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THE DYNAMICS OF A VERTICALLY TRANSMITTED DISEASE

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Abstract. An SIRS epidemiological model for a vertically transmitted disease is discussed. We give a complete global analysis in terms of three explicit threshold parameters which respectively govern the existence and stability of an endemic proportion equilibrium, the increase of the total population and the growth of the infective population. This paper generalizes the results of Busenberg and van den Driessche.

Key words : Epidemiological model, endemic proportions, global stability, Poincaré index, threshold, vertical transmission.
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1. Introduction

In 1990, a complete global analysis of an SIRS model of disease transmission in a population with varying size was given by Busenberg and van den Driessche [4]. In an SIRS epidemiological model, we divide the population into three groups, Susceptible, Infective and Removed individuals, and the problem is to examine the behavior of the size of each group when the time goes to infinity. They considered a disease with horizontal transmission, that is a disease which is transmitted by contact between an infective and a susceptible individual. We intend to generalize their results for a vertically transmitted disease, that is a disease which is also transmitted from infective parents to their newborns. The assumption of vertical transmission has two consequences. First it causes some newborns to die and forces us to assume that the birth rate differs from one group to another. (See the demographic assumption in [3, 10, 11].) The second fact is that some newborns are infected, hence a group of newborns enter to the infective class [1, 2, 7]. We also assume that a part of these infected newborns are known and removed after their birth. We shall show that the latter parameter can play an important role in the epidemic process.

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We consider an SIRS epidemiological model for a vertically transmitted disease. In our model, the incidence function is of proportionate mixing type introduced by Nold [12]. Natural births and deaths are assumed to be proportional to the class numbers with different rates. We also assume that a proportion of the infected newborns are known and removed. We follow [4] to examine our model equation which is homogeneous of degree one. We consider the proportions system and show that this system has no periodic orbit in its feasibility region. This reduces our analysis to the discussion of existence and stability of rest points of a planar system. The technique used here to show the uniqueness of endemic equilibria is based on the Poincaré index. This technique has no hard analysis and can be easily applied to other similar systems [14, 15]. The reader can verify that our results hold for similar SIRI systems as well [8].

We first in the next section state the model and a result concerning the non-existence of certain types of solutions [5]. We consider the proportions system and prove that every solution in the feasibility region tends to a rest point of this system. In Section 3., we introduce a quadratic planar system with the same dynamics as the proportions system and then we discuss the existence and stability of rest points of this quadratic planar system. This gives a complete global analysis of the proportions system which is used to provide a global analysis of the original system is Section 4.

2. The model

In order to derive our model equations, we divide the population into three classes, the susceptible, the infective and the removed (or recovered) individuals with total numbers S, I and R respectively,. We set $N = S + I + R$ which is the total size of the population. The following parameters are used in our model equations:

b_0: per capita birth rate of susceptible individuals,
b_1: per capita birth rate of infective individuals born uninfected,
β: per capita birth rate of infective individuals born infected,
b_2: per capita birth rate of removed individuals,
d: per capita disease free death rate,
ε_1: excess per capita death rate of infected individuals,
ε_2: excess per capita death rate of removed individuals,
α: per capita removal rate of infective individuals,
γ: per capita recovery rate of removed individuals,
λ: effective per capita contact rate of infective individuals.

As mentioned before, we assume that the infected newborns enter the classes I and R of proportions β_1 and β_2 respectively, hence $\beta = \beta_1 + \beta_2$. In this paper, all the above parameters, are positive, however some of them can also

be zero. These hypotheses yield the following system of differential equation in $\mathbb{R}_3^+$, where " $'$ " denotes the derivatives with respect to t, the time.

$$\begin{cases} S' = (b_0 - d)S + b_1 I + (b_2 + \gamma)R - \lambda \dfrac{IS}{N} & (2-1) \\ I' = (\beta_1 - d - \varepsilon_1 - \alpha)I + \lambda \dfrac{IS}{N} & (2-2) \\ R' = (\beta_2 + \alpha)I - (d + \varepsilon_2 + \gamma)R & (2-3) \end{cases}$$

where $\lambda \dfrac{IS}{N}$ is of the proportionate or random mixing type [9, 12]. By adding the above three equations, the total population equation is

$$N' = b_0 S + (b_1 + \beta - \varepsilon_1)I + (b_2 - \varepsilon_2)R - dN.$$

If we consider the proportions $s = \dfrac{S}{N}$, $i = \dfrac{I}{N}$, $r = \dfrac{R}{N}$, we get the following system of equations.

