PHENOMENOLOGICAL STUDY OF BACKWARD BIFURCATION IN EPIDEMIOLOGICAL MODELS

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Abstract

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ABSTRACT submitted by **Manuhwa Byron** for the Degree of MSc in Mathematics and entitled **PHENOMENOLOGICAL STUDY OF BACKWARD BIFURCATION IN EPIDEMIOLOGICAL MODELS**
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This thesis is about the phenomenological study of bifurcations in epidemiological models, in particular, in backward bifurcation. We consider models that exhibit such bifurcation and also consider the factors that cause them. In order to make the reader understand backward bifurcation, we first consider transcritical bifurcation and show how it is related to backward bifurcation. We consider our own examples to show these bifurcations and strengthen the cases of occurrence of such bifurcation for certain range of parameters.

Declaration

No portion of the work referred to in this thesis has been submitted in support of an application for another degree or qualification of this or any other university or other institution of learning.

Dedication

I dedicate this thesis to the Lord God Almighty who made this project possible. He continues to guide my footsteps. I also dedicate this project to men and women who were inspired by the Holy Spirit to guide and advise me. Thank you Lord.

Acknowledgements

I would like to thank the N.U.S.T. (National University of Science and Technology) epidemiological disease study group and work team for their excellent support in the development of this thesis. Of particular thanks, is Zindoga Mukandavire who helped me with the numerical analysis and especially in coding mathematical programs in C++. Without these programs, we would not have obtained any good results. I also thank Dr W. G. Garira who guided me in this thesis. To my other international colleagues and advisors such as Pauline Van Den Driessche and Herbert Hethcote, I say thank you so much.

Chapter 1

Introduction

A *bifurcation* is the qualitative change of flow as the parameters of a system are varied. In particular, fixed points can be created or destroyed, or their stability can change [7]. The parameter values at which they occur are called *bifurcation points*. Bifurcations are important, as they provide models of *transitions* and *instabilities* as some *control parameter* is varied [7].

Different types of bifurcations have been observed to occur in epidemiological models. The epidemiological models include the SI, SIS and SIR models, where S are the susceptible class, I, the infective class, and R, the recovered or removed class and the bifurcations include the transcritical (*forward*), subcritical (*backward*) and hopf bifurcations. The most common control *threshold* parameter in these models is the basic reproduction number, R_0, defined as the number of secondary infections produced by an infected individual in a susceptible population [1]. It is arguably the most important quantity in the study of epidemics and notably in comparing population dynamical effects of control strategies [1] and is treated as a bifurcation parameter so that the bifurcation usually occurs at $R_0 = 1$. This is true in the case of forward bifurcation. The forward bifurcation exhibits an absence of positive equilibria near the disease-free equilibrium when $R_0 < 1$, and a low level of endemicity when R_0 is slightly above one. This is biologically meaningful and means that introduction of an infection for $R_0 \leq 1$ will result in the dying out of the infection, that is the infectives decrease to zero, and the susceptibles increase to a steady equilibrium state. Conversely, introduction

of an infection for $R_0 > 1$ will result in the infection rising and eventually reaching a steady endemic equilibrium. Thus the disease-free equilibrium is stable for $R_0 \leq 1$, and unstable for $R_0 > 1$, whilst the reverse occurs for the endemic equilibrium. However, study of more complicated epidemiological models has shown behaviors that diverge from this classic threshold behavior.

Backward bifurcations have recently received much attention due to the adaptation, continual evolution of infectious agents, drug resistant infection and the re-emergence of diseases. In particular, the increased re-activation of re-emergence of tuberculosis due to the human immuno-deficiency syndrome (HIV) has drawn a lot of attention recently. Expectedly, other biological factors such as immigration may influence backward bifurcation. In addition to exhibiting qualities of a forward bifurcation, that is a stable disease-free equilibrium for $0 \leq R_0 < 1$ and a stable endemic equilibrium for $R_0 > 1$, there is a coexistence of the two qualitatively different states for some parameter values $0 < R_0 < 1$. Backward bifurcations also allow multiple stable states with fixed parameters [6]. Further, small changes in parameter values, may result in large changes in equilibrium behavior. Biologically, this means that once R_0 crosses one, the disease can invade to a relatively high endemic level, and further reducing it to below one will not necessarily make the disease disappear. Therefore the presence of backward bifurcation in epidemiology has serious biological and mathematical consequences; in particular, it may be possible for a disease to persist under conditions which would otherwise preclude an invasion of disease.

Several epidemiological models that exhibit bifurcations have been studied. Lajmanovich and York considered an SIS model and showed that the disease-free equilibrium is globally stable for $R_0 \leq 1$ and that a *unique* globally stable endemic equilibrium exists for $R_0 > 1$, exhibiting a forward bifurcation. Other examples of models considered which exhibit forward bifurcations are in [1] and [17]. With this kind of bifurcation, in the case of disease control, in order to eradicate an already established infection, reducing the reproduction number R_0 to below one suffices. This is not so with the backward bifurcation.

Dushoff and Huang studied the backward bifurcation and catastrophe in a simple SI model in [6], Huang *et al* considered a multi-group model for dynamics o f HIV/AIDS transmission in [11]. Backward bifurcation of endemic equilibria occurs as a result of the incorporation of several groups of susceptible, or infective In terms of disease control, merely reducing the reproduction number R_0 to below one does not suffice in eradication of an infection, therefore another control strategy has to be implementated.

Individuals with different susceptibilities or infective rates to the disease [13]. Replacing standard incidence by a power law also leads to backward bifurcation. In this thesis we study the backward bifurcations and phenomena that influence or cause these bifurcations in epidemiological models. More precisely, we consider epidemiological models that result in the backward bifurcation. We digress a bit in the next chapter and show how we obtain forward bifurcation. This we believe is a prerequisite into understanding the backward bifurcation and its relation to the forward bifurcation. We will review the models studied by Hethcote [5], Dushoff [6] and Martcheva and Thieme [13] and also use various bifurcation techniques to show existence of backward bifurcations. We use different examples in these epidemiological models, and interpret our results. In the last chapter we do not consider numerical analysis due to time constraints.

1.1 Project layout

We begin by introducing a simple SIR model in chapter 2 and show how we obtain the threshold parameter R_0. We then show its relation to the forward bifurcation. In chapters 3 and 4 we show how backward bifurcation occurs as a result of incorporation of several groups with different susceptibilities, of infectiveness. We also discuss how varying certain parameters influence backward or forward bifurcation. In the case of chapter 3, we have one large susceptible class. We also include numerical analyses to validate our results. In chapter 5 we include vaccination and immigration in an SIS model and show their connection to backward bifurcation. In chapter 6, we deal with the concept of super-infection in a non-linear continuous model studied in [13]. We however show the role of

super-infection on backward bifurcation.

In each chapter therefore we will have an introduction to the chapter, a clear statement of the model, model analysis and a brief discussion.

Chapter 2

Forward bifurcation in an SIR model

2.1 Introduction

The simple SIS model has been studied in [4], and exhibits forward bifurcation. It was modelled by Kermack and Mckendrick(1932) who were perhaps the first to notice forward bifurcation behavior in an epidemiological model [6]. This model therefore shows the classical threshold behavior. We aim to obtain the threshold parameter R_0, and show how a forward bifurcation is related to it, by use of a simple SIR model. We also show that in a simple SIR model where the immigration (noted by births only) in the model is equal to removal rate (death in this case), we obtain forward bifurcation. We consider the SIR model with vital dynamics.

A parameter associated with the reproductive number is the contact number, σ, and is defined as the average number of adequate contacts of a typical infective during the infectious period [1]. Though many models are silent about this parameter, we use it in our model. The contact number σ remains constant as the infection spreads, so it is always equal to the basic reproduction number R_0, and thus can be used interchangeably with R_0. Thus

$$R_0 \geq \sigma$$

with equality of the two quantities at the times of invasion. Note that $R_0 = \sigma$ for most models, and $\sigma > R$ after the invasion for all models, where R is the replacement number defined as the actual number of secondary infections produced by a typical infective during the entire period of infectiousness.

2.2 The model

In this model, we divide the population into the susceptible, infectives and recovered classes. We assume that individuals move from the susceptible class to the infective then later to the recovered class. We introduce parameters of the model as;

$I(t)$ = number of infectives at time t th j Td d Tj Tj ψTd ψTp $lThe$ n ψ ψ m ij

infectives. Since β is assumed to be the average number of adequate contacts,(i.e. contacts adequate for transmission) of a person per unit time, then $\frac{\beta I}{N} = \beta i$ is the average number of contacts with infectives per unit time of one susceptible, and $\frac{\beta I}{N} S = \beta si$ is the number of new cases per unit time due to the susceptibles $S = Ns$.

We now formulate the model. We have

$$\begin{aligned} \frac{dS}{dt} &= -\beta SI + \mu(N - S) & S(0) = S_0 \geq 0 \\ \frac{dI}{dt} &= \beta SI - (\mu + \nu)I & I(0) = I_0 \geq 0 \\ \frac{dR}{dt} &= \nu I - \mu R & R(0) = R_0 \geq 0 \end{aligned} \tag{2.1}$$

where $S(t) + I(t) + R(t) = N$

$s(t) = \frac{S(t)}{N}$, $i(t) = \frac{I(t)}{N}$, and $r(t) = \frac{R(t)}{N}$ are fractions of the susceptibles, infectives, and recovered respectively.

Dimensionalizing (2.1) gives

$$\begin{aligned} \frac{ds}{dt} &= -\beta si + \mu(1 - s) & s(0) = s_0 \geq 0 \\ \frac{di}{dt} &= \beta si - (\mu + \nu)i & i(0) = i_0 \geq 0 \\ \frac{dr}{dt} &= \nu i - \mu r & r(0) = r_0 \geq 0 \end{aligned} \tag{2.2}$$

Before we go any further we simplify (2.2). Because the first two equations in (2.1) are independent of the third one and its dynamic behavior is trivial when $I(0) = 0$ for some $t > 0$, it suffices to consider the first two equations with $I > 0$. Thus we restrict our attention to the following reduced model:

$$\begin{aligned} \frac{ds}{dt} &= -\beta si + \mu(1 - s) & s(0) = s_0 \geq 0 \\ \frac{di}{dt} &= \beta si - (\mu + \nu)i & i(0) = i_0 \geq 0 \end{aligned} \tag{2.3}$$

with $r(t) = 1 - s(t) - i(t)$. The triangle T in the si plane is given by

$$T = \{(s, i) \mid s \geq 0, i \geq 0, s + i \leq 1\}$$

and is positively invariant and unique for all positive time, thus the model is mathematically and epidemiologically well posed [1]. This epidemiological model is well posed because unique solutions exist in T and for given initial conditions, solutions starting in T exist, are unique and stay in T. The contact number σ remains equal to the basic reproduction number R_0 for all time, hence no new classes of infectives occur after the invasion.

