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MULTIPLE EQUILIBRIA FOR AN SIS EPIDEMIOLOGICAL SYSTEM

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Abstract. In this paper, we give a complete global analysis of an SIS epidemiological model in a population of varying size with two dissimilar groups of infective individuals. The main arguments are based on the discussion of the existence and stability of equilibria of the proportions system. We use the Poincaré index together with perturbation and numerical methods to show that the endemic proportions need not be unique.

Key Words. differential infectivity, disease transmission, endemic proportions, epidemiological model, perturbation, Poincaré index.

1. Introduction

Most mathematical models for the dynamics of disease transmission in a population are multigroup models in which heterogenous subpopulations may participate in the epidemic process with different parameters [6]. Recently Hyman, Li and Stanley [14] introduced a new model based on different infection levels among individuals which causes different levels of infectivity. This model, which was called the differential infectivity model, is different from all previous ones. In the differential infectivity model, the susceptible group is assumed to be homogeneous and the infective population is subdivided into groups according to their infectiveness. Upon infection, an individual enters one of these subpopulations with a probability. By using this model, they showed that HIV is primarily spread by a small, highly infectious group of superspreaders. (See [13, 14, 15] for more details.)

In this paper we examine an SIS model of disease transmission in a population of varying size with a homogeneous susceptible group and two dissimilar groups of infective individuals. We assume that a new infected individual enters one of these two groups with constant proportions. Therefore the model discussed here is a very simple differential infectivity model. In our model, the incidence function is of proportionate mixing type introduced by Nold [17]. The demographic assumptions are also very simple, Natural births and deaths are assumed to be proportional to the class numbers. All newborn susceptibles and the excess deaths due to the disease among infectives are also proportional. We could have considered more complicated demographic or vertical transmission assumptions [1, 2], but these parameters have no mathematical significance and one can easily conclude that our main results would still be valid. Indeed we shall show that multiple equilibria can occur even in this simple case. The existence of multiple equilibria or limit cycles has been previously shown for more complicated systems [10, 12, 16].

In the next section, We first introduce our model equations which give a homogeneous system of degree one. For such a system, it is easier to consider the proportions system. In section 3, we state a result concerning the nonexistence of

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certain types of solutions for this system [5]. This result helps us to show that every solution in the feasibility region tends to a rest point of this system. The rest of this paper is mainly concerned with the discussion of the existence and stability of equilibria of the proportions system. The technique used here is based on a careful choice of Jordan curves and counting the number of rest points inside them. This technique has no hard analysis and can be easily applied to other similar systems [20, 21]. In section 4, we reduce our system to a planar one to obtain some information about the local behavior near a rest point. In section 5, we obtain a partial result in a special case which is used in section 6 to show the existence of multiple equilibria in the general case. Finally in section 7, we provide some numerical simulations of our system in the case of multiple equilibria.

2. The Model

In order to derive our model, we divide the population into three classes: susceptibles and two groups of infectives, the number in each class is denoted by S, I_1 and I_2 respectively. We set $N = S + I_1 + I_2$ which is the total size of the population and we use the following parameters which are assumed to be positive unless otherwise specified:

b : per capita birth rate ,
d : per capita disease free death rate,
ε_1 : excess per capita death rate of I_1,
ε_2 : excess per capita death rate of I_2,
λ_1 : effective per capita contact rate of I_1,
λ_2 : effective per capita contact rate of I_2,
γ_1 : per capita recovery rate of I_1,
γ_2 : per capita recovery rate of I_2.

We also assume that the susceptible individuals who have been infected, enter the groups I_1 and I_2 of constant proportions p and q respectively, hence $p + q = 1$. The above hypotheses lead to the following system of differential equations in $\mathbb{R}^3_+$, where "$'$" denotes the derivative with respect to time t,

$$\begin{cases} S' = bN - dS + \gamma_1 I_1 + \gamma_2 I_2 - \lambda_1 \frac{I_1 S}{N} - \lambda_2 \frac{I_2 S}{N}, & (2-1) \\ {I'}_1 = p\left(\lambda_1 \frac{I_1 S}{N} + \lambda_2 \frac{I_2 S}{N}\right) - (d + \varepsilon_1 + \gamma_1) I_1, & (2-2) \\ {I'}_2 = q\left(\lambda_1 \frac{I_1 S}{N} + \lambda_2 \frac{I_2 S}{N}\right) - (d + \varepsilon_2 + \gamma_2) I_2, & (2-3) \end{cases}$$

and $\frac{\lambda_j I_j}{N}$ is of the proportionate (or random) mixing type [11, 17]. The total population equation is obtained by adding the above three equations:

$$N' = (b - d)N - \varepsilon_1 I_1 - \varepsilon_2 I_2. \qquad (2-4)$$

Now if we consider the proportions $s = \frac{S}{N}, i_1 = \frac{I_1}{N}$ and $i_2 = \frac{I_2}{N}$, we get the following system of equations:

$$\begin{cases} s' = b(1 - s) + \gamma_1 i_1 + \gamma_2 i_2 + (\varepsilon_1 - \lambda_1) i_1 s + (\varepsilon_2 - \lambda_2) i_2 s, & (2-1a) \\ i_1' = ps(\lambda_1 i_1 + \lambda_2 i_2) + i_1(\varepsilon_1 i_1 + \varepsilon_2 i_2) - (b + \varepsilon_1 + \gamma_1) i_1, & (2-2a) \\ i_2' = qs(\lambda_1 i_1 + \lambda_2 i_2) + i_2(\varepsilon_1 i_1 + \varepsilon_2 i_2) - (b + \varepsilon_2 + \gamma_2) i_2. & (2-3a) \end{cases}$$

