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GLOBAL STABILITY RESULTS ON AN EPIDEMIOLOGICAL MODEL WITH A CORE GROUP (A NOTE ON THE PAPER "LOCAL STABILITY RESULTS ON A MODEL FOR TYPHOID FEVER WITH A CORE GROUP") *

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Abstract

A SIRS epidemiological model with two subpopulations and vital dynamics is analyzed. Both subpopulations sizes are considered constant by assuming that the birth and the death rates are equal. We consider the case where one subpopulation is a core , that is a very infectious small group, responsible for a big fraction of the incidence. For this case thresholds are determined and the main equilibrium points for the four dimensional system are shown to be globally stable by using a known Theorem of Markus on asymptotically autonomous systems. This system models the dynamics of typhoid fever , where the core is the group of food handlers . The results presented in this work are an extension of those presented in [3].

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1. Introduction

The spread of an infectious disease in a population depends not only on the character of the disease,but also on the structure and behavior of the population. Therefore the study of *heterogeneous* epidemic models is very important. Many previous results have been obtained in this direction (See [3] for a brief bibliographical discussion of [7] ,[1], [14], [8], [9]). We can see that *global* stability of the endemic equilibrium for many of the analyzed models is still an open problem .

In the present paper we extend the results presented in [3] in two directions : first we can *weaken* the assumptions made in [3] in order to obtain only *local* stability , and second we can obtain *global* stability for both the disease free and the endemic equilibrium . We recall that the model is an epidemiological SIRS *core-noncore* model [5] , where the infectious contacts of the core people with the noncore ones are responsible for most of the total incidence. Our aim is to model the spread of typhoid fever in a modern big city , where many poeple eat in restaurants . In this case the *food handlers* constitute the *core* group

2. The Model

Let N be the total size of the population, N_1 the size of the core and N_2 the size of the noncore. Then $N = N_1 + N_2; N_i = S_i + I_i + R_i, i = 1, 2$, where S, I, R denote the number of susceptibles , infectious and removed (immune non infectious)individuals of each subpopulation. We assume that both subpopulations N_1 and N_2 are constant by setting the birth rate equal to the death rate .Note that ,in the case of the core group, the birth and the death rate have the meaning of a *rate of change* of the food handlers,not necessarily equal to the birth and death rate of the population . Let $x_i = I_i/N_i$, $y_i = R_i/N_i$,$i = 1, 2$; (λ_{ij}) is the *transmission matrix*, that is , λ_{ij} is the average number of infectious contacts (also called *adequate* contacts,see [5]) of an infective in group j with persons in group i per unit time . Let $p = N_1/N_2$, δ_i the birth (or death) rate of subpopulation i , γ is the recovery removal rate ($1/\gamma$ is the average infectious period) , w_i is the rate of loss of temporary immunity for group i and v_i is the immunization rate by vaccination in group i. We can accept *different* values of duration of immunity because the vaccination on both groups can be different (for example, food handlers can get more dose of vaccine).

The model is then given by the following four dimensional system of autonomous differential equations :

$$\begin{aligned} x_1' &= (1 - x_1 - y_1)(\lambda_{11}x_1 + \frac{\lambda_{12}}{p}x_2) - x_1(\delta_1 + \gamma) \\ y_1' &= v_1 + (\gamma - v_1)x_1 - (v_1 + \delta_1 + w_1)y_1 \\ x_2' &= (1 - x_2 - y_2)(\lambda_{22}x_2 + \lambda_{21}px_1) - x_2(\delta_2 + \gamma) \\ y_2' &= v_2 + (\gamma - v_2)x_2 - (v_2 + \delta_2 + w_2)y_2 \end{aligned} \tag{1}$$

with the conditions : $x_i, y_i \geq 0; x_i + y_i \leq 1, i = 1, 2.$

Let D be the domain $x_i, y_i \geq 0; x_i + y_i \leq 1, i = 1, 2$ in the four dimensional space R^4 . It is easy to see ,by applying Nagumos's Lemma,that domain D is positively invariant for system (1). This system satisfies the existence ,uniquenes and prolongability conditions so that solutions of (1) starting in D exists for all time and remain in D . Thus the model is well-posed.