2.3 Equilibrium points

From equations in (2.3) we want to find equilibrium points. We thus equate the equations in (2.3) to zero and find the fixed points. We have

$$\begin{aligned}
\frac{ds}{dt} &= -\beta s^* i^* + \mu(1 - s^*) = 0 \\
\frac{di}{dt} &= \beta s^* i^* - (\mu + \nu) i^* = 0 \\
\text{then} \quad & -\beta s^* i^* + \mu(1 - s^*) = 0 \\
\frac{di}{dt} &= \beta s^* i^* - (\mu + \nu) i^* = 0
\end{aligned}$$

thus

$$i^*[\beta s^* - (\nu + \mu)] = 0 \tag{2.4}$$

implying that $i^* = 0$ or $[\beta s^* - (\nu + \mu)] = 0$

For the latter equilibrium point we get that

$$s^* = \frac{(\nu + \mu)}{\beta}$$

Making i^* subject of the formula in (2.4) and substituting the value of s^* we get

$$\begin{aligned} i^* &= \frac{\mu(1-s^*)}{\beta s^*} \\ &= \frac{\mu(\frac{1}{s^*}-1)}{\beta} \end{aligned} \tag{2.5}$$

Therefore we have two values for i^*; that is $i^* = 0$, and $i^* = \frac{\mu(1-s^*)}{\beta s^*}$ and one for s^* as given above. We therefore interpret the fixed point at $i^* = 0$ as the disease-free equilibrium point, and denote the disease-free equilibrium point as $P_0(s_{df}, i_{df})$. Since $s(t) = 1 - i(t) - r(t)$, where $r(t)$ at time $t = 0$ is equal to zero, i.e. $r(0) = 0$, we have $s(0) = 1$. The fixed point at the disease-free equilibrium point therefore is given by $P_0(s_{df}, i_{df}) = (1, 0)$. We have $r(0) = 0$ because at the beginning of the endemic, there are no infectives, thus no recovered individuals. The other equilibrium point at $i^* = \frac{\mu(1-s^*)}{\beta s^*}$ is a point where the infection has been introduced in the population, thus will be interpreted as the endemic equilibrium point. We will denote this by $P_e(s_e, i_e)$. We expect that $r(t) > 0$, since the disease does not cause deaths.
$P_e(s_e, i_e) = (\frac{(\nu+\mu)}{\beta}, \frac{\mu(\frac{1}{s^*}-1)}{\beta})$. We now want to determine the stability of the system of equations in (2.3) so we linearize the equations.

2.4 Stability Analysis

We consider the Jacobian matrix method for (2.3). The Jacobian of the linearized system (2.3) at a general point (s^*, i^*) is given as :

$$J_{(s^*,i^*)} = \begin{pmatrix} -\beta i^* - \mu & -\beta s^* \\ \beta i^* & \beta s^* - (\mu + \nu) \end{pmatrix} \tag{2.6}$$

we continue to analyze the equilibrium points.

2.4.1 Disease-free equilibrium

We will first transform the fixed points to the origin via the relevant translation coordinates. Introducing translation coordinates in (2.3):

Let

$$s_1 = s^* - 1 \quad \text{, and} \quad i_1 = i^*$$
$$\frac{ds}{dt} = \frac{ds_1}{dt} \quad , \frac{di}{dt} = \frac{di_1}{dt}$$

Then

$$\begin{aligned} \dot{s_1} &= -\beta s^* i^* + \mu s^* \\ &= -\beta(s_1+1)i_1 + \mu(1-(s_1+1)) \\ &= -\beta s_1 i_1 - \beta i_1 - \mu s_1 \end{aligned}$$

and also

$$\begin{aligned} \dot{i_1} &= \beta s^* i^* - (\mu+\nu)i_1 \\ &= \beta(1+s_1)(i_1) - (\mu+\nu)I_1 \\ &= \beta i_1 + \beta s_1 i_1 - (\mu+\nu)i_1 \\ &= \beta s_1 i_1 + [\beta - (\mu+\nu)]i_1 \end{aligned}$$

The linear system becomes:

$$\begin{pmatrix} \dot{s}_1 \\ \dot{i}_1 \end{pmatrix} = \begin{pmatrix} -\beta i_1 - \mu & -\beta(1+s_1) \\ \beta i_1 & \beta - (\mu+\nu) \end{pmatrix} \begin{pmatrix} s_1 \\ i_1 \end{pmatrix} \tag{2.7}$$

To get the characteristic equation;

$$det[J - \lambda I] = \begin{vmatrix} \beta i_1 - \mu - \lambda & -\beta(1+s_1) \\ \beta i_1 & \beta - (\mu+\nu) - \lambda \end{vmatrix} = 0 \tag{2.8}$$

Evaluating (2.8) at $P_0(s_{df}, i_{df}) = (1, 0)$

$$\begin{vmatrix} -\mu - \lambda & -\beta(1+s_1) \\ 0 & \beta - (\mu+\nu) - \lambda \end{vmatrix} = 0 \tag{2.9}$$

The characteristic equation becomes :

$$\lambda^2 + \lambda(\mu + (\nu+\mu) - \beta) + \mu((\nu+\mu) - \beta) \tag{2.10}$$

Clearly $\lambda_1 = -\mu < 0, \quad \lambda_2 = \beta - (\nu + \mu) < 0$ if $\beta < (\nu + \mu)$.

In order for the equilibrium point $P_o(s_{df}, i_{df})$ to be asymptotically stable, both λ_1, and λ_2 must be less than zero (negative). This implies that a small population of infectives once introduced into the system of equations would not cause persistent infection. However, if $\lambda_2 > 0$ (since λ_1 is always negative), the equilibrium point becomes unstable and introduction of infectives results in persistent infection(*endemic infection*). We, from λ_2, conclude that asymptotic stability exists for $\frac{\beta}{(\mu+\nu)} = R_0 < 1$. By the Hurwitz criteria, $tr(J) < 0$ for $\beta < (\mu + \gamma)$, hence the system is asymptotically stable. Note that in this model the reproductive number R_0 is obtained from the dominant eigenvalue of the Jacobian matrix which is $\lambda_2 = \beta - (\mu + \nu)$. Equating λ to zero (*to get* R_0), we get, R_0 as

$$R_0 = \frac{\beta}{(\mu + \nu)}$$

The contact number σ remains equal to the basic reproduction number R_0 for all time because no new class of susceptibles and of infectives is introduced after the invasion of the infection. We then can write i^* in terms of R_0 as $i^* = \frac{\mu(\sigma-1)}{\beta}$.

Since, for $\lambda_2 < 0$ the system (2.3) is asymptotically stable, we have $\beta-(\nu+\mu) < 1$. This results in $\frac{\beta}{(\nu+\mu)} < 1$ hence $R_0 < 1$ hence the following;

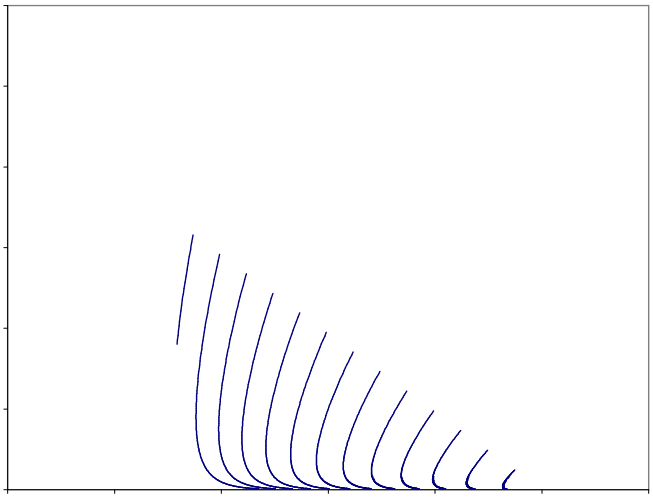
Proposition 1. *The system (2.3) is asymptotically stable for* $\lambda_2 < 0$ *, where* $\beta - (\nu + \mu) < 1$.

Once asymptotical stability has been ascertained (by Proposition 1), it does not necessarily follow that the system (2.3) will be globally stable. We deduce global stability by using the lyapunov function

$$\begin{aligned} V(s,i) &= \frac{s_1^2 + i_1^2}{2} \\ \dot{V}(s,i) &= s_1 + i_1 \end{aligned} \tag{2.11}$$

and observe that $V(0,0) = 0$ and $\dot{V}(s,i) = s_1 + i_1 > 0$ in any neighborhood of $(0,0)$. Then $(0,0)$ is globally stable for $\varepsilon < 0$.

Figure 2.1 illustrates the stability of the system for $R_0 < 1$, for the given parameters. The phase portrait shows the infectives being introduced at $s + i = 1$. The infectives rate reduces rapidly at first, then slows down to a steady equilibrium of zero.



At this point, $R_0 > 1$ which implies that $\lambda_1, \lambda_2 > 0$. From the characteristic equation the real part of both eigenvalues is negative when

$$\mu(\nu + \mu)(\sigma - 1) > 0$$

, since $\mu > 0$, and $\sigma > 0$. Hence the endemic equilibrium $P_e(s_e, i_e) = (\frac{1}{\sigma}, \frac{\mu(\sigma-1)}{\beta})$ is asymptotically stable.

All the initial points are in the first quadrant because s and i represents population proportions and are therefore nonnegative. We note that the endemic equilibrium exists for $R_0 < 1$ but is unimportant as it does not exist within the triangle T.