In order to determine the asymptotic behavior of the solutions of this system of equations, we use the following concept of ODE system. Given an autonomous system of ordinary differential equations in $\mathbb{R}^n$

$$\frac{dx}{dt} = f(x). \qquad (2-5)$$

We will denote by $x.t$ the value of the solution of this system at time t that is x initially. For $V \subset \mathbb{R}^n$ and $J \subset \mathbb{R}$, we let $V.J = \{x.t : x \in V, t \in J\}$. The set V is called invariant if $V.\mathbb{R} = V$ and it is called positively invariant if $V.\mathbb{R}_+ \subset V$. For $Y \subset \mathbb{R}^n$ the ω-limit set of Y is defined to be the maximal invariant set in the closure of $Y.[0, \infty)$. A closed curve connecting several rest points whose segments between successive rest points are heteroclinic orbits is called phase polygon. By a sink we mean a rest point at which all the eigenvalues of the linearized system have negative real parts. A rest point is called a source if these eigenvalues have positive real parts and it is called a saddle point if some of these eigenvalues have positive real parts and the others have negative real parts. A rest point is called nondegenerate if all of these eigenvalues are nonzero and it is called hyperbolic if all of its eigenvalues have nonzero real parts.

3. Some Basic Results

We start our analysis with some basic results about the system $(2-1a)-(2-3a)$. If we set $\sum = s + i_1 + i_2$, then $\sum' = (1 - \sum)(b - \varepsilon_1 i_1 - \varepsilon_2 i_2)$. Therefore the plane $\sum = 1$ is invariant. We consider the feasibility region

$$D = \{(s, i_1, i_2) : s + i_1 + i_2 = 1, s \geq 0, i_1 \geq 0, i_2 \geq 0\}$$

which is a triangle and on its sides we have

$$s = 0 \Rightarrow s' = b + \gamma_1 i_1 + \gamma_2 i_2, \quad i_1 = 0 \Rightarrow i_1' = p\lambda_2 s i_2, \quad i_2 = 0 \Rightarrow i_2' = q\lambda_1 s i_1.$$

Since all parameters are positive, D is positively invariant and the disease free equilibrium $(1, 0, 0)$ is the only rest point on ∂D, the boundary of D. Indeed any solution of the system $(2 - 1a) - (2 - 3a)$ with initial point in $\partial D - \{(1, 0, 0)\}$, immediately gets into $\overset{\circ}{D}$, the interior of D. From now on, we examine the dynamics of this system in the feasibility region D. The following theorem is a special case of the results of [5] concerning the nonexistence of certain types of solutions.

Theorem 3.1. *Let in (2-5), f be a smooth vector field in $\mathbb{R}^3$ and $\gamma(t)$ be a closed piecewise smooth curve which is the boundary of an orientable smooth surface $S \subset \mathbb{R}^3$. Suppose $g : U \longrightarrow \mathbb{R}^3$ is defined and is smooth in a neighborhood U of S. Moreover it satisfies $g(\gamma(t)).f(\gamma(t)) \geq 0$ and $(curl g) \cdot n < 0$, where n is the unit normal to S. Then γ is not a finite union of the orbits of the system (2-5).*

In order to apply the above theorem, we define $g = g_1 + g_2 + g_3$ where

$$g_1(i_1, i_2) = \left[0, -\frac{f_3(i_1, i_2)}{i_1 i_2}, \frac{f_2(i_1, i_2)}{i_1 i_2}\right],$$

$$g_2(s, i_2) = \left[\frac{f_3(s, i_2)}{s i_2}, 0, -\frac{f_1(s, i_2)}{s i_2}\right],$$

$$g_3(s, i_1) = \left[-\frac{f_2(s, i_1)}{s i_1}, -\frac{f_1(s, i_1)}{s i_1}, 0\right],$$

and f_1, f_2 and f_3 denote the right hand side of $(2 - 1a), (2 - 2a)$ and $(2 - 3a)$ reduced to functions of two variables by using $\sum = 1$, respectively. Now after some manipulations [4, 7], we get

$$(\mathrm{curl} g).(1, 1, 1) = -\left(\frac{p\lambda_2}{i_1^2} + \frac{q\lambda_1}{i_2^2} + \frac{b + \gamma_1}{i_2 s^2} + \frac{b + \gamma_2}{i_1 s^2}\right).$$

Corollary 3.2. *The system* $(2-1a)-(2-3a)$ *has no periodic orbits, homoclinic orbits or phase polygons in* $\overset{\circ}{D}$.

Proof. Use Theorem 3.1. for $f=(f_1,f_2,f_3)$. Here we have $g.f=0$ and $(\mathrm{curl}g).(1,1,1)<0$ in $\overset{\circ}{D}$. □

Lemma 3.3. *The* ω*-limit set of any orbit of the system* $(2-1a)-(2-3a)$ *with initial point in* D *is a rest point.*

Proof. Suppose the contrary, so that the ω-limit set has a regular point in $\overset{\circ}{D}$. Let x be such a point and h be its first return map. For a point y near x on the transversal, let V be the region surrounded by the orbit γ from y to $h(y)$ and the segment between them. This region is known as Bendixson sack. (See Figure 3.1.)