The qualitative analysis of system (1) is very difficult because of the dimension,even the equilibrium points are difficult to be found explicity. But ,if we assume that $\lambda_{12} = 0$, then system (1) decomposes into two two-dimensional systems and a complete analysis can be made. We recall that in [3] the assumption was $\lambda_{12} = \lambda_{22} = 0$. In fact, with the former supposition ,the first two equations :

$$\begin{aligned} x_1' &= (1 - x_1 - y_1)\lambda_{11}x_1 - x_1(\delta_1 + \gamma) \\ y_1' &= v_1 + (\gamma - v_1)x_1 - (v_1 + \delta_1 + w_1)y_1 \end{aligned} \tag{2}$$

can be solved independent on the other two variables . Once a suitable solution $x_1(t)$ is obtained , we can introduce it in the second part of the system :

$$\begin{aligned} x_2' &= (1 - x_2 - y_2)(\lambda_{22}x_2 + \lambda_{21}px_1(t)) - x_2(\delta_2 + \gamma) \\ y_2' &= v_2 + (\gamma - v_2)x_2 - (v_2 + \delta_2 + w_2)y_2 \end{aligned} \tag{3}$$

Note that this last system *is not autonomous*. System (2) correspond to the one group model analyzed by Hethcote [7] .

The hypotesis $\lambda_{12} = 0$ means that the infections on the core people produced by the noncore one is neglected.This is, in our opinion, a reasonable simplification.

Let D_1 be the domain $x_1, y_1 \geq 0; x_1 + y_1 \leq 1$ and D_2 the domain $x_2, y_2 \geq 0; x_2 + y_2 \leq 1$. Then : $D = D_1 \times D_2$. By analyzing systems (2) and (3) we obtain the following two threshold parameters :

$$\sigma_i = \frac{\lambda_{ii}(\delta_i + w_i)}{(\delta_i + \gamma)(v_i + \delta_i + w_i)} \tag{4}$$

$i = 1, 2$

Lemma 1. a) *If $\sigma_1 \leq 1$, then the only equilibrium point of system(2) in domain D_1 is the disease-free equilibrium :*

$$\bar{x_1} = 0 \ ; \ \bar{y_1} = v_1/(v_1 + \delta_1 + w_1) \tag{5}$$

which is globally asymptotically stable in D_1.

b) If $\sigma_1 > 1$, there are two equilibrium points in D_1 : the disease free equilibrium $(0, \bar{y_1})$ and :

$$x_1* = \frac{(\delta_1+\gamma)(v_1+\delta_1+w_1)(\sigma_1-1)}{\lambda_{11}(\gamma+\delta_1+w_1)}$$
$$y_1* = 1 - \frac{\delta_1+\gamma}{\lambda_{11}}(1+\frac{(v_1+\delta_1+w_1)(\sigma_1-1)}{\gamma+\delta_1+w_1}) \tag{6}$$

In this case the point $(0,\bar{y_1})$ *is unstable while point* (x_1*, y_1*) *is globally asymptotically stable in domain* $D_1 - \{(x_1,y_1) : x_1 = 0, 0 \leq y_1 \leq 1\}$.

Proof. The equilibrium points are easy to find by analyzing the isoclines $x_1' = 0, \quad y_1' = 0$.

The Jacobian matrix of (2) at point $(0,\bar{y_1})$ is :

$$J(0,\bar{y_1}) = \begin{pmatrix} (\delta_1+\gamma)(\sigma_1-1) & 0 \\ (\gamma - v_1) & -(v_1+\delta_1+w_1) \end{pmatrix}$$

We obtain explicity the eigenvalues of $J(0,\bar{y_1})$:

$$\begin{aligned} \lambda_1 &= (\delta_1+\gamma)(\sigma_1-1) \\ \lambda_2 &= -(v_1+\delta_1+w_1) \end{aligned}$$

We can see that,if $\sigma_1 \leq 1$,both eigenvalues are negative and if $\sigma_1 \geq 1$ the eigenvalue λ_1 is positive.In this last case the equilibrium point $(0,\bar{y_1})$ is a saddle point where the stable manifold in D_1 is the line $\{(0,y) : 0 \leq y \leq 1\}$. If $\sigma_1 = 1$, then the point $(0,\bar{y_1})$ is the only equilibrium point in the invariant set D_1 (is coincident with the point (x_1*, y_1*)). Applying Dulac's test [10] to the function $\rho(x,y) = 1/x$, we see that there is no periodic orbits in D_1

The Jacobian matrix of (2) at point (x_1*, y_1*) is :

$$J(x_1*, y_1*) = \begin{pmatrix} -\gamma_{11}x_1* & -\gamma_{11}x_1* \\ \gamma - v_1 & -(v_1+\delta_1+w_1) \end{pmatrix}$$

The eigenvalues are the solution of the characteristic equation :

$$\lambda^2 + \lambda(\lambda_{11}x_1* + v_1+\delta_1+w_1) + \lambda_{11}x_1*(\gamma+\delta_1+w_) = 0$$

Since $\lambda_{11}x_1*(\gamma+\delta_1+w_1) > 0$, both eigenvalues have negative real parts ,hence the point (x_1*, y_1*) is locally asymptotically stable.Since there is no periodic orbits , this point is globally stable □