Let $s_2 = s^* - (\mu + \nu)/\beta$, and $i_2 = i^* - \mu(\sigma - 1)/\beta$
Then

$$\begin{aligned}
\dot{s}_2 &= -\beta s^* i^* + \mu(1 - s^*) \\
&= -\beta\left(s_2 + \frac{\nu + \mu}{\beta}\right)\left(i_2 + \frac{\mu(\sigma - 1)}{\beta}\right) + \mu\left(1 - s_2 - \frac{(\nu + \mu)}{\beta}\right) \\
&= -\beta s_2 i_2 + \mu(1 - s_2) - (\nu + \mu)i_2 - \mu\frac{(\sigma - 1)(\nu + \mu)}{\beta} - s_2\mu(\sigma - 1) \\
&\quad -\mu\frac{(\nu + \mu)}{\beta} \\
&= -\beta s_2 i_2 - \mu(\sigma - 1)s_2 - (\nu + \mu)i_2 - \mu(\frac{(\sigma - 1)}{\sigma}) + \mu(1 - s_2) - \mu s_2 \\
&= -\beta s_2 i_2 - \mu\sigma s_2 - (\nu + \mu)s_2
\end{aligned}$$

and

$$\begin{aligned}
\dot{i}_2 &= \beta s^* i^* - (\nu + \mu)i^* \\
&= \beta(s^* - \frac{(\mu + \nu)}{\beta}\frac{(i^* - \mu(\sigma - 1)}{\beta} \\
&= \beta s_2 i_2 + \mu(\sigma - 1)s_2
\end{aligned}$$

Upon linearizing, we get the Jacobian

$$\begin{vmatrix} -\beta i_2 - \mu\sigma - \lambda & -\beta s_2 - (\nu + \mu) \\ \beta i_2 + \mu(\sigma - 1) & \beta s_2 - \lambda \end{vmatrix} = 0$$

thereby getting the characteristic equation as

$$\lambda^2 + \lambda(\beta(i_2 - s_2) + \mu\sigma) + \beta(\gamma i_2 + \mu(i_2 - s_2)) + \mu(\nu + \mu)(\sigma - 1) = 0 \qquad (2.14)$$

Thus

$$\lambda_{1,2} = \frac{-(\beta(i_2 - s_2) + \mu\sigma)\sqrt{(\beta(i_2 - s_2) + \mu\sigma)^2 - 4(\beta(\nu i_2 + \mu(i_2 - s_2)) + \mu(\nu + \mu)(\sigma - 1)}}{2}$$

We note that there is a clear relationship between i_2 and s_2. Recall that $\sigma > 0$, $\mu > 0$, $\beta > 0$ and also $i_2 > 0$ and $s_2 > 0$. We vary the values of the parameters including i_2 and s_2. Since the real part of the quadratic formula is negative for $i_2 \geq s_2$, the endemic equilibrium is asymptotically stable. Choosing the same lyapunov function as before (equation (2.11)), we find that the endemic equilibrium point is globally stable. We also note that for $s_2 > i_2$, this point becomes unstable. Therefore the endemic point is unstable for $R_0 = \sigma \leq 1$.

Regardless of whether or not R_0 can be calculated explicitly, its role on the study of the stability of the equilibria can still be determined. Most reasonable epidemic models support at least two equilibria: a disease-free equilibrium, and a positive (stable) endemic equilibrium. For $R_0 < 1$ the disease-free equilibrium is the only equilibrium that is stable. For $R_0 > 1$ the endemic equilibrium is stable.

Figure 2.2 shows the introduction of infection for $R_0 > 1$ with the indicated parameters. As seen the infection rates increase slowly, then decrease rapidly to an endemic steady state P_e. The susceptiles also decrease as the infectives increase, and increase slowly so as to finally reach a steady endemic state.

We expect that a bifurcation occurs at $R_0 = 1$, which has the characteristics of a *forward* or *transcritical* bifurcation. At this point asymptotical stability is

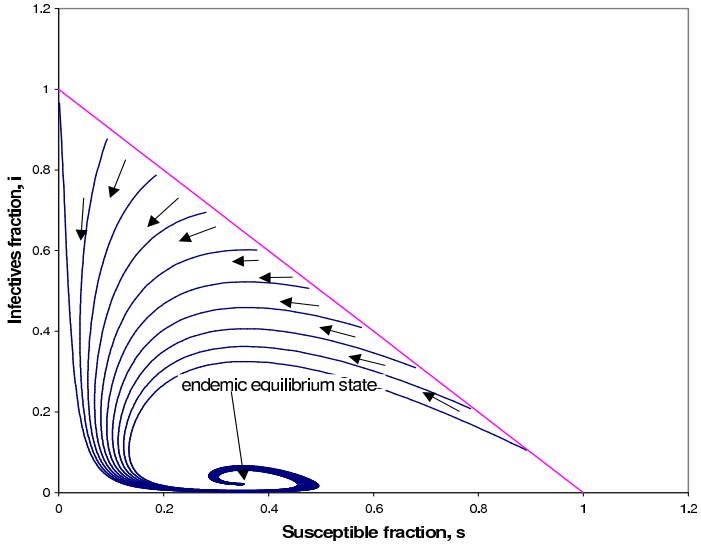


Figure 2.2: Phase plane portrait for the classic SIR endemic model with contact number $\sigma = 3$, average infectious period $1/\nu = 3$ and average lifetime $1/\mu = 60$ days in the si phase plane. This short period of time has been chosen so that the endemic equilibrium is clearly above the horizontal axis and the spiraling into the endemic equilibrium can be seen.

transferred from the infectious-free state to the new(emerging) endemic (positive) equilibria.

We investigate the occurrence of bifurcations in this model in the next section

2.5 Bifurcation Analysis

We describe a transcritical bifurcation. This is a basic mechanism by which fixed points change stability as some parameter is varied. In the diagrams below, σ is the bifurcation parameter that is being varied. Figures 2.3, figure 2.4 and figure 2.5 show the stability of the fixed points a and b when σ is varied. For $0 < \sigma < 1$, the fixed point a is stable while, b is unstable. For $\sigma = 0$ there is one fixed point a which is stable, and for $\sigma > 1$ a is unstable, and b stable. These scenarios are shown in figures 2.4, figure 2.5 and figure 2.3 respectively

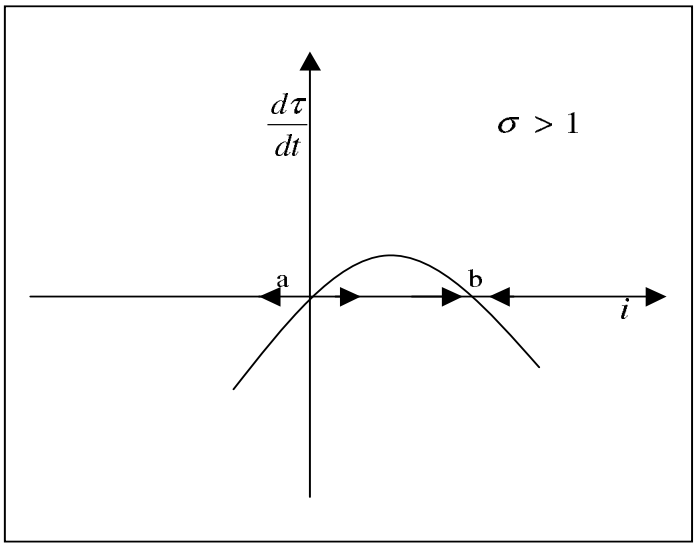


Figure 2.3: The schematic diagram of $d\tau/dt$ and i when $\sigma > 1$. This graph shows that the fixed point a=0 is unstable and b $= 1 - 1/\sigma$ is stable.

2.5.1 Analytic approach to bifurcation

We consider the following equation from (2.3)

$$\frac{di}{dt} = \beta si - (\mu + \nu)i \tag{2.15}$$

We consider the change in stability of (2.3) as R_0 varies. Expressing the above equation in terms of R_0, we get:

$$\begin{aligned}
\frac{di}{dt} &= \beta si - (\nu + \mu)i \\
&= \beta si - (\nu + \mu)(\beta/(\nu + \mu))i \underbrace{((\nu + \mu)/\beta)}_{=1/\sigma} \\
&= \beta si - \beta i/\sigma \\
&= \beta(si - i/\sigma)
\end{aligned}$$

since we have $s + i \leq 1$ then for the triangle T , $s \leq 1 - i$.
Substitute $s = 1 - i$ in (6). We get,

$$\frac{di}{dt} = \beta(i(1 - i) - i/\sigma) \tag{2.16}$$

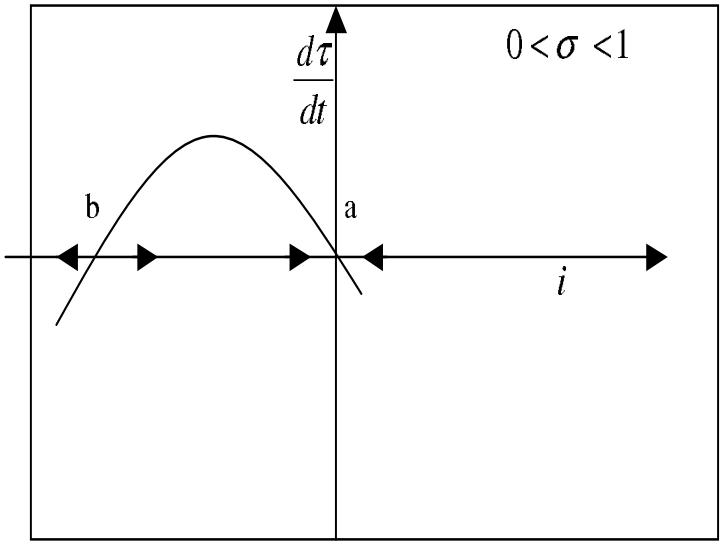


Figure 2.4: The schematic diagram of $d\tau/dt$ and i when $0 < \sigma < 1$. This graph shows that the fixed point a=0 is stable and b $= 1 - 1/\sigma$ is unstable.