Now by Stokes' theorem

$$\int\int_V (\mathrm{curl}g).(1,1,1)d\sigma = \int_\gamma g.f dt + \int_0^1 g(ty+(1-t)h(y)).(y-h(y))dt.$$

Since $g.f=0$ and $h(x)=x$, the right hand side of the above equality tends to zero when y tends to x. But the left hand side tends to the integral over the region bounded by the ω-limit set. This is a contradiction since $(\mathrm{curl}g).(1,1,1)<0$ in $\overset{\circ}{D}$. □

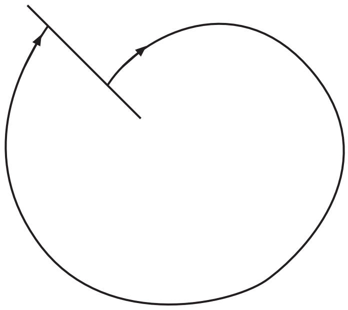

Figure 3.1. The Bendixson sack.

Remark 3.4. When the ω-limit set lies in $\overset{\circ}{D}$, the above result is easily concluded by the generalized Poincaré-Bendixson theorem [19, 18] and Corollary 4.2. Similarly if the α-limit set of an orbit of the system $(2-1a)-(2-3a)$ lies in $\overset{\circ}{D}$, it must be a single point.

4. The Planar System

Using the equality $s+i_1+i_2=1$, we see that our system is essentially two dimensional. Thus we can eliminate one of the variables, say s, to arrive at the following quadratic planar system

$$\begin{cases} i_1' = (p\lambda_1-b-\varepsilon_1-\gamma_1)i_1+p\lambda_2 i_2-(i_1+i_2)(p\lambda_1 i_1+p\lambda_2 i_2)+i_1(\varepsilon_1 i_1+\varepsilon_2 i_2), & (3-1)\\ i_2' = q\lambda_1 i_1+(q\lambda_2-b-\varepsilon-\gamma_2)i_2-(i_1+i_2)(q\lambda_2 i_2-q\lambda_1 i_1)+i_2(\varepsilon_1 i_1+\varepsilon_2 i_2). & (3-2)\end{cases}$$

The dynamics of the system $(2-1a)-(2-3a)$ on D is equivalent to the dynamics of this planar system in the positively invariant region

$$D_1=\{(i_1,i_2)|i_1\geq 0, i_2\geq 0, i_1+i_2\leq 1\}.$$

The matrix of the linearization of the system $(3-1),(3-2)$ at the origin is:

$$C=\left[\begin{array}{ll} p\lambda_1-b-\varepsilon_1-\gamma_1 & p\lambda_2 \\ q\lambda_1 & q\lambda_2-b-\varepsilon_2-\gamma_2 \end{array}\right],$$

with $\det C = (b+\varepsilon_1+\gamma_1)(b+\varepsilon_2+\gamma_2) - p\lambda_1(b+\varepsilon_2+\gamma_2) - q\lambda_1(b+\varepsilon_1+\gamma_1)$. We set $R_0 = \frac{p\lambda_1}{b+\varepsilon_1+\gamma_1} + \frac{q\lambda_2}{b+\varepsilon_2+\gamma_2}$. Hence if $R_0 < 1$, then $\det C > 0$ and $\operatorname{trace} C < 0$ and if $R_0 > 1$ then $\det C < 0$. Thus we have proved the following proposition.

Proposition 4.1. *If* $R_0 < 1$ *(resp.* $R_0 > 1$*) then the origin is a sink (resp. a saddle) for the system* $(3-1),(3-2)$.

Lemma 4.2. *The trace of the linearization of the system* $(3-1),(3-2)$ *at a rest point in* $\overset{\circ}{D}_1$ *is negative.*

Proof. We compute the trace at a rest point in $\overset{\circ}{D}_1$.

$$\begin{aligned}\frac{\partial i_1'}{\partial i_1} &= p\lambda_1 - b - \varepsilon_1 - \gamma_1 + (\varepsilon_2 - p\lambda_1 - p\lambda_2)i_2 + 2(\varepsilon_1 - p\lambda_1)i_1,\\ \frac{\partial i_2'}{\partial i_2} &= q\lambda_2 - b - \varepsilon_2 - \gamma_2 + (\varepsilon_1 - q\lambda_2 - q\lambda_1)i_1 + 2(\varepsilon_2 - q\lambda_2)i_2.\end{aligned}$$

From $i_1' = 0$ and $i_2' = 0$ we have

$$\begin{aligned}\frac{\partial i_1'}{\partial i_1} &= -p\lambda_2\frac{i_2}{i_1} + p\lambda_2\frac{i_2^2}{i_1} + (\varepsilon_1 - p\lambda_1)i_1 = -p\lambda_2\frac{i_2}{i_1}(1-i_2) + (\varepsilon_1 - p\lambda_1)i_1,\\ \frac{\partial i_2'}{\partial i_2} &= -q\lambda_1\frac{i_1}{i_2} + q\lambda_1\frac{i_1^2}{i_2} + (\varepsilon_2 - q\lambda_2)i_2 = -q\lambda_1\frac{i_1}{i_2}(1-i_1) + (\varepsilon_2 - q\lambda_2)i_2.\end{aligned}$$