In order to analize the non autonomous system (3) we consider the *associate autonomous* system :

$$x_2' = (1 - x_2 - y_2)(\lambda_{22}x_2 + \lambda_{21}px_1(\infty)) - x_2(\delta_2 + \gamma)$$
$$y_2' = v_2 + (\gamma - v_2)x_2 - (v_2 + \delta_2 + w_2)y_2 \tag{7}$$

where $x_1(\infty)$ is the asymptotic value of $x_1(t)$ in system (2) .Note that,by Lemma 1 , $x_1(\infty) = 0$ or $x_1(\infty) = x_1*$

Lemma 2. a) *If $x_1(\infty) = 0$ then two possibilities arise :*

i) If $\sigma_2 \leq 1$, then the only equilibrium point of system (7) in domain D_2 is the disease-free equilibrium :

$$\bar{x_2} = 0 \quad ; \quad \bar{y_2} = v_2/(v_2 + \delta_2 + w_2) \tag{8}$$

which is globally asymptotically stable in D_2 .

ii) If $\sigma_2 > 1$, there are two equilibrium points in D_2 : the disease free equilibrium $(0, \bar{y_2})$ and :

$$x_2* = \frac{(\delta_2 + \gamma)(v_2 + \delta_2 + w_2)(\sigma_2 - 1)}{\lambda_{22}(\gamma + \delta_2 + w_2)}$$
$$y_2* = 1 - \frac{\delta_2 + \gamma}{\lambda_{22}}(1 + \frac{(v_2 + \delta_2 + w_2)(\sigma_2 - 1)}{\gamma + \delta_2 + w_2}) \tag{9}$$

In this case the point $(0, \bar{y_2})$ is unstable while point (x_2, y_2*) is globally asymptotically stable in domain $D_2 - \{(x_2, y_2) : x_2 = 0, 0 \leq y_2 \leq 1\}$*

b) If $x_1(\infty) = x_1*$ then there is only one equilibrium point in domain D_2 .This point is the inner point $(\hat{x_2}, \hat{y_2})$ of D_2 ,where $\hat{x_2}$ is the positive root of the quadratic equation :

$$\lambda_{22}(\gamma + \delta_2 + w_2)x^2 +$$
$$+[(v_2 + \delta_2 + w_2)(\delta_2 + \gamma) - \lambda_{22}(\delta_2 + w_2) + \lambda_{21}p(\gamma + \delta_2 + w_2)x_1*]x$$
$$-\lambda_{21}p(\delta_2 + w_2) = 0 \tag{10}$$

and

$$\hat{y_2} = (v_2(1 - \hat{x_2}) + \gamma\hat{x_2})/(v_2 + \delta_2 + w_2) \tag{11}$$

This point is globally asymptotically stable in D_2.

Proof. Note that system(7) with $x_1(\infty) = 0$ is *the same* system(2) by substituting suscript 2 in all parameters.

If $x_1(\infty) = x_1*$ the only suitable equilibrium point is given by the intersection of the isoclines

$$x_2' = 0 : y_2 = 1 - x_2 - (\delta_2 + \gamma)x_2/(\lambda_{21}px_1* + \lambda_{22}x_2)$$

$$y_2' = 0 : y_2 = -x_2 + (1 - (\delta_2 + \gamma)/\lambda_{11})$$

By applying Dulac's Lemma to the function $\rho(x, y) = 1/x$ we prove that there are no periodic orbits in D_2 . □

We are going to analyze the non autonomous system (3) by using some results of Markus [12] on *asymptotically autonomous* systems .(See also Thieme [13]) . Let us consider the systems

$$x' = f(t, x) \tag{12}$$

$$y' = g(y) \tag{13}$$

in R^n .System (12) is called *asymptotically autonomous*, with *limit equation (13)* , if

$f(t, x) \longrightarrow g(x)$ *for* $t \longrightarrow \infty$,

locally uniformly in $x \in R^n$, i.e.,for x in any compact susbset of R^n .

Theorem 1 [Markus]. *Let (12) asymptotically autonomous with limit (13), f continous and locally Lipschitz in x , g continously differentiable , $y*$ a locally asymptotically stable equilibrium of (13) . Then there exists $r > 0$ and $T_1 > 0$ such that the solution $\phi(t, T_1, \zeta)$ of (12) starting at $\zeta, \mid \zeta - y* \mid < r$ at time T_1 converges to $y*$ for $t \longrightarrow \infty$.*

By using this theorem we show the following Lemma :

Lemma 3. *Let H be a compact set, positively invariant for systems (12) and (13) ,$y* \in H$ be the globally asymptotically stable equilibrium point in H for system (13). Then* $\lim_{t\to\infty} \phi(t, 0, \zeta) = y*, \forall \zeta \in H$.