we see that

$$\beta = 0 \qquad \text{or} \qquad i(1-i) - i/\sigma = 0$$

Thus $\beta = 0$ or $i(1-i) = \frac{i}{\sigma}$, implying that $i = 0$ or $i = 1 - i$.
These fixed points are shown in the figure plotted below. Hence we see that for $\sigma < 0$ there are two fixed points, $i = 0$ is stable and $i < 0$ unstable. These two fixed points coalesce at $\sigma = 1$ and for $\sigma > 1$, $i = 0$ is unstable and $i = 1 - 1/\sigma$ is stable. Thus, an exchange of stability occurs at $\sigma = 1$. This type of bifurcation is a transcritical bifurcation. hence we cite the following theorem [1] which is stated without proof:

Theorem 1. *Let $(s(t), i(t))$ be a solution of (2.3) in T. If $\sigma \leq 1$ or $i_0 = 0$, then solution paths starting in T approach the disease-free equilibrium given by $s = 1$ and $i = 0$. If $\sigma > 1$ then all solution paths with $i_0 > 0$ approach the endemic equilibrium given by $s_e = 1/\sigma$ and $i_e = \mu\frac{(\sigma-1)}{\beta}$*

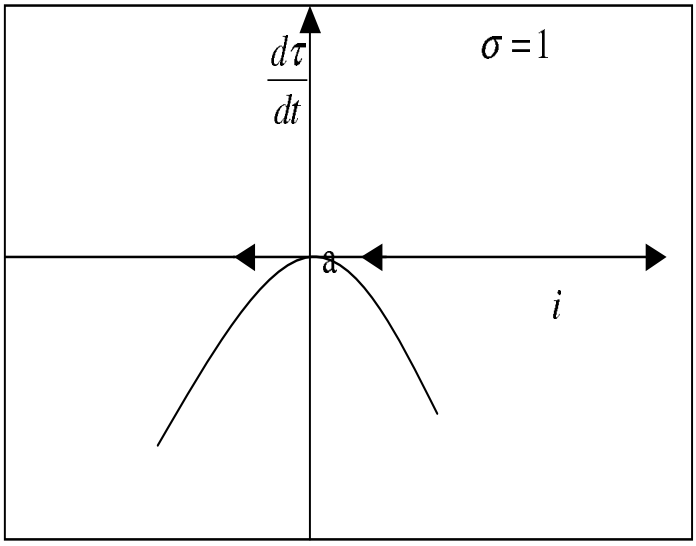


Figure 2.5: The schematic diagram of $d\tau/dt$ and i when $\sigma = 1$. The fixed point a=0 is half stable.

2.6 Discussion:

In this model, at disease free equilibrium where all the population is in the susceptible compartment, the basic reproduction number R_0 is $\frac{\beta}{\gamma+\mu}$. R_0 remains fixed for a given set of parameters, and introduction of infection, for $R_0 < 1$, the disease dies down, and when infection is introduced for $R_0 > 1$, a steady endemic state occurs. In other words, when R_0 first crosses one, the disease can invade to low endemic levels. If R_0 drops to below one, the disease dies down. This means therefore that a globally stable endemic state is maintained for $R_0 > 1$.
This model exhibits forward bifurcation. We summarize the Characteristics of the forward bifurcation. These include:

1. the absence of positive equilibria near the disease-free equilibrium when $R_0 < 1$ and,

2. a low level of endemicity when R_0 is slightly above 1.

and illustrate it in the figure below (figure 2.6). We also observe how the assumption that immigration (births in this case) equal deaths influence forward bifurcation. Where births are not equal to deaths, we may observe different bifurcation. Figure 2.6 illustrates the forward bifurcation. Note that the infection rises after $R_0 = 1$. Figure 2.6 clearly shows that the disease-free equilibrium

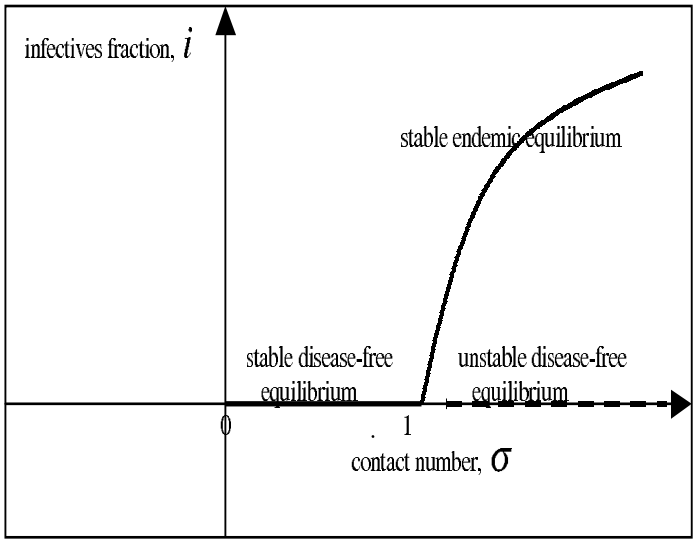


Figure 2.6: Bifurcation diagram for the SIR endemic model, which shows that the disease-free and endemic equilibria exchange stability when contact number, σ is 1. The bold lines show stability and dashed lines show instability.

is stable for $R_0 \leq 1$, and unstable for $R_0 > 1$, denoted by a dotted line. The endemic equilibrium state is unstable for $R_0 \leq 1$ and stable for $R_0 > 1$.

Chapter 3

Backward bifurcation in SI model

3.1 Introduction

In the previous chapter we showed that in an epidemiogical model which exhibits forward bifurcation, there is non-existence of equilibria near the disease-free equilibrium when $R_0 < 1$. However, the SI model we consider may exhibit backward bifurcation. It has been studied by Dushoff in [10] and exhibits backward bifurcation for some parameter values. Our contribution in this chapter is to strengthen the case considered by Dushoff, and further discuss a bifurcation technique considered developed by Huang *et al* of determining the sign of bifurcation using center manifolds. Van Den Driessche developed a technique for determining subcriticality of a bifurcation in [9], which we will refer to.

We begin by considering the case where the probability of reducing different infected states depends not only on the state of the individual , but also on the level of disease in the population. This is possibly predicated on the two assumptions as follows;

- There is a connection between the level of the disease in the populations and the distribution of exposure intensifies that individuals face.
- the intensity of initial exposure has an effect on immunological outcome.

The first assumption is clearly reasonable for a variety of diseases. For example, if there is a high level of malaria in the population, the probability of several infected bites in a short time (or a bite from a multiply infected mosquito) is increased. Similarly, in a population with a high level of cholera, the chance of receiving a strong dose at first exposure is higher [10]. In sexually transmitted diseases, the relationship between population level of the disease and initial dose may be small.

The second assumption is also true for a variety of diseases, although by no means all. Many intestinal infections are thought to require a threshold level of invading organisms in order to become established. Schweitzer and Anderson (1992, 1993) provide theoretical support for the second assumption. They suggest that under some circumstances a low level of exposure to an infectious organism may lead to active immunity and a short-lasting or a virulent infection, while a larger infection may overwhelm the immune system and lead to far greater subsequent transmission.

If a disease is more likely to result in heavy infections at high levels of prevalence, it is possible that this could result in higher reproductive rates for the disease at intermediate levels of prevalence, in spite of the fact that higher rates of prevalence are associated with smaller numbers of susceptibles. It seems plausible that a disease that reproduces sufficiently well in heavily infected people may be able to persist in a population once established, even if it is unable to invade [10]. We strengthen the case of the model discussed in [10] and use a different example to show that this model may exhibit backward bifurcation, for a certain range of parameters.
We now introduce the model.

3.1.1 The SI model

This model considers a disease-host system which has two possible outcomes: low-level infection or high-level infection.

3.1.2 Assumptions

- The rate of disease is proportional to force of infection, and also that probability of an infection becoming a high-level infection is a function of the same level of infection,
- constant population size,
- no disease induced death,
- there is no lasting immunity.

Let x, y and z be the proportions of the susceptibles, proportion of individuals with low-level and high level infections respectively. We write the equations as:

$$\begin{aligned} \dot{x} &= -\lambda x + my + nz \\ \dot{y} &= \lambda(1 - g(\lambda))x - my \\ \dot{z} &= \lambda g(\lambda)x - nz \end{aligned} \tag{3.1}$$

and

$$s + i = 1$$

where $\lambda = \alpha y + \beta z$ is the force of infection, and $g(\lambda)$ is the function that gives the proportion of infections that will be high-level infections.
Individuals depart from the infected class at rate λ. They either become heavily infected at the rate $g(\lambda)$ hence enter the heavily infected class; otherwise they enter the lightly infected class. They leave the two infected classes at the rates m and n respectively. The "departure rates" m and n include both recovery from the disease and natural mortality. We will assume that y and z are the lightly infected, and highly infected classes respectively. g will be defined to be an increasing function of λ, so that the proportion of heavy infections increases as the infection increases.

We note that this is an SI model. We use x, y and z in place of s, i_1 and i_2 respectively, to avoid confusion and complexity of terms in latter sections.

To analyze this model we will disregard the first equation $\dot{x}$ (as we focus more on the infective class and also) because the population is constant. We make mention of the fact that in a constant population where the births only occur into the susceptible class, susceptible individuals who die are replaced by individuals who are born, and hence do not appear in the model.

We let $\mathbf{Y}$ equal to the vector (y, z); and linearizing we get :

$$\begin{aligned} \dot{y} &= \alpha y(1-g(\lambda))x + \beta z(1-g(\lambda))x - my \\ \dot{z} &= \alpha y g(\lambda) + \beta z g(\lambda)x - nz \end{aligned}$$

then (3.2) becomes:

$$H(\mathbf{Y}) = \begin{bmatrix} \alpha(1-g(\lambda))x - m & \beta(1-g(\lambda))x \\ \alpha g(\lambda) & \beta g(\lambda)x - n \end{bmatrix} \tag{3.2}$$

where $x = 1 - y - z$ and λ is as defined before.

We look for the equilibrium points of this system by equating $\dot{y}$ and $\dot{z}$ to zero.