Now by using the equality $s + i_1 + i_2 = 1$, we obtain

$$\frac{\partial i_1'}{\partial i_1} + \frac{\partial i_2'}{\partial i_2} = (\varepsilon_1 - \lambda_1)i_1 + (\varepsilon_2 - \lambda_2)i_2 - p\lambda_2\frac{i_2 s}{i_1} - q\lambda_1\frac{i_1 s}{i_2}.$$

Then from $(2-1a)$ we get

$$s' = b(i_1+i_2) + \gamma_1 i_1 + \gamma_2 i_2 + (\varepsilon_1 - \lambda_1)i_1 s + (\varepsilon_2 - \lambda_2)i_2 s = 0.$$

Thus $(\varepsilon_1 - \lambda_1)i_1 s + (\varepsilon_2 - \lambda_2)i_2 s < 0$ and it follows that $\frac{\partial i_1'}{\partial i_1} + \frac{\partial i_2'}{\partial i_2} < 0$. □

Corollary 4.3. *The system* $(3-1),(3-2)$ *has no source points in* $\overset{\circ}{D}_1$.

Corollary 4.4. *Every nondegenerate rest point of the system* $(3-1),(3-2)$ *in* $\overset{\circ}{D}_1$ *is hyperbolic.*

The above two corollaries are immediate consequences of Lemma 4.2. Notice that a nondegenerate rest point of the system $(3-1),(3-2)$ is obtained by a transversal intersection of the two conic sections $i_1' = 0$ and $i_2' = 0$ in the (i_1, i_2) plane. We desire to show that this intersection is almost always transversal. Let Ω be the set of all admissible values of parameters involved in the system (3-1),(3-2). If we set $q = 1-p$, then Ω can be considered as a subset of $\mathbb{R}^8$ with its standard measure. Let $\Omega_0 \subset \Omega$ be the set of all values of parameters at which the system (3-1),(3-2) has a degenerate rest point in D_1. The following theorem asserts that Ω_0 is nowhere dense in Ω.

Theorem 4.5. Ω_0 *is a closed subset of* Ω *with zero measure.*

Proof. Ω_0 is closed for the continuity of the eigenvalues of a matrix with respect to its entries. In Order to prove that Ω_0 has zero measure, we use Sard's theorem. At a rest point of the system (3-1),(3-2), we have $s' = 0$. If we use the relation $s + i_1 + i_2 = 1$ in $(2-1a)$, we can write:

$$(1)\qquad i_1 = \frac{\big(b + \gamma_2 + (\varepsilon_2 - \lambda_2)s\big)(1-s)}{\gamma_2 - \gamma_1 + (\lambda_1 - \lambda_2 - \varepsilon_1 + \varepsilon_2)s}, \qquad (3-3)$$

$$(2)\qquad i_2 = \frac{\big(b + \gamma_1 + (\varepsilon_1 - \lambda_1)s\big)(1-s)}{\gamma_1 - \gamma_2 + (\lambda_2 - \lambda_1 - \varepsilon_2 + \varepsilon_1)s}. \qquad (3-4)$$

Note that if $\gamma_2 - \gamma_1 + (\lambda_1 - \lambda_2 - \varepsilon_1 + \varepsilon_2)s = 0$ at a rest point in $\overset{\circ}{D}_1$, then $(b + \gamma_2)(\varepsilon_1 - \lambda_1) = (b + \gamma_1)(\varepsilon_2 - \lambda_2)$ which is an algebraic hypersurface in Ω and hence it has zero measure. Thus the above equations are valid almost everywhere in Ω. From $i_1' = 0$ we have

$$\frac{(b+\varepsilon_1+\gamma_1)i_1 - i_1(\varepsilon_1 i_1 + \varepsilon_2 i_2)}{(\lambda_1 i_1 + \lambda_2 i_2)s} = p.$$

If we substitute i_1 and i_2 from the equations (3-3) and (3-4) in the left hand side of this equality, we get $h(s) = p$ where h is a function in terms of s. At a rest point in $\overset{\circ}{D}_1$, we have $(\lambda_1 i_1 + \lambda_2 i_2)s > 0$ and if this rest point is degenerate, then p is a critical value of h. Now by Sard's theorem, the set of critical values of h has zero measure (indeed finite since h is rational function in s). It follows that Ω_1 meets almost all lines parallel to the p-axis in subsets with zero measure. Now the proof is complete by Fubini's Theorem. □

Remark 4.6. In the above argument, if $G(s) := \gamma_2 - \gamma_1 + (\lambda_1 - \lambda_2 - \varepsilon_1 + \varepsilon_2)s$ does not vanish at a rest point of the system (3-1),(3-2), then we can use (3-3), (3-4) and one of the relations $i_1' = 0$ or $i_2' = 0$ to obtain an equation in the form of $\frac{F(s)}{G(s)^2} = 0$ where $F(s)$ is a quartic in s with coefficient in terms of parameters. A nondegenerate rest point of the system (3-1),(3-2) in $\overset{\circ}{D}_1$ corresponds to a simple root of $F(s) = 0$. Notice that if $G(s) = 0$, then $b + \gamma_2 + (\varepsilon_2 - \lambda_2)s = 0$ and $b + \gamma_1 + (\varepsilon_1 - \lambda_1)s = 0$. Thus $b + \gamma_2 + \varepsilon_2 - \lambda_2 < 0$ and $b + \gamma_1 + \varepsilon_1 - \lambda_1 < 0$. Therefore $G(s) \neq 0$ when $R_0 \leq 1$.