$$\begin{cases} s' = b_0 s + b_1 i + (b_2 + \gamma)r - b_0 s^2 - (b_1 + \beta + \lambda - \varepsilon_1)is - (b_2 - \varepsilon_2)sr & (2-1)' \\ i' = (\beta_1 - \varepsilon_1 - \alpha)i + (\lambda - b_0)is - (b_1 + \beta - \varepsilon_1)\ i^2 - (b_2 - \varepsilon_2)\ ir & (2-2)' \\ r' = (\beta_2 + \alpha)i - (\varepsilon_2 + \gamma)r - b_0 sr - (b_1 + \beta - \varepsilon_1)ir - (b_2 - \varepsilon_2)r^2 & (2-3)' \end{cases}$$

This system is called proportions system and the feasibility region of this system is the triangle

$$D = \{(s, i, r) | s \geq 0, i \geq 0, r \geq 0, s + i + r = 1\}.$$

If we set $\Sigma = s + i + r$ then $\Sigma' = (1 - \Sigma)(b_0 s + (b_1 + \beta - \varepsilon_1)i + (b_2 - \varepsilon_2)r)$. Thus the plane $\Sigma = 1$ is invariant. Moreover, on the sides of D, we have:

$$\begin{cases} s = 0 \Rightarrow s' = b_1 i + (b_2 + \gamma)r \geq 0, \\ i = 0 \Rightarrow i' = 0 \quad \text{hence the line } \{i = 0\} \text{ is invariant,} \\ r = 0 \Rightarrow r' = (\beta_2 + \alpha)i. \end{cases}$$

Therefore, D is positively invariant. On the invariant line $\{\Sigma = 1\} \cap \{i = 0\}$, we have

$$r' = -(\varepsilon_2 + \gamma)r - b_0 r(1 - r) - (b_2 - \varepsilon_2)r^2 = -(b_0 + \varepsilon_2 + \gamma)r + (b_0 - b_2 + \varepsilon_2)r^2.$$

It follows that this invariant line contains two rest points, the Disease-Free Equilibrium $(1, 0, 0)$ and possibly another one which is outside of D. It is easy to see that the DFE attracts the side $D \cap \{i = 0\}$. Furthermore, our vector field is strictly inward on the other sides of D. Thus $\overset{\circ}{D}$, the interior of D, is positively invariant too. The following theorem reduces our problem to the discussion of existence and stability of rest points in D.

Theorem 1. *The ω-limit set of any solution for the system $(2-1)' - (2-3)'$ with initial point in D is a rest point in D.*

Proof. In [5], it's proved that such systems have no periodic orbits or phase polygons in $\overset{\circ}{D}$. Now the proof is finished by generalized Poincaré-Bendixson theorem [13]. □

3. The planar system

The proportions systems has an invariant plane $s+i+r=1$ which contains the feasibility region D, hence it is essentially two dimensional. Thus we can eliminate one of the variable to arrive at the following quadratic planar system:

$$\begin{cases} i' = (\lambda+\beta_1-b_0-\varepsilon_1-\alpha)i + (b_0+\varepsilon_1-\lambda-b_1-\beta)i^2 + (b_0+\varepsilon_2-\lambda-b_2)ir & (3-1) \\ r' = (\beta_2+\alpha)i - (b_0+\varepsilon_2+\gamma)r + (b_0+\varepsilon_1-b_1-\beta)ir + (b_0+\varepsilon_2-b_2)r^2 & (3-2) \end{cases}$$

The dynamics of the system $(2-1)'-(2-3')$ in D is equivalent to the dynamics of this planar system in the positively invariant region $D_1 = \{(i,r) : i \geq 0, r \geq 0, i+r \leq 1\}$. This quadratic system has at most four rest points and since D_1 misses a rest point on $i=0$, there are at most three rest points in D_1. One of these rest points is the origin which comes from the DFE. The matrix of the linearization of the system $(3-1),(3-2)$ at the origin is:

$$\begin{bmatrix} \lambda+\beta_1-b_0-\varepsilon_1-\alpha & 0 \\ \beta_2+\alpha & -(b_0+\varepsilon_2+\gamma) \end{bmatrix}$$

with the eigenvalues $\lambda+\beta_1-b_0-\varepsilon_1-\alpha$ and $-(b_0+\varepsilon_2+\gamma)$. Now we define the first threshold parameter $R_0 = \dfrac{\lambda+\beta_1}{b_0+\varepsilon_1+\alpha}$ which governs the stability of the origin.