3.2 Equilibria of the system

$$\begin{aligned} 0 &= [\alpha(1-\hat{g})x - m]y + [\beta(1-\hat{g})x]z \\ 0 &= [\alpha\hat{g}x]y + [\beta\hat{g}x - n]z \end{aligned}$$

leading to

$$y = \frac{-[\alpha(1-\hat{g})x - m]z}{[\beta(1-\hat{g})x]}$$

and subsequently

$$z = \frac{[\alpha\hat{g}x][\beta(1-\hat{g})x]}{[\beta\hat{g}x - n][\alpha(1-\hat{g})x - m]}$$

The Jacobian matrix $H(\mathbf{Y})$ at disease-free equilibrium is given by

$$H(\mathbf{0}) = \begin{bmatrix} \alpha(1-\hat{g})x - m & \beta(1-\hat{g})x \\ \alpha\hat{g}(\lambda) & \beta\hat{g}x - n \end{bmatrix} \tag{3.3}$$

where $(\mathbf{Y}) = (\mathbf{0}) = (y_{df}, z_{df})^T = (0,0)^T$, and $\hat{g} \equiv g(0)$.

Since we have two classes of infectives we calculate the basic reproduction number R_0 for each class, as these may not be the same.

From (3.3), the eigenvalues are $\lambda_1 = \alpha s - m$ and $\lambda_2 = \beta s - n$. Since $s = 1 - x - y$, $s = 1$ at disease-free equilibrium. Thus from $\lambda_1 = \alpha - m$ we get that $R_0^y = \frac{\alpha}{m}$, similarly, $R_0^z = \frac{\beta}{n}$, since bifurcations in simple models are expected to occur at $R_0 = 1$. Hence

$$R_0 = R_0^y + R_0^z \tag{3.4}$$

Solving (3.3) for stability we see that at the disease free equilibrium, the system (3.2)is asymptotically stable for $\alpha < m$ and $\beta < n$.

Since we are dealing with the infective classes (y, z) only, we have $y + z \leq 1$, where $x = 0$). We obtain a feasible region similar to T defined in chapter one. This approach has the limitation that we cannot analyze further that the Jacobian of the resultant matrix, hence we consider a different approach.

In simple disease models, the bifurcation point at $R_0 = 1$ is generally characterized by a forward bifurcation. In cases where the replacement number R increases

as the disease invades, backward bifurcations are possible. These are characterized by a low-level unstable equilibrium that exists when $R_0 < 1$ and which serves as a break point (threshold) above which the disease persists if established, even though it cannot invade. We explore the method of determining dynamical behavior when an infection is introduced at $R_0 = 1$.

The sign of the bifurcation at $R_0 = 1$ can be determined by examining whether the disease can invade at the bifurcation point. At this bifurcation point, the reproduction number R is exactly 1 at the disease-free equilibrium, so a disease which increases its reproduction number R by invading will invade and one that does not, will not invade. We introduce our bifurcation parameter μ such that $R_o < 1$ for $\mu < 0$ and $R_0 > 1$ for $\mu > 0$. Please note that the parameter R has been discussed in chapter 1[section on threshold parameters] and remains the same. The criterion of the disease invading depends on the dominant eigenvectors of the jacobian matrix. Note that from these dominant eigenvectors we get values of R_0.

More generally, we consider a multi-group version of (3.2):

$$\dot{y_i} = \lambda f_i x - m_i y_i \qquad\qquad , i = [1, n] \tag{3.5}$$

where $\lambda = \sum_j \alpha_j y_j$, $x = 1 - \sum_j y_j$, and the proportion of infections in each subgroup, $f(\lambda_i)$ satisfies $\sum_i f_i = 1$. The reproductive number is given by

$$R_0 = \sum_j \hat{f}_i \tag{3.6}$$

where $R_j = \frac{\alpha_j}{m_i}$, and $\hat{f}_j \equiv f_j(0)$. We may write (3.6) in vector form as:

$$\dot{Y} = H(\mathbf{Y})Y$$

where $H(\mathbf{Y}) = L(Y) - diag\{m_i\}$ and $L = [f_i \alpha_j x]_{ij}$. We note that the notation $\in [(i,j)]_{ij}$ refers to a matrix $\mathbf{M}$ whose elements are given by $\mathbf{M}_{ij} = \in (i,j)$. $[\in]_i$ refers to a vector $\mathbf{V}$, where $\mathbf{V}_i = \in (i)$.
At the bifurcation point the a reproduction number $R_0 = 1$, the dominant eigenvalue of the jacobian matrix is zero, and is associated with a unique right eigenvector, which we will call the dominant eigenvector,$\mathbf{V}$, thus we have that $H(\mathbf{0})\mathbf{V} = 0$. This eigenvector gives the distribution of infected individuals in different groups in the direction in which the disease initially spreads (see [6]). In the case where

the disease does not spread, the dominant eigenvector gives the asymptotic distribution of infecteds in different groups as the disease dies out.
At the disease free equilibrium we have :

$$L(\mathbf{0}) = [\hat{f}_i \alpha_j]_{ij} \tag{3.7}$$

Hence:

$$\hat{f}_i \sum_j \alpha_j V_j = m_i V_i \tag{3.8}$$

We will assume that $\mathbf{V}$ is chosen so that $\sum_j \alpha_j V_j = 1$. Then

$$V_i = \frac{\hat{f}_i}{m_i}$$

At bifurcation point, we also have that $\mathbf{W}\mathrm{H}(\mathbf{0}) = \mathbf{0}$, where $\mathbf{W}$ is the dominant left eigenvalue. Caswell provided a biological interpretation of dominant left eigenvectors. The left eigenvector gives the projection of a vector onto the dominant eigenvector in the eigenvector basis. The dominant left eigenvector reflects how much an infected individual in each subgroup contributes to the spread of the disease, as it begins to invade.
Using (3.8)

$$\alpha_j \sum_i \hat{f}_i W_i = m_j W_j$$

We also assume that $\sum_i \hat{f}_i W_i = 1$. Then

$$W_j = \frac{\alpha_j}{m_j} = R_j$$

The dominant eigenvector $\mathbf{V}$ gives the direction of the initial spread of the disease, while the dominant left eigenvector denoted by $\mathbf{W}$ gives the contribution of infecteds in each group to the spread of the disease.

Intuitively speaking, we develop a criterion for whether the disease can invade when $R_0 = 1$ by assuming that the disease invades a small amount along the dominant eigenvector, calculating the vector field at a point along the dominant eigenvector to find out if the component of the vector field in the direction of the dominant eigenvector is positive or negative.

To calculate the rate of change of H along the eigenvector, we first calculate its rate of change with respect to each dynamic variable:

$$\frac{\partial H}{\partial y_k}(\mathbf{0}) = \frac{\partial L}{\partial y_k}(\mathbf{0}) = [\alpha_k \delta_i \alpha_j - \hat{f}_i \alpha_j]$$

where $\delta_i = \frac{df_i}{d\lambda}$ evaluated at $\lambda = 0$.

At $R_0 = 1$ or $\mu = 0$ the dominant right eigenvector $\mathbf{V}$ is given by $(\frac{(1-\hat{g})}{m}, \frac{\hat{g}}{n}))$ and $\mathbf{W}$ is given by (R_1, R_2). From center manifold theory [S. Wiggins, Theorem 2.1.1], we know it is sufficient to examine if the disease initially invades a small distance $\in$ along the manifold.

The rate of change of H is given by

$$H_{\in} = \frac{d}{d \in}(H_{\in}\mathbf{V}) \qquad \text{where} \quad \mathbf{Y} = \in \mathbf{V}$$

$$\text{and} \qquad \dot{Y} = \in H(\mathbf{0})V + \in^2 H_{\in}(\mathbf{0})\mathbf{V} + \mathbf{Order(3)}$$

where $H_{\in}$ is given by,

$$H_{\in}(\mathbf{0}) = \sum_k V_k \frac{\partial H}{\partial y_k}(\mathbf{0}) = [\delta_i \alpha_j \sum_k \alpha_k V_k - \hat{f}_i \alpha_j \sum_k V_k]_{ij}$$

We further define

$$\hat{\alpha} = \frac{\sum_k \alpha_k V_k}{\sum_k V_k} = \frac{1}{\sum_k V_k}$$

to be the mean transmission coefficient as the disease tries to invade6 11.ET 2 TfΩ42.9161 -4dΩ(=

those due to public health interventions. We note that in this example $g(\lambda) = 0$, hence $R_0 = R_o^y = \frac{\alpha}{m}$.

Figure 3.1 shows the occurrence of steady endemic states for the susceptible, low-level infectives and high-infective classes respectively, at $R_0 > 1$. We introduced low levels of infectives and notice that though the infectives decline, they each approach a unique stable endemic equilibrium. The susceptibles also increase to a unique stable equilibrium point. This is common in epidemiological models which exhibit forward bifurcations as shown in figure 3.3. Surprisingly the proportion of low-level infecteds decreases sharply at first, then slows down drastically and maintain a constant, while the high-level infecteds decrease at a slower rate to maintain a constant which is still lower than that of the low-level infectives class. We also that for a certain range of parameters, introducing more low-level infectives than high-level infectives will result in backward bifurcation. Figure 3.2 depicts a scenario where the infection is more dominant in the low-level infectives class, in a time course of the infection. We used $y = 0.3$ and $z = 0.1$. We see that the low level infectives rise rapidly and dominate over the slower high-level infectives class. From the diagrams we conclude that whenever the low-level infectives are more dominant, we get a forward bifurcation (as similar to [10, p. 184]). This is not so when we introduce a higher portion of the high-level infectives class.

Figure 3.3 shows a forward bifurcation, where in this case $y = 0.3$, and $z = 0.2$. When $R_0 < 1$, the disease free equilibrium is locally asymptotically stable and also globally stable (as was shown in chapter 2). The endemic equilibrium is unstable for $R_0 < 1$. For $R_0 > 1$ we see that the endemic equilibrium is stable and the disease approaches a stable endemic state, whereas the disease-free equilibrium is unstable in this region. This means that for $R_0 < 1$, introduction of infectives will lead to the infection dying out. Introduction of infection at $R_0 > 1$ results in a low level of endemicity. Decreasing R_0 again to less that unity will result in the eradication of the disease.

The occurrence of stable endemic state is further supported by our analysis depicted in figure 3.1. We introduced an infection in the region $R_0 > 1$, and found out that though the infectives decline, they each approach an endemic state or constant, as the susceptibles also increase to a constant rate.