5. A Special Case

In order to continue the study of the planar system, we need a partial result from the special case $b_1 = \gamma_1 = \gamma_2 = 0$. In this case the line $\{s' = 0\}$ is invariant with two rest points $(1,0)$ and $(0,1)$. The matrix of linearization of the planar system at $(1,0)$ is

$$C_1 = \begin{bmatrix} \varepsilon_1 - p\lambda_1 & \varepsilon_2 - p\lambda_1 \\ -q\lambda_1 & \varepsilon_1 - \varepsilon_2 - q\lambda_1 \end{bmatrix}.$$

Since the line $\{i_1 + i_2 = 1\}$ is invariant, $\begin{bmatrix} 1 \\ -1 \end{bmatrix}$ is an eigenvector of C_1. The eigenvalue related to this eigenvector is $\varepsilon_1 - \varepsilon_2$. Thus the other eigenvalue of C_1 is $\varepsilon_1 - \lambda_1$. Similarly the matrix of linearization at $(0,1)$ is

$$C_2 = \begin{bmatrix} \varepsilon_2 - \varepsilon_1 - p\lambda_2 & -p\lambda_2 \\ \varepsilon_1 - q\lambda_2 & \varepsilon_2 - q\lambda_2 \end{bmatrix}.$$

Here $\varepsilon_2 - \varepsilon_1$ is the eigenvalue of C_2 related to the invariant line $\{i_1 + i_2 = 1\}$ and the other eigenvalue is $\varepsilon_2 - \lambda_2$.

Proposition 5.1. *If* $b = \gamma_1 = \gamma_2 = 0$ *,* $R_0 < 1$ *,* $\varepsilon_1 < \varepsilon_2$ *and* $\varepsilon_1 < \lambda_1$*, then the planar system (3-1), (3-2) has a saddle point in* $\overset{\circ}{D}_1$.

Proof. These assumptions mean that $(0,0)$ and $(1,0)$ are sinks and $(0,1)$ is a source. Since our planar system is quadratic, there is at most one rest point in $\overset{\circ}{D}_1$ and it must be nondegenerate. Let B_1, B_2 and B_3 be small disks (with respect to an adapted norm if needed) centered at $(0,0)$, $(1,0)$ and $(0,1)$ respectively. (See Figure 4.1.) If we set $\Gamma_0 = \partial((D_1 - B_3) \cup B_1 \cup B_2)$, then Γ_0 is a Jordan curve containing all rest points in $\overset{\circ}{D}_1$ and the vector field X related to our planar system is never outward on it. For such a Jordan curve we know that $I_X(\Gamma_0) = 1$ where $I_X(\Gamma_0)$ is the Poincaré index of Γ_0 with respect to the vector field X. (See [20] for an elementary proof.) Therefore there is a rest point in $\overset{\circ}{D}_1$ whose Poincaré index is -1. Since this rest point is nondegenerate, it must be a saddle point.□

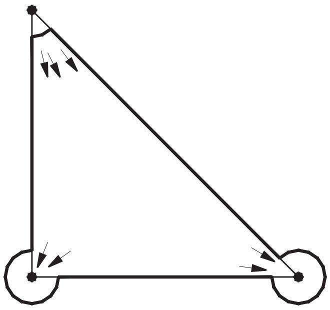

Figure 4.1. The Jordan curve Γ_0

Remark 5.2. In the above proposition, we exhibited a special case of the planar system (3-1),(3-2) in which there are two sinks in D_1. This helps us to find an example of multiple equilibria for the case $R_0 < 1$. (See Theorem 6.1.) When $R_0 > 1$, the origin is a saddle point and both $(1,0)$ and $(0,1)$ cannot be sinks simultaneously. Since our planar system is quadratic, it has at most four rest points and if one of $(0,1)$ or $(1,0)$ is sink, then the fourth one lies outside of the convex hull of $(0,0)$, $(1,0)$ and $(0,1)$ that is D_1. Therefore there is at most one sink in D_1 when $b_1 = \gamma_1 = \gamma_2 = 0$ and $R_0 > 1$.

6. The General Case

In this section we give a complete global analysis of the planar system (3-1),(3-2). We first consider the case $R_0 < 1$ in which the origin is a sink or equivalently the DFE (disease free equilibrium) is locally stable. A natural question here is whether the DFE is a Globally Asymptotically Stable (GAS). This has been shown to be true for most models, but for our differential infectivity model, multiple equilibria may occur. The following theorem gives a complete global analysis of the system in this case.

Theorem 6.1. *If $R_0 < 1$ then one of the following statements holds:*
A) The origin is globally asymptotically stable (GAS) in D_1.
B) There exist a sink and a saddle point in $\overset{\circ}{D}_1$.
C) There is a unique rest point in D_1 which is degenerate.
Moreover each of the above occurs for suitable values of involved parameters.

Proof. The proof will be given in three steps.