Theorem 2. *The origin is globally asymptotically stable in the feasibility region D_1 when $R_0 \leq 1$ and it is a saddle point when $R_0 > 1$.*

Proof. By Theorem 1 it is enough to prove that if $R_0 \leq 1$, then the origin is the only rest point in D_1. If there exists a rest point in $\overset{\circ}{D}_1$, we have $i' = 0$ and $i \neq 0$ at this point. Thus it belongs to the line

$$(\lambda+\beta_1-b_0-\varepsilon_1-\alpha)+(b_0+\varepsilon_1-\lambda-b_1-\beta)i+(b_0+\varepsilon_2-\lambda-b_2)r = 0. \quad (3-3)$$

Since $s' = 0$ at this point, from $(2-1)'$ we obtain

$$b_0 s + b_1 i + (b_2+\gamma)r - b_0 s^2 - (b_1+\beta+\lambda-\varepsilon_1)is - (b_2-\varepsilon_2)sr = 0.$$

and by using the relation $s+i+r=1$, we can write

$$b_1 i + (b_2+\gamma)r + (b_0+\varepsilon_1-b_1-\beta-\lambda)is + (b_0+\varepsilon_2-b_2)sr = 0.$$

Multiplying (3-3) by $(-s)$ and adding it to the above expression, we get the following equality

$$b_1 i + (b_2+\gamma)r + \lambda sr + (b_0+\varepsilon_1+\alpha-\lambda-\beta_1)s = 0.$$

But the left hand side is positive when $R_0 \leq 1$ and this is a contradiction. $\square$

When $R_0 > 1$, the origin is a saddle point and it does not attract any point of $D_1 - \{i=0\}$. Thus the orbits with initial point in $D_1 - \{i=0\}$ must be

attracted by some rest points in $\overset{\circ}{D}_1$ by Theorem 1. These rest points belong to the line (3-3) and the conic section

$$r' = (\beta_2 + \alpha)i - (b_0 + \varepsilon_2 + \gamma)r + (b_0 + \varepsilon_1 - b_1 - \beta)ir + (b_0 + \varepsilon_2 - b_2)r^2 = 0.$$

It follows that there are at most two rest points in $\overset{\circ}{D}_1$. Notice that a nondegenerate rest point of the planar system is obtained by a transverse intersection of the line (3-3) and the above conic section. The following lemma has two immediate consequences which will be very helpful.

Lemma 3. *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.

$$\begin{aligned}\frac{\partial i'}{\partial i} &= (\lambda + \beta_1 - b_0 - \varepsilon_1 - \alpha) + 2(b_0 + \varepsilon_1 - \lambda - b_1 - \beta)i + (b_0 + \varepsilon_2 - \lambda - b_2)r,\\ \frac{\partial r'}{\partial r} &= -(b_0 + \varepsilon_2 + \gamma) + (b_0 + \varepsilon_1 - b_1 - \beta)i + 2(b_0 + \varepsilon_2 - b_2)r.\end{aligned}$$

From $i' = 0$ and $r' = 0$ at a rest point, we can write

$$\frac{\partial i'}{\partial i} = (b_0 + \varepsilon_1 - \lambda - b_1 - \beta)i \quad \text{and} \quad \frac{\partial r'}{\partial r} = (b_0 + \varepsilon_2 - b_2)r - (\beta_2 + \alpha)\frac{i}{r}.$$

Since $s' = b_1 i + (b_2 + \gamma)r + (b_0 + \varepsilon_1 - \lambda - b_1 - \beta)si + (b_0 + \varepsilon_2 - b_2)sr$, it follows that $(b_0 + \varepsilon_1 - \lambda - b_1 - \beta)si + (b_0 + \varepsilon_1 - \lambda - b_1 - \beta)sr < 0$ and hence $\dfrac{\partial i'}{\partial i} + \dfrac{\partial r'}{\partial r} < 0$. □