In this case we see that the disease can maintain itself once established, for a

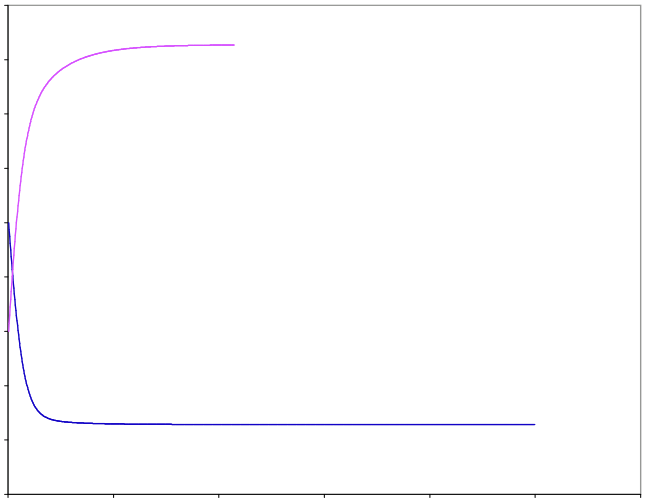


Figure 3.2: The figure shows a time course comparison of the two infective groups I_1 and I_2 in the endemic state.

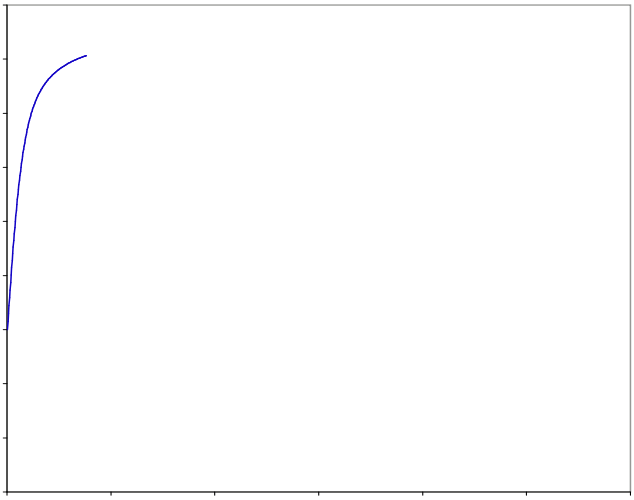


Figure 3.3: A forward bifurcation, with $\alpha = 0.8$, $\beta = 3$, $\sigma = 0.1$, $I_1 = 0.3$, $I_2 = 0.2$, $m = 1$ and $n = 5$. The disease was introduced at time $t = 0$.

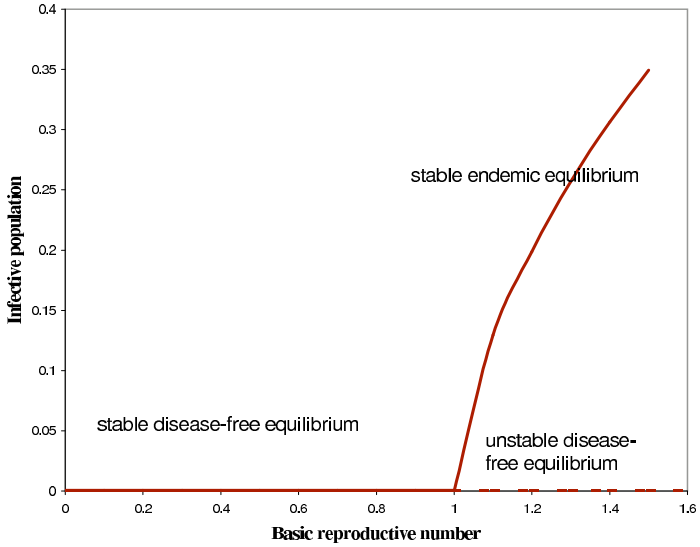
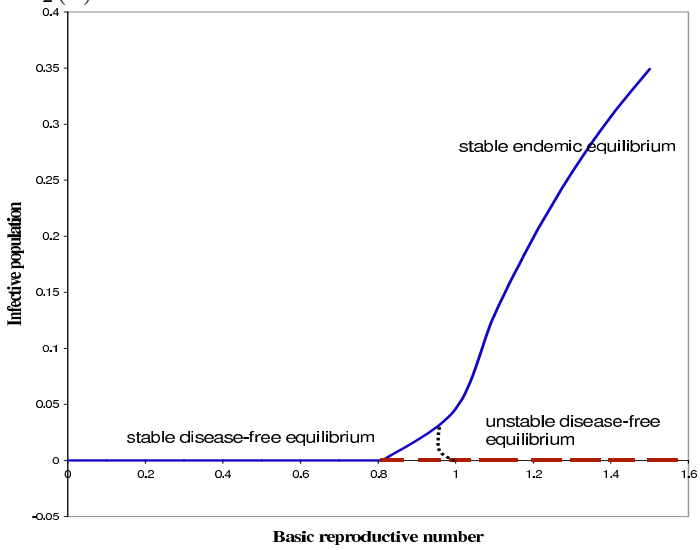


Figure 3.4: A backward bifurcation, with $\alpha = 0.8$, $\beta = 0.7$, $m = 1$, $n = 5$, $I_1(0) = 0.3$ and $I_2(0) = 0.7$



Chapter 4

Backward bifurcation in multi-group SI model

4.1 Background

Multi-group models are models which incorporate several groups of compartmentalized classes such as susceptibles, and infectives. Various epidemiological multi-group models have been studied and are shown to exhibit forward bifurcation such as in [9], [6] and [13]. We consider a simple holding parameters constant in an epidemiological model and get forward bifurcation, then extend to the case where we vary our parameters per each group i.

We introduce the epidemiological model analyzed by Dushoff [6] but however we use a different approach to show existence of backward bifurcation.

We begin by a brief discussion of practical criteria for backward bifurcation.

4.2 A practical criterion for backward bifurcations

It has been noted that as a disease invades the susceptible class in the population, it tends to reduce its reproductive rate, as the amount of susceptibles is depleted. For a backward bifurcation to occur, other factors must outweigh this tendency, so that as the disease invades its reproductive rate *increases*. If a disease lowers its reproductive rate by invading, it would be expected that when $R_0 < 1$ and cannot invade a *naive* population, it could never persist at all. Further, when R_0 is slightly above one, the disease would be expected to reach a low endemic level, because of this negative feedback [6].

On the other hand, a disease that increases its reproductive rate by invading may be able to survive when established in a population, even when $R_0 < 1$ and it cannot invade. Similarly when R_0 is even very slightly above one, the positive feedback between increase of the disease and the rate of spread may lead to a relatively high endemic rate of infection. In particular, when $R_0 = 1$, each infection exactly replaces itself in the linear approximation ($i = 1$, and $\sigma = R_0 = 1$). Hence, whether the disease invades at $R_0 = 0$ will be determined by whether the reproductive rate increases or decreases as the disease increases along the center manifold. We thus expect the disease to invade at $R_0 = 1$ in the case of a backward bifurcation, but not in the forward bifurcation case. We now introduce the SI model.

4.3 A simple multi-group model

This model is a simplified version of the one developed for AIDS by Huang *et al.* We use the model by Dushoff *et al* [6]. In general, we write

$$\begin{aligned} \frac{di_i}{d\tau} &= \beta_i s_i i_i - \mu_i(\sigma_i + 1) i_i \\ \frac{ds_i}{d\tau} &= \Lambda_i - \beta_i s_i i_i - \mu_i s_i \end{aligned} \tag{4.1}$$

Here i_i and s_i represent the fractions of infectives and susceptibles, respectively, in the group i. Individuals are recruited into the susceptible pool at rate Λ_i, and contract the disease at rate $\beta_i s_i i_i$. Both $\beta_i s_i i_i$ and Λ_i can be functions of any or

all of the dynamic variables. Susceptibles die at rate μ_i, while infected individuals experience disease-induced mortality at a rate that is σ_i times as great, as well as mortality from other sources at the rate μ_i.

Since $\beta_i s_i i_i$ often is the most complicated term in such a model, we re-write (4.1) in terms of i_i and s_i, where $\tau_i = s_i + i_i$ is the total number of people in the group i as ;

$$\begin{aligned} \frac{di_i}{d\tau} &= \beta_i s_i i_i - \mu_i(\sigma_i + 1)i_i \\ \frac{dt_i}{d\tau} &= \Lambda_i - \mu_i \tau_i - \mu_i \sigma_i i_i \end{aligned} \tag{4.2}$$

In this model proportional mixing is assumed, the mixing rate of each group is assumed, and the probability of transmission between any two groups and the rate of recruitment into each group is fixed. The rate of recruitment into each group is fixed. This model is a non simple model ass there is proportional mixing and disease-induced death. We assume that if the mixing rate of group i is c_i, then the total mixing activity is $\sum_j c_j t_j$, and the proportion of group i's contacts that are with members of group j is $\frac{c_j t_j}{\sum_k c_k t_k}$. Let λ_{ij} be the fraction of contacts between group i susceptibles and group j infectives which lead to infection. Since the proportion of group j that is infected is $\frac{I_j}{t_j}$, and the total number of contacts made by group i susceptibles is $c_i S_i$, the rate at which the group i susceptibles become infected is

$$\beta_i s_i i_i = c_i s_i \frac{\sum_j c_j \lambda_{ij} i_j}{\sum_j c_j t_j} \tag{4.3}$$

We now define the total mixing activity as $N(t) = \sum_j c_j t_j$, for convenience,let the transmission rate from group j to group i, $l_{ij} = c_i c_j \lambda_{ij}$ and the total death rate of infectives, $m_i = \mu_i(\sigma_i + 1)$. Then (4.2) becomes:

$$\begin{aligned} \frac{di_i}{d\tau} &= \frac{s_i}{N(t)} \sum_j i_{ij} i_j - m_i i_i \\ \frac{dt_i}{d\tau} &= \Lambda_i - \mu_i \tau_i - \mu_i \sigma_i i_i \end{aligned} \tag{4.4}$$

The most important assumption for backward bifurcations to occur is that the mixing rates c_i remain constant as subgroup sizes change. We assume that all the l_{ij} are positive, and hence every subgroup has at least some transmission of the disease to every other subgroup.