Step 1. We first prove that if all rest points in D_1 are nondegenerate, then (A) or (B) occurs. Since our planar system is quadratic, it has at most four rest points all hyperbolic by Corollary 4.4. Similar to the proof of Proposition 5.1, we choose a Jordan curve containing all rest points in D_1 and we calculate the number of rest points inside this curve. Let W be a small disk centered at the origin (with respect to an adapted norm if necessary) and $\Gamma = \partial(D_1 \cup W)$. (See Figure 6.1.) Then our vector field is always tangent or inward on Γ hence the Poincaré index of this Jordan curve relative to our system is 1. Let $\mu_0(\Gamma)$, $\mu_1(\Gamma)$ and $\mu_2(\Gamma)$ be the number of sinks, saddles and sources inside Γ. If all rest points in D_1 are hyperbolic, we get

$$\left.\begin{array}{c}\mu_0(\Gamma) - \mu_1(\Gamma) + \mu_2(\Gamma) = 1\\ \mu_0(\Gamma) + \mu_1(\Gamma) + \mu_2(\Gamma) \le 4\\ \mu_2(\Gamma) = 0 \text{ by Corollary 4.3.}\end{array}\right\} \quad \Rightarrow \quad \begin{array}{c}\mu_0(\Gamma) = 1,\ \mu_1(\Gamma) = \mu_2(\Gamma) = 0\\ \text{or}\\ \mu_0(\Gamma) = 2,\ \mu_1(\Gamma) = 1,\ \mu_2(\Gamma) = 0.\end{array}$$

The first case gives (A) and the second one gives (B).

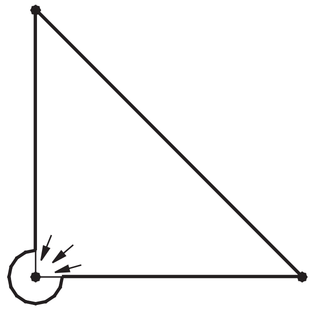

Figure 6.1. The Jordan curve Γ.

Step 2. Now we prove that both (A) and (B) occur for suitable value of parameters. Notice that $(2-1a)$ can be written in the following form by using the relation $s+i_1+i_2=1$.

$$\begin{aligned} s' &= (b+\gamma_1)i_1+(b+\gamma_2)i_2+(\varepsilon_1-\lambda_1)i_1 s+(\varepsilon_2-\lambda_2)i_2 s \\ &= (b+\gamma_1)i_1(1-s)+(b+\gamma_2)i_2(1-s)+(\varepsilon_1+\gamma_1-\lambda_1)i_1 s+(\varepsilon_2+\gamma_2-\lambda_2)i_2 s. \end{aligned}$$

If $\lambda_1 \leq b+\varepsilon_1+\gamma_1$ and $\lambda_2 \leq b+\varepsilon_2+\gamma_2$, then $s'>0$ in $D_1-\{(0,0)\}$ and hence i_1+i_2 is a Liapunov function for the planar system in D_1. Therefore $(0,0)$ is GAS in D_1 and we obtain an example for (A). In order to show that (B) occurs, we use Proposition 5.1. Under the assumptions of this proposition, all rest points are hyperbolic and there exists a saddle point in $\overset{\circ}{D}_1$. Now by the stability of hyperbolic rest points, for small values of b, γ_1 and γ_2, the planar system has only hyperbolic rest points and one of them is a saddle point in $\overset{\circ}{D}_1$. Now the results of the first step show that (B) occurs in this case. (See Figure 6.2.)

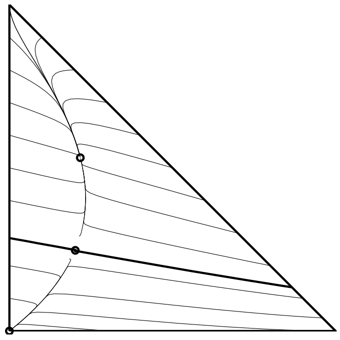

Figure 6.2. A sample phase portrait of the case (B).

Step 3. Finally we examine the degenerate case. Recall that Ω is the set of all possible values of parameters. It is easy to see that $\Omega \cap \{R_0<1\}$ is connected and both (A) and (B) occur in open subsets of $\Omega \cap \{R_0<1\}$. Therefore by Corollary 4.4, there must be a degenerate case. It remains to show that in this case the degenerate rest point is unique in $\overset{\circ}{D}_1$. Suppose that there is another rest point in $\overset{\circ}{D}_1$ in the presence of the degenerate rest point. Then by Remark 4.6, this rest point gives a simple root of $G(s)=0$, hence it is nondegenerate and the degenerate one gives a square root. Now $\Omega_1 \cap \{R_0<1\}$ has zero measure by Theorem 4.5. Thus after a perturbation, we get an odd number of hyperbolic rest points in $\overset{\circ}{D}_1$ which contradicts the results of Step 1. □

Theorem 6.2. *If $R_0>1$, then one of the following statements holds:*

Aa*) There exists a unique rest point in $\overset{\circ}{D}_1$ which is a sink and attracts $D_1-\{(0,0)\}$.*

Ba*) There are two sinks and a saddle point in* $\overset{\circ}{D}_1$.

Ca*) There exists a degenerate rest point in* $\overset{\circ}{D}_1$.

Moreover each of them occurs for suitable values of parameters.

Proof. When $R_0 > 1$, the origin is a saddle point and for the right angle of D_1 at the origin, a part of the unstable manifold of the origin lies outside of D_1. Since D_1 is positively invariant, the stable manifold of the origin cannot have any point of $\overset{\circ}{D}_1$. Moreover our vector field is strictly inward on $\partial D_1 - \{(0,0)\}$, hence the stable manifold meets D_1 only at the origin. (See Figure 6.3.)