Corollary 4. *The system (3-1),(3-2) has no source point in $\overset{\circ}{D}_1$*

Corollary 5. *Every nondegenerate rest point in $\overset{\circ}{D}_1$ is hyperbolic.*

Theorem 6. *If $R_0 > 1$, then there exists a unique rest point (i^*, r^*) in $\overset{\circ}{D}_1$ which is hyperbolic and attracts $D_1 - \{i = 0\}$.*

Proof. When $R_0 > 1$, the origin is a saddle point with the unstable eigenvector

$$\begin{bmatrix} \lambda + \beta_1 - b_0 - \varepsilon_1 - \alpha + b_0 + \varepsilon_2 + \gamma \\ \beta_2 + \alpha \end{bmatrix}.$$

Since $R_0 > 1$, we have $\lambda + \beta_1 - b_0 - \varepsilon_1 - \alpha > 0$ and hence this vector belongs to the first quadrant of the plane (i, r). Since $\overset{\circ}{D}_1$ is positively invariant it follows that a branch of the unstable manifold of the origin lies in $\overset{\circ}{D}_1$. This helps us to find a piece-wise smooth Jordan curve C on which our vector field X is either tangent or inward. (See Figure 1) The Poincaré index of such a Jordan curve is 1. (See [14], Lemma 5.1.)

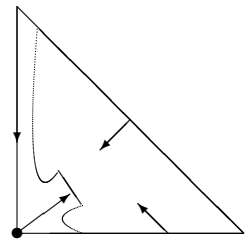

Figure 1. The Jordan curve C

We choose this Jordan curve so that it contains all rest points in $\overset{\circ}{D}_1$. If there are two rest points in $\overset{\circ}{D}_1$, they are obtain by a transverse intersection of the line (3-3) and the conic section $r' = 0$ and hence both are nondegenerate. Thus their Poincaré index must be ± 1 which contradicts $I_X(C) = 1$. Therefore there is a unique rest point in $\overset{\circ}{D}_1$ which attracts $D_1 - \{i = 0\}$ by Theorem 1. It remains to prove that this rest point is hyperbolic. Suppose the contrary, then it must be nondegenerate by Corollary 5 Thus it is obtained by a tangent (non-transverse) intersection of the line (3-3) and the conic section $r' = 0$. With a slight perturbation in γ, we will have either two transverse intersection in $\overset{\circ}{D}_1$ or nothing. (γ appears only in the coefficient of r in $r' = 0$ and does not appear in (3-3) and R_0). This is a contradiction with the uniqueness of the rest point in $\overset{\circ}{D}_1$ proven above. □

Theorem 2 and Theorem 6 provide a complete global analysis of the planar system (3-1),(3-2) in $\overset{\circ}{D}_1$. Since the dynamics of this system in $\overset{\circ}{D}_1$ is equivalent to the dynamics of proportions system $(2-1)' - (2-3)'$ in D, we have proved the following result which gives a complete global analysis of the proportions system in the feasibility region D.

Theorem 7. *Consider the proportions system* $(2-1)' - (2-3)'$.

(i) *If* $R_0 \leq 1$, *then the disease free equilibrium proportions* $(1, 0, 0)$ *is globally asymptotically stable in* D.

(ii) *If* $R_0 > 1$, *then there is a unique rest point* (s^*, i^*, r^*) *which is globally asymptotically stable in* $D - \{i = 0\}$.

4. Analysis of the model equations

Consider the original model equation (2-1)-(2-3) and recall that the population equation is $N' = b_0 S + (b_1 + \beta - \varepsilon_1)I + (b_2 - \varepsilon_2)R - dN$. Thus

$$\frac{N'}{N} = b_0 s + (b_1 + \beta - \varepsilon_1)i + (b_2 - \varepsilon_2)r - d. \qquad (4-1)$$

If $R_0 \leq 1$, then $(s,i,r) \longrightarrow (1,0,0)$ by Theorem 7, hence $\dfrac{N'}{N} \longrightarrow b_0 - d$. Moreover if $R_0 > 1$ and $I > 0$, then $(s,i,r) \longrightarrow (s^*,i^*,r^*)$, i.e. the unique rest point in $\overset{\circ}{D}_1$, and

$$\frac{N'}{N} \longrightarrow b_0 s^* + (b_1 + \beta - \varepsilon)i^* + (b_2 - \varepsilon_2)r^* - d.$$