4.4 Bifurcation Analysis

In this section we use the Jacobian matrix approach to find R_0, and compare it to the 'next-generation approach'. From (4.1), i.e.

$$\begin{aligned} \frac{di_i}{d\tau} &= \beta_i s_i i_i(s_i, i_i) - \mu(\sigma_i + 1)i_i \\ \frac{ds_i}{d\tau} &= \Lambda_i - \beta_i s_i i_i - \mu_i s_i \end{aligned}$$

We have that $s_i = \frac{\Lambda_i - \beta_i s_i i_i}{\mu_i}$ and that $i_i = \frac{\beta_i s_i i_i}{\mu_i(\sigma_i+1)}$ at equilibrium point. The Jacobian of (4.1) is:

$$J = \begin{pmatrix} -\beta_i i_i - \mu_i & -\beta_i s_i \\ \beta_i i_i & \beta_i s_i - \mu_i(\sigma_i + 1) \end{pmatrix}$$

$$J = \begin{pmatrix} -\beta_i i_i - \mu_i & -\beta_i s_i \\ \beta_i i_i & \beta_i s_i - \mu_i(\sigma_i + 1) \end{pmatrix}$$

The characteristic equation at disease-free equilibrium becomes:

$$det[J - \lambda] = \begin{vmatrix} -\mu_i - \lambda & -\beta_i \frac{\Lambda_i}{\mu_i} \\ 0 & \beta_i - \mu_i(\sigma_i + 1) - \lambda \end{vmatrix} = 0$$

giving us eigenvalues $\lambda_{1i} = -\mu_i$ and $\lambda_{2i} = \beta_i s_i - \mu_i(\sigma_i + 1)$, hence $R_0^i = \frac{\beta_i}{\mu_i(\sigma_i+1)}$ for each i, as there are i groups.

Adopting the next generation matrix method [9], we define R_0 as the dominant eigenvalue of the next-generation matrix.

Using the method applied in [9], we have for the next generation matrix;

$$F = [\beta_i], \quad \mathcal{F} = \begin{bmatrix} 0 \\ \beta_i \end{bmatrix}, \quad \mathcal{V} = \begin{bmatrix} -\Lambda_i + \beta_i + \mu_i s_i \\ \mu_i(\sigma_i + 1) \end{bmatrix}$$

then, since $m = 1$ we have

$$V = \begin{bmatrix} \mu_i(\sigma_i + 1) \end{bmatrix}, \quad V^{-1} = \frac{1}{\mu_i(\sigma_i + 1)}$$

Since $R_0 = FV^{-1}$, we get

$$FV^{-1} = \sum_i \frac{\beta_i}{\mu_i(\sigma_i + 1)}$$

resulting in the following theorem;

Theorem 2. *Let (4.1) be the system of equations given, and let $\beta_i s_i i_i = i_i f s_i i_i$ for mathematical convenience. Then at disease-free equilibrium $i_i = 0$ and $s_i = \Lambda_i/\mu_i$, and at endemic state, where $i_i > 0$, we find that $R_0^i = \frac{f(s_{df},0)}{\mu_i(\sigma_i+1)}$*

Since we are dealing with the eigenvalues of each of the i's we obtain $2n$ eigenvalues system with two equilibrium points, and two steady states for each i, where $i = 1, 2, 3....n$.

4.5 Numerical analysis

At the disease-free equilibrium, $s = \sum_i s_i = n$, $i_i = 0$. The eigenvalues are $\lambda_{1i} = -\mu_i$ and $\lambda_{2i} = \beta_i - \mu_i(\sigma_i + 1)$. For stability to occur, the eigenvalues must be less than zero, hence for $\lambda_{2i}, \beta_i < \mu(\sigma_i + 1)$, therefore $s_i = \frac{\beta_i}{\mu(\sigma_i+1)}$. By Hurwitz condition, the system is asymptotically stable for $\beta_i < \mu_i(\sigma_i + 1)$

We see that since this model exhibits an even number of equilibrium points, for $i = 1$ and the contact rates between groups are constant, we expect to get a forward bifurcation for $i = 1$. We will also consider the case $i = 2$, and perhaps $i = 3$. We also note that assuming the contact rates $c_i = c_j$,we get forward bifurcations, as obtained in [9]. This shows how crucial a role mixing plays in the dynamics of the model.

Figure 4.1 indicates a of the susceptibles class and infectives class for $R_0 < 1$ The infective population declines and approaches the zero equilibrium slowly. The susceptibles, which initially start with a lower population, increase sharply, then slow down to a stable equilibrium. Figure 4.2 illustrates the phase portrait of the infectives for $R_0 < 1$. Regardless where we begin, each of the trajectories

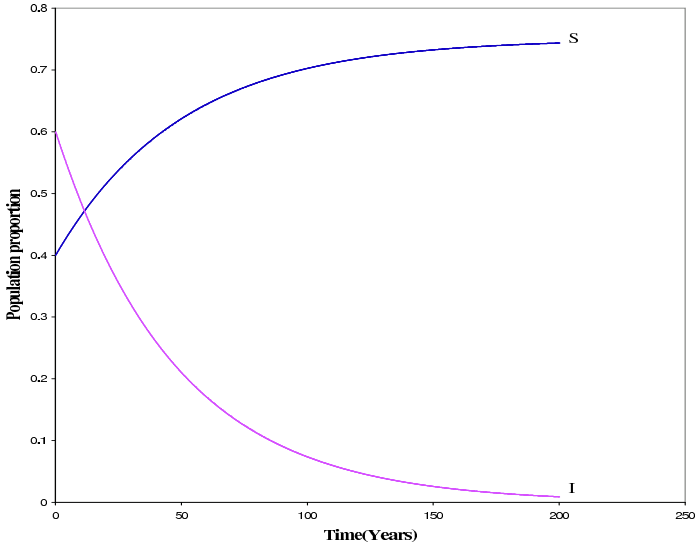


Figure 4.1: Time course showing the susceptible population against the infectives for $R_0 < 1$, with $s(0) = 0.4$ and $I(0) = 0.6$ at time $t = 0$

approaches a steady equilibrium, while the trajectories in figure 4.3 approach zero. In the case of $i = 2$, we face a similar scenario as depicted in the three above figures if we hold c_i, β_i, Λ_i constant. The model exhibits forward bifurcation, though we do not include it in our figures here. We however recall that in a simple SI model transcritical bifurcation is expected. We illustrate a case where these constants vary per subgroup, hence expect backward bifurcation.

Figure 4.4 shows the time series behavior of the model with $i = 2$. s_1 decreases at a slower rate than s_2, but the two groups of susceptibles settle to a similar steady state for some time, then finally s_1 approaches a steady state slightly higher than that of s_2. The infectives rise to a maximum then decrease to a steady endemic state,I_1being less than I_2 at time t.

4.6 Discussion

We have seen in the example the significance of varying parameters for each group and their resultant bifurcation. When we vary these parameters we get backward bifurcation, whilst maintaining them as a constant results in forward bifurcation

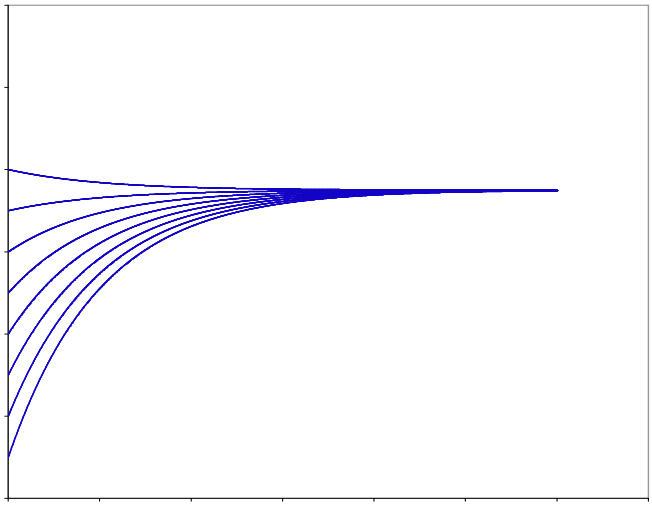


Figure 4.2: Phase portrait for $R_0 < 1, l = 0.015, \sigma = 0.05$ and $\mu = 0.02$

in this model. This result is similar to that of [9, section 5]. The concept of free mixing may thus result in backward bifurcation as shown in this case, for unique independent parameter values per group i.

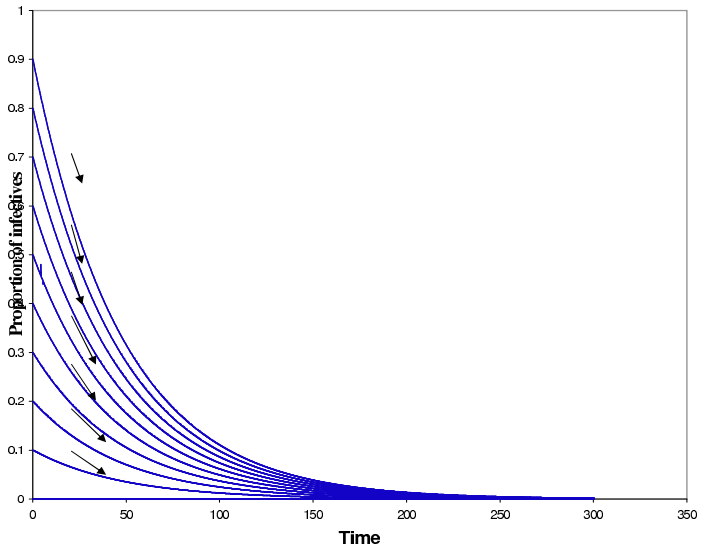


Figure 4.3: Phase portraits showing that if infectives are introduces for $R_0 < 1$, the infection eventually dies out

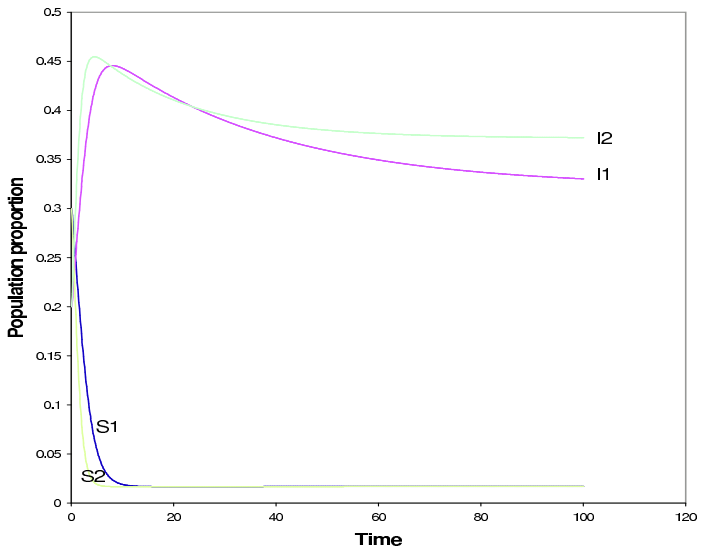


Figure 4.4: Time course of the multi-group model with $i = 2$, with varying constants for each group. We used $\beta_1 = 0.2$, $\beta_2 = 0.4$, $s_1 = s_2 = 0.2$, $I_1 = I - 2 = 0.3$, $\sigma_1 = 0.1$, $\sigma_2 = 0.15$, $\mu_1 = 0.01$, $\mu_2 = 0.02$

Chapter 5

Backward bifurcation in $SVIS$ model

5.1 Background and Introduction

In this chapter, we consider the SIS model with vaccination, thus becoming the $SVIS$ model. The simple SIS model exhibits forward bifurcation [4]. With the introduction of vaccination, this model may exhibit backward bifurcation. Increasing the level of nonlinearity of the system in the model changes the dynamics and bifurcation of the epidemiological model.