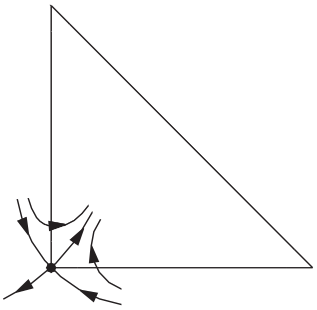

Figure 6.3. The dynamics near the origin.

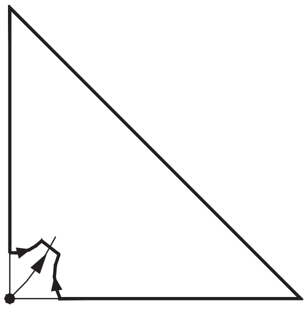

Figure 6.4. The Jordan curve Γ'.

Now we can construct a Jordan curve Γ' containing all rest points in $\overset{\circ}{D}_1$ such that our vector field is either tangent or inward on it. (See Figure 6.4.) The Poincaré index of this Jordan curve relative to our system is 1. If all rest points in $\overset{\circ}{D}_1$ are hyperbolic, we can again use the Poincaré theorem to obtain

$$\left.\begin{array}{c} \mu_0(\Gamma') - \mu_1(\Gamma') + \mu_2(\Gamma') = 1 \\ \mu_0(\Gamma') + \mu_1(\Gamma') + \mu_2(\Gamma') \le 3 \\ \mu_2(\Gamma') = 0 \text{ by Corollary 4.3.} \end{array}\right\} \quad \Rightarrow \quad \begin{array}{c} \mu_0(\Gamma') = 1,\ \mu_1(\Gamma') = \mu_2(\Gamma') = 0 \\ \text{or} \\ \mu_0(\Gamma') = 2,\ \mu_1(\Gamma') = 1,\ \mu_2(\Gamma') = 0. \end{array}$$

The first case gives (Aa) and the second one gives (Ba). It is enough to prove at both (Aa) and (Ba) occur for suitable values of parameters. Since $\Omega \cap \{R_0 > 1\}$ is connected and both (Aa) and (Ba) occur in an open subset of $\Omega \cap \{R_0 > 1\}$, it follows that (Ca) also occurs . As we mentioned in Remark 5.2, there is at most one sink in D_1 for small values of b , γ_1 and γ_2 for the case $R_0 > 1$. Therefore the technique used in Theorem 6.1 just gives examples for the case (Aa). For this reason we give a computer assisted proof to show that (Ba) occurs too. The program used here to detect examples for the case (Ba) is a randomness method based on Remark 4.6. This program generates random points in Ω and detects those values of parameters for which $R_0 > 1$, $G(s) \neq 0$ and $\frac{F(s)}{1-s}$ has three roots with $(s, i_1, i_2) \in D$. Among 13^8 random points in Ω, three percent satisfied $R_0 > 1$ and about 300 examples for (Ba) were found. (Cf. Section 7.) This completes the proof of Theorem 6.2. □

7. Numerical Results

In this section, we present some results of our computer program which helped us to find examples of multiple equilibria for the planar system (3-1),(3-2) when $R_0 > 1$. In this case, the origin is a saddle point, hence by Lemma 3.3, there exist other rest points in $\overset{\circ}{D}$ which are known as endemic equilibria. For most of epidemiological models, it has been shown the endemic equilibrium is unique, but our computer program showed the existence of multiple equilibria i.e. two sinks and a saddle point in $\overset{\circ}{D}$. In Table 7.1., we have listed some values of parameters for which $R_0 > 1$ and multiple equilibria occurs. These values have been selected among about 300 examples obtained by the program. We have arranged the rows of the results table with respect to p assuming that $p \geq q$. In the first ten examples $p > 0.96$, hence $q < 0.04$. Therefore multiple equilibria may occur even if q is near zero. Now consider I_2 as the superspreaders in the sense of [14, 15]. We see that this small group could even change the dynamics of the epidemic process . Another interesting point is that there are two examples with $b < 0.001$.

#	p	b	ε_1	ε_2	λ_1	λ_2	γ_1	γ_2
1	0.9991	0.0275	0.2735	0.1125	0.3981	0.9196	0.0468	0.0093
2	0.9917	0.0003	0.1144	0.0537	0.5259	0.9099	0.4427	0.0014
3	0.9910	0.0155	0.6906	0.4602	0.7765	0.9834	0.0478	0.0027
4	0.9892	0.0204	0.2006	0.0780	0.5217	0.8225	0.2320	0.0065
5	0.9881	0.0120	0.4110	0.1523	0.6242	0.8968	0.2156	0.0202
6	0.9793	0.0531	0.1977	0.0357	0.3191	0.7648	0.1023	0.0106
7	0.9747	0.0228	0.4658	0.1998	0.4791	0.8001	0.0064	0.0627
8	0.9698	0.0051	0.5211	0.3589	0.5596	0.7969	0.0513	0.0072
9	0.9694	0.0284	0.4530	0.2647	0.4767	0.7510	0.0162	0.0019
10	0.9671	0.0266	0.3323	0.1945	0.4584	0.8603	0.0856	0.0030
11	0.9568	0.0124	0.5849	0.4568	0.6227	0.9144	0.0211	0.0035
12	0.9357	0.0009	0.2823	0.1099	0.4369	0.7247	0.3652	0.0150
13	0.9204	0.0028	0.6612	0.3666	0.7371	0.8693	0.1399	0.0253
14	0.9019	0.0048	0.3591	0.1872	0.4573	0.8497	0.3230	0.0140
15	0.8654	0.0020	0.5847	0.3654	0.5767	0.8744	0.1196	0.0233
16	0.8393	0.0130	0.4676	0.3011	0.4060	0.7295	0.0414	0.0208
17	0.7435	0.0019	0.6037	0.4353	0.5536	0.9610	0.2890	0.0013

Table 7.1.