We define the second threshold parameter which governs the total population as follows.

$$R_1 = \begin{cases} \dfrac{b_0}{d} & \text{if } R_0 \leq 1, \\ \dfrac{b_0 s^* + (b_1+\beta)i^* + b_2 r^*}{d + \varepsilon_1 i^* + \varepsilon_2 r^*} & \text{if } R_0 > 1. \end{cases}$$

Since $I = 0$ is invariant with a linear equation, we may assume that $I > 0$. Now from (2-2), we write

$$\frac{I'}{I} = (\beta_1 - d - \varepsilon_1 - \alpha) + \lambda s. \qquad (4-2)$$

If $R_0 \leq 1$, then $\dfrac{I'}{I} \longrightarrow \beta_1 - d - \varepsilon_1 - \alpha + \lambda$ and if $R_0 > 1$, $\dfrac{I'}{I} \longrightarrow \beta_1 - d - \varepsilon_1 - \alpha + \lambda s^*$. So we define the third threshold parameter which governs the total number of infective individuals.

$$R_2 = \begin{cases} \dfrac{\beta_1 + \lambda}{d + \varepsilon_1 + \alpha} & \text{if } R_0 \leq 1, \\ \dfrac{\beta_1 + \lambda s^*}{d + \varepsilon_1 + \alpha} & \text{if } R_0 > 1. \end{cases}$$

Notice that d does not appear in the proportions system and hence (s^*,i^*,r^*) is independent of d. The following results provide a rather complete global analysis of the model equations (2-1)-(2-3).

Lemma 8. *If $I(t) \leq M$ for every $t \geq t_0$, then $R(t) \longrightarrow 0$ and if $I(t) \longrightarrow \infty$, then $R(t) \longrightarrow \infty$.*

Proof. From (2-3), we have $R'(t) = (\beta_2+\alpha)I(t) - (d+\varepsilon_2+\gamma)R(t)$. If $I(t) \leq M$ for $t \geq t_0$, then $R'(t) \leq M(\beta_2+\alpha) - (d+\varepsilon_2+\gamma)R(t)$ and by Gronwall's inequality [13], $R(t) \leq M(\beta_2+\alpha)e^{-(d+\varepsilon_2+\gamma)(t-t_0)}$ which follows that $R(t) \longrightarrow 0$. Now suppose that $I(t) \longrightarrow \infty$. Then by (2-3), we have $R'(t) + (d + \varepsilon_2 + \gamma)R(t) = (\beta_2+\alpha)I(t)$ which implies that $\dfrac{d}{dt}(R(t)e^{(d+\varepsilon_2+\gamma)t}) = (\beta_2 + \alpha)I(t)e^{(d+\varepsilon_2+\gamma)t}$. For every $M \in \mathbb{R}^+$, there is a $t_0 \in \mathbb{R}$ such that $I(t) > M$ for $t > t_0$. Thus

$$(R(t) - R(t_0))e^{(d+\varepsilon_2+\gamma)t} = \int_{t_0}^{t} (\beta_2+\alpha)I(t)e^{(d+\varepsilon_2+\gamma)t} > M(\beta_2+\alpha)\int_{t_0}^{t} e^{(d+\varepsilon_2+\gamma)t}dt.$$

$$\Rightarrow R(t) > \left(R(t_0) - \frac{M(\beta_2+\alpha)}{d+\varepsilon_2+\gamma}\right) e^{-(d+\varepsilon_2+\gamma)(t-t_0)} + \frac{M(\beta_2+\alpha)}{d+\varepsilon_2+\gamma}.$$

Since $e^{-(d+\varepsilon_2+\gamma)(t-t_0)}$ goes to zero as $t \longrightarrow \infty$, $R(t) > \dfrac{M(\beta_2+\alpha)}{2(d+\varepsilon_2+\gamma)}$ for large values of t. It means that $R(t) \longrightarrow \infty$. □

Theorem 9. *(i) If $R_1 > 1$, then $N(t) \longrightarrow \infty$ and if $R_1 < 1$, then $N(t) \longrightarrow 0$. (ii) If $R_2 > 1$, then $(I(t), R(t)) \longrightarrow (\infty, \infty)$ and if $R_2 < 1$, then $(I(t), R(t)) \longrightarrow (0, 0)$.*