Proof. Let $\psi(t, T, \zeta)$ be the solution of (13) starting at ζ at time T , and let $r > 0$ according to Markus Theorem . Due to the compacity of H and the continous dependence on the initial conditions , we can find a time t_1 , not depending on ζ , such that $\mid \psi(t, 0, \zeta) - y* \mid < r/2, \forall t > t_1, \forall \zeta \in H$. Let $L > 0$ such that $\mid g(y) - g(x) \mid \leq L \mid y - x \mid$. Than there is a time t_2 such that

$\mid g(x) - f(t, x) \mid < (r \exp(-t_1 L))/2t_1, \forall t > t_2, \forall x \in H$. Now , for an arbitrary $\zeta \in H$, let $\phi(t) = \phi(t, 0, \zeta)$, $\psi(t) = \psi(t, t_2, \phi(t_2))$. Then :

$$| \phi(t) - \psi(t) | \leq \int_{t_2}^{t} | f(u, \phi(u)) - g(\psi(u) | \, du \leq$$

$$\leq \int_{t_1}^{t_1+t_2} | f(u, \phi(u) - g(\phi(u)) | \, du + L \int_{t_1}^{t} | \phi(u) - \psi(u) | \, du \quad \forall t \in [t_1, t_1 + t_2] \, .$$

Using Gronwall's inequality :

$$| \phi(t) - \psi(t) | \leq [\int_{t_1}^{t+t_2} | f(u, \phi(u)) - g(\phi(u)) | \, du] \exp L(t - t_1) \leq r/2$$

Hence, $| \phi(t_1 + t_2) - y* | < r$ and the result follows from Markus Theorem □
Since domain D_2 is invariant for both systems (3) and (7) and system (3) is asymptotically autonomous with limit (7) , then the main stability results given in Lemma 2 for the autonomous system (7) are valid for the nonautonomous system (3). We can sumarize our results in the following Theorem.

Theorem 2. *Let $\lambda_{12} = 0$ in the four dimensional system (1).Then :*

a) If $\sigma_1 \leq 1$ Then :

If $\sigma_2 \leq 1$, then the only equilibrium point of (1) in domain D is the disease-free equilibrium : $(0, \bar{y}_1, 0, \bar{y}_2)$ which is globally asymptotically stable in D.

b) If $\sigma_1 > 1$ .Then :

i) If $\sigma_2 \leq 1$, there are two equilibrium points in domain D : the disease free point $(0, \bar{y}_1, 0, \bar{y}_2)$,which is unstable , and the endemic point $(x_1*, y_1*, x_2, \bar{y}_2)$ which is globally asymptotically stable in

$D - \{(0, y_1, x_2, y_2) : 0 \leq y_1 \leq 1, (x_2, y_2) \in D_2\}$

ii) If $\sigma_2 > 1$, there are three equilibrium points : the disease free point $(0, \bar{y}_1, 0, \bar{y}_2)$ which is unstable , the point $(0, \bar{y}_1, x_2*, y_2*)$ which is also unstable , and endemic point $(x_1*, y_1*, \hat{x}_2, \hat{y}_2)$ which is globally asymptotically stable in

$D - \{(0, y_1, x_2, y_2) : 0 \leq y_1 \leq 1, (x_2, y_2) \in D_2\}$

3. REMARKS.-

a) The condition $\sigma_1 > 1$ implies that the core population can maintain an endemic level in the *whole* population, even when the non-core satisfies $\sigma_2 \leq 1$. In this case the endemicity on the non-core is maintained only by the core.

b) The case : $\sigma_1 \leq 1, \sigma_2 > 1$ has been excluded of the Theorem because Lemma 3 is not applicable (the invariant compact set D_2 is not the domain of attraction of the non trivial equilibrium point due to the existence of a second equilibrium point on the boundary). In this case there are two equilibrium points : $(0, \bar{y}_1, 0, \bar{y}_2)$ and $(0, \bar{y}_1, x_2*, y_2*)$. The first is unstable while the second one seems to be globally asymptotically stable in domain: $D - \{(0, y_1, x_2, y_2) : 0 \leq y_1 \leq 1, (x_2, y_2) \in D_2\}$

In this case the endemicity on the non-core population is maintained by itself, without the action of the core.

c) The point $(x_1*, y_1*, 0, 0)$ *is not* an equilibrium point of the system in all the cases. That means only that the core is not isolated, so that any endemicity of the core is transfered to the non-core .

d) Parameter estimation and some illustrative computer simulations can be founded in [3].

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