The following figures are phase portraits of some of the above examples. Notice that the origin is a saddle point and there are two sinks and one saddle point in $\overset{\circ}{D}_1$ and the stable manifold of the saddle point in $\overset{\circ}{D}_1$ separates the basins of attraction of the two sinks. In these examples, one of the sinks is near the origin and the other one is far from it and near the line $\{s = 0\}$. Therefore the choice of initial values becomes very important in these examples. Unfortunately in most cases, there is little data on how infections are distributed among subgroups and we have to select an initial condition on some intuitive justification [15]. If the choice of initial distribution affects the results, then the researcher has to be extremely careful when using numerical simulations to study the epidemic process.

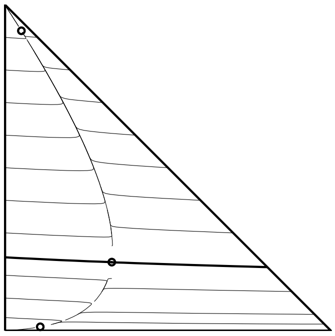

Figure 7.2. The phase portrait of #2

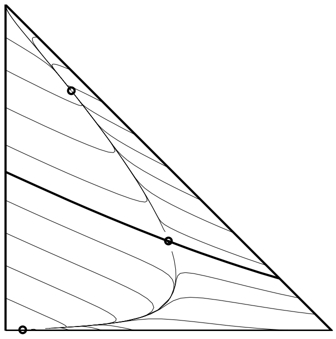

Figure 7.3. The phase portrait of #8

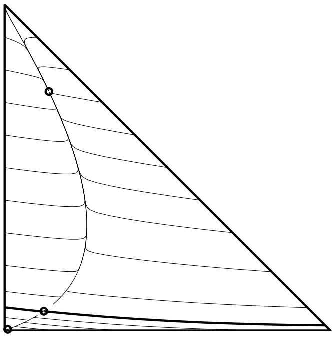

Figure 7.4. The phase portrait of #12

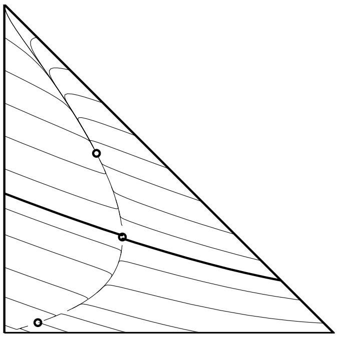

Figure 7.5. The phase portrait of #15

Concluding Remarks. Our analysis is based on two essential facts:

1. The reproduction rate $R_0 = \frac{p\lambda_1}{b+\varepsilon+\gamma_1} + \frac{q\lambda_2}{b+\varepsilon+\gamma_2}$ which governs the stability of the disease free equilibrium. This threshold clearly shows the effect of each parameter on the epidemics process. For instance in the differential infectivity model, we have a group of superspreaders, say I_2, with $\lambda_2 \gg \lambda_1$. This group may be very small with $q \ll 1$, but the assumption $\lambda_2 \gg \lambda_1$ causes the term $q\lambda_2$ to be significant in R_0 and it can force R_0 to be greater than one. In most cases, the initial condition of our population gives a point which is close to the DFE. When $R_0 > 1$, the DFE is unstable, hence the solution of our system gets far from it and tends to an endemic equilibrium. This proves the assertion of [15] that the disease is primarily spread by a small, highly infectious, group of superspreaders.
2. The existence of multiple equilibria in both cases $R_0 < 1$ and $R_0 > 1$. This does not happen in the model proposed by Hyman, Li and Stanley [14, 15]. The existence of multiple equilibria has many consequences. The most important one is that the initial conditions may also be important besides the involved parameters. This role of the initial conditions is more crucial when the population equation (2-4) is considered in the following form:
$$\frac{N'}{N} = b - d - \varepsilon_1 i_1 - \varepsilon_2 i_2.$$
To see this, suppose that a solution $(s(t), i(t), r(t))$ of the system $(2-1a)-(2-3a)$ tends to an equilibrium (s^*, i^*, r^*). If we set $R_1 = \frac{b}{d+\varepsilon_1 i_1^* + \varepsilon_2 i_2^*}$, then $N(t) \to \infty$ if $R_1 > 1$, and $N(t) \to 0$ if $R_1 < 1$. (See [3, 21] for more details.) Now each endemic equilibrium gives an R_1 and when there are two endemic equilibria, we may get different values for R_1 at these two points. This could be considered as the sensitivity of the dynamics of the epidemic to the initial distribution of infected population [15].

Acknowledgments

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