptotically stable.

If $R_0 = 1$, we have $\dot{V}_1 \leq 0$ It is easy to see that $\dot{V}_1 = 0$ if and only if $S = N\ or\ I = O$. Then, the largest compact invariant set of (2) where $P = 0$ is the set $\{(S, I, R\} \in \Gamma, V_1 \leq 0\}$ is the singleton set $\{E_0\}$. Therefore Lassalle's invariance principle implies that the endemic equilibrium point E_0 is globally asymptotically stable.

Theorem

If $P = 0, R_0 > 1$ and $N_1 \in \left(0, \frac{A}{\sigma}\right) then$ endemic equilibrium point E_1 is locally asymptotically stable.

Proof

From system (2), replace S by $N - I - R$. This leads to

$$\dot{I} = PA + \frac{\lambda}{N}(N - I - R)I - (\gamma + \sigma + \alpha)I$$

$$\dot{R} = \gamma I - \sigma R \qquad \rightarrow (8)$$

$$\dot{N} = A - \alpha I - \sigma N$$

At the endemic equilibrium points E_1 we then obtain the characteristic equation

$$(\lambda^* + \sigma)(\lambda^{*2} + a_1\lambda^* + a_2) = 0.$$

Where

$$a_1 = \gamma + \sigma + \alpha - (\lambda / N_1)(N_1 - 2I_1 - R_1) + \sigma \equiv f(N_1, I_1, R_1)$$

$$a_2 = \sigma[\gamma + \sigma + \alpha - (\lambda / N_1)(N_1 - 2I_1 - R_1)] + (\lambda / N_1^2)\alpha I_1(I_1 + R_1) + (\lambda / N_1)\gamma I_1 \equiv g(N_1, I_1, R_1)$$

It is easy to see that a1>0 and a2>0 if $\gamma+\sigma+\alpha-(\lambda/N_1)(N_1-2I_1-R_1)>0 \quad \rightarrow(9)$

substitute I_1 and R_1 we obtain

$$\lambda-(\gamma+\sigma+\alpha)-(2\lambda/\alpha N_1)(A-\sigma N_1)-(\lambda\gamma/(\alpha\sigma N_1))(A-\sigma N_1)<0 \quad \rightarrow(10)$$

Then from 10 and $F(N_1)=0$ we obtain

$$-(\lambda/\alpha N_1)(A-\sigma N_1)<0 \quad \rightarrow(11)$$

since all parameters are positive and $N_1 \in (0,A/\sigma)$, equation (11) is always true. This implies that a1>0 and a2>0. Thus according to the Routh – Hurwitz criterion if p=0, $R_0>1$ and $N_1 \in (0,A/\sigma)$ then the endemic equilibrium point E_1 is locally asymptotically stable.

Conclusion

We Proved that the disease free point E_0 exists when $N=\frac{A}{\sigma}$ and P = O, which means that the new members of population are susceptible only. We showed by using an appropriate Lyapunov function that of $R_o \leq 1$, the disease free equilibrium point Eo is globally asymptotically stable, So that the disease always dies out If Ro >1 or o< $p \leq 1$, Which means that the new members of population include both susceptible Population and infective Population, the disease free equilibrium point Eo becomes unstable while the endemic equilibrium point emerges as the unique equilibrium point and becomes and asymptotically stable.

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