Proof. First suppose that $R_0 \leq 1$ which implies that $(s, i, r) \longrightarrow (1, 0, 0)$ by Theorem 7. Thus $\dfrac{N'}{N} \longrightarrow b - d$ by (4-1) and $\dfrac{I'}{I} \longrightarrow \beta_1 - d - \varepsilon_1 - \alpha + \lambda$ by (4-2). If $R_1 < 1$, then $b - d < 0$, hence $N(t) \longrightarrow 0$. Similarly if $R_1 > 1$, then $b-d > 0$, hence $N(t) \longrightarrow 0$. Furthermore If $R_2 < 1$, then $B_1-d-\varepsilon_1-\alpha+\lambda < 0$, hence $I(t) \longrightarrow 0$ and by the above lemma $R(t) \longrightarrow 0$. Similarly if $R_2 > 1$, then $\beta_1 - d - \varepsilon_1 - \alpha + \lambda > 0$, hence $I(t) \longrightarrow \infty$ and by the above lemma $R(t) \longrightarrow \infty$.

Now suppose that $R_0 > 1$. We assumed that $I(t) > 0$, hence $i > 0$ and $(s, i, r) \longrightarrow (s^*, i^*, r^*)$ by Theorem 7. Thus $\dfrac{N'}{N} \longrightarrow b_0 s^* + (b_1 + \beta - \varepsilon_1) i^* + (b_2 - \varepsilon_2) r^* - d$ which is positive if $R_1 > 1$, hence $N(t) \longrightarrow \infty$ and negative if $R_1 < 1$, hence $N(t) \longrightarrow 0$. Moreover $\dfrac{I'}{I} \longrightarrow (\beta_1 - d - \varepsilon_1 - \alpha) + \lambda s^*$ which is positive if $R_2 > 1$, hence $I(t) \longrightarrow \infty$ and then $R(t) \longrightarrow \infty$ by the above lemma. Similarly $\beta_1 - d\varepsilon_1 - \alpha + \lambda s^* < 0$ if $R_2 < 1$ and then $(I(t), R(t)) \longrightarrow (0, 0)$. □

5. Conclusion

In order to give a complete global analysis of our system, we defined three threshold parameters R_0, R_1 and R_2 and the results are summarized in the following table which is the same as Table 1. in [4].

R_0	R_1	R_2	$N \longrightarrow$	$(s, i, r) \longrightarrow$	$(S, I, R) \longrightarrow$
≤ 1	< 1	$< 1^\alpha$	0	$(1, 0, 0)$	$(0, 0, 0)$
> 1	< 1	$< 1^\alpha$	0	(s^*, i^*, r^*)	$(0, 0, 0)$
≤ 1	> 1	< 1	∞	$(1, 0, 0)$	$(\infty, 0, 0)$
≤ 1	> 1	> 1	∞	$(1, 0, 0)$	(∞, ∞, ∞)
> 1	> 1	$> 1^\alpha$	∞	(s^*, i^*, r)	(∞, ∞, ∞)

$^\alpha$ Given R_0 and R_1, this condition is automatically satisfied.

Now we make some comparison between the results in [4] and the above results.

1. If we set $b_0 = b_1 = b_2 = b$ and $\beta_1 = \beta_2 = \beta = 0$ in the system (2-1)-(2-3), we obtain the system (2-1)-(2-3) in [4]. Moreover by these assumptions, we get the same threshold parameters as in [4].

2. Comparing their threshold parameters with our ones, we see that the effect of b_0, b_1 and b_2 appears more clearly instead of b. For example when $R_0 > 1$, our R_1 is $\frac{b_0 s^* + (b_1+\beta) i^* + b_2 r^*}{d+\varepsilon_1 i^* + \varepsilon_2 r^*}$, but they obtain $R_1 = \frac{b}{d+\varepsilon_1 i^* + \varepsilon_2 r^*}$ in which the effects of b_0, b_1 and b_2 are hidden in b.

3. There are two vertical transmission parameter, β_1 and β_1, in our model. The effect of β_1 in R_0 and R_2 is crucial. Since $\beta_1 + \beta_2 = \beta$, we can decrease β_1 by increasing β_2. Therefore removing more infected newborns causes more safe situation.

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