We aim to show that levels of nonlinearity, by use of Rolle's theorem may change the resultant bifurcation. We will use a different example and range of parameters to strengthen the case of [14]. We also interpret our results and discuss how the immigration rate may influence dynamics of the model.We compartmentalize the total population $N(t)$ at time t, into three compartments as follows, $S(t)$ is the number of susceptibles in the population, $I(t)$ is the number of infectives at any time t, and $V(t)$ is the number of numbers who are vaccinated at time t. We note that the total population at time t is denoted by $N = S + I + V$. We assume that each infective makes βN contacts sufficient to transmit infection in unit time, where β is a constant. We assume standard incidence in this model. The susceptible population is vaccinated at a constant rate φ, and the rate at which the vaccine wears off is θ. Please note that in this epidemiological model

we assume that the vaccination is temporal and does not lead to full immunity. There are disease induced and natural deaths. The population is replenished in two ways, birth and immigration. We assume that all newborns enter the susceptible class at a constant rate, Λ, and the inflow of immigrants is a constant A where some portion of them, p, is infective.

We thus summarize the assumptions in this model as:

- $S(t), I(t), V(t)$ and $N(t)$ are the numbers of susceptibles, infectives, vaccinated, and the total population at time t, respectively.
- There is a constant flow of a new members into the population per unit time, where fraction p of immigrants are infective, $(0 \leq p \leq 1)$
- The vaccine has the effect of reducing infection by a factor of σ so that $\sigma = 0$ means that the vaccine is completely effective in preventing infection, while $\sigma = 1$ means that the vaccine is utterly ineffective.
- The rate at which the susceptible population is vaccinated is φ and the rate at which the vaccine wears off is θ
- The disease is fatal and α is the rate of disease induced death. In our model there is no disease induced death.
- the constant per capita natural death rate is given by, $\mu > 0$ in each class.
- The recovery rate of infectives is γ in unit time
- βN is the infectious contact rate per unit time.
- Λ is the constant natural birth rate, with all newborns coming into the susceptible class.

We have the following formulation of the model:

$$\begin{aligned} \dot{S} &= (1-p)A + \Lambda - \beta SI - (\mu + \varphi)S + \gamma I + \theta V \\ \dot{I} &= pA + \beta SI + \sigma\beta VI - (\mu + \gamma)I \\ \dot{V} &= \varphi S - \sigma\beta VI - (\mu + \theta)V \end{aligned} \tag{5.1}$$

Parameter	Symbol
Number of susceptibles at time t	$S(t)$
Number of vaccinated individuals at time t	$V(t)$
Number of infectives at time t	$I(t)$
Number of immigrants	A
Proportion of infectives among immigrants	p
Birth rate	Λ
Contract rate	β
Recovery rate	γ
Vaccination rate	φ
Factor by which vaccine reduces infection	σ
Drug wearing or failure rate	θ
Natural death rate	μ
Disease related death	α
The basic reproduction number	R_0
The vaccine reproduction number	$R(\varphi)$

Table 5.1: Table of notation

We note that as earlier indicated, the total population is the sum of the three classes;

$$N(t) = S(t) + I(t) + V(t)$$

Thus it follows that

$$\dot{N} = \dot{S} + \dot{I} + \dot{V} = A + \Lambda - \mu N$$

This system can be seen to be asymptotically autonomous, and we see that the $\lim_{t\to\infty} N(t) = \dfrac{A+\Lambda}{\mu}$ which we will equate to some constant K

Before we go any further we consider some basic definitions.

Definition 1. *Consider the differential equation*

$$\frac{dx}{dt} = \dot{x} = f(x) \tag{5.2}$$

where $x = x(t) \in \Re^n$ is a vector valued function of an independent variable and $f : U \to \Re^n$ is a smooth function defined on some subset $U \subseteq \Re^n$. Systems of the form (5.2) which do not contain time explicitly are called autonomous.

Definition 2. *The system*

$$\dot{y} = f(t, y)$$

is said to be asymptotically autonomous on the set Ω if and only if

1. $\lim_{t\to\infty} f(t,y) = h(y)$ *for* $y \in \Omega$ *and this convergence is uniform for* y *in closed bounded subsets of* Ω

2. *For every* $\varepsilon > 0$ *and every* $y \in \Omega$ *there exists a* $\delta(\varepsilon, y) > 0$ *such that* $\mid f(t,x) - f(t,y) \mid < \varepsilon$ *, whenever* $\mid x - y \mid < \delta$ *for* $0 \leq t < \infty$

Using the *theory of autonomous systems* we can reduce (1) to a two dimensional system, and replacing S with $K - I - V$:

$$\begin{aligned} \dot{I} &= pA + \beta[K - I - (1-\sigma)V]I - (\gamma + \mu)I \\ \dot{V} &= \varphi[K - I - V] - \sigma\beta VI - (\gamma + \mu)V \end{aligned} \tag{5.3}$$

5.2 Equilibria

In this section we equate the right hand side of the equations in (3) to zero and get:

$$\begin{aligned} \beta(1-\sigma)V &= \frac{pA}{I} + \beta(K - I) - (\gamma + \mu) \\ \varphi(K - I) &= V[\sigma\beta I + (\mu + \theta + \varphi)] \end{aligned}$$

We solve the above system by solving for V in the last equation and substituting it in the first equation;

$$V = \frac{\varphi(K - I)}{[\sigma\beta I + (\mu + \theta + \varphi)]}$$

$$\begin{aligned} \frac{\varphi(K - I)}{[\sigma\beta I + (\mu + \theta + \varphi)]} &= \frac{pA}{I} + \beta(K - I) - (\gamma + \mu) \\ \beta\varphi(1-\sigma)(K - I) &= [\sigma\beta I + (\mu + \theta + \varphi)][\frac{pA}{I} + \beta(K - I) - (\gamma + \mu)] \end{aligned} \tag{5.4}$$

Expanding the last equation we get

$$\beta\varphi(1-\sigma)(K - I)I = [\sigma\beta I + (\mu + \theta + \varphi)][\frac{pA}{I} + \beta(K - I) - (\gamma + \mu)]I$$

$$\beta\varphi(1-\sigma)(K-I)I = -\sigma\beta^2 I^3 - I^2[-\beta\varphi(1-\sigma) - \sigma\beta^2 K + \sigma\beta(\gamma+\mu) + \beta(\mu+\theta+\varphi)]$$
$$- I[\beta\varphi(1-\sigma)K - \sigma\beta pA + \beta K(\mu+\theta+\varphi) - (\gamma+\mu)(\mu+\theta+\varphi)]$$
$$+ pA(\mu+\theta+\varphi)$$

and the cubic polynomial takes the form:

$$f(I) = EI^3 + BI^2 + CI + D = 0 \tag{5.5}$$

with

$$\begin{aligned} E &= \beta\sigma \\ B &= (\mu+\theta+\sigma\varphi) + \sigma(\gamma+\mu) - \sigma\beta K \\ C &= -p\sigma A - K(\mu+\theta+\sigma\varphi) + \frac{(\gamma+\mu)(\mu+\theta+\varphi)}{\beta} \\ D &= \frac{pA(\mu+\theta+\varphi)}{\beta} \end{aligned}$$

At disease free equilibrium, where $I = 0$, $f(0) = D$. Thus the cubic function yields a disease-free equilibrium at the point $I = 0$, hence

$$V_{dfe} = \frac{\varphi(K)}{(\mu+\theta+\varphi)}$$

We consider the equilibrium points of (5). We note that some coefficients of the polynomial are fixed for all parameters. $E \geq 0$ and $D \leq 0$ for all the non-negative parameters. If $D \neq 0$, then there is either one or three positive roots since $f(0) < 0$ and $\lim_{t\to\infty} f(I) = \infty$. Differentiating (5) with respect to I, we get $\dot{f}(I) = 3EI^2 + 2BI + C$. If $f(0)$ has three positive roots then it follows that $\dot{f}(I) = 0$ has two positive roots according to *Rolle's Theorem*. Thus, $B < 0$ and $C > 0$ are the necessary conditions for the system (5.2) to have three endemic steady states.

hence the resultant proposition;

Proposition 2. *If the system (5.2) has three distinct endemic steady states then two conditions on the parameters must be satisfied:*

$$(\mu+\theta+\varphi) + \sigma(\gamma+\mu) - \sigma\beta K < 0$$

and

$$-p\sigma A - K(\mu+\theta+\varphi) + (\gamma+\mu)(\mu+\theta+\varphi) > 0$$

5.3 Stability Analysis

Proposition 3. *The sign of the slope of the bifurcation curve, I vs β, of the system (5.1) is determined by the sign of $(3EI^2 + 2BI + C)$ where*

$$\begin{aligned} E &= \beta\sigma \\ B &= (\mu+\theta+\sigma\varphi) + \sigma(\gamma+\mu) - \sigma\beta K \\ C &= -p\sigma A - K(\mu+\theta+\sigma\varphi) + \frac{(\gamma+\mu)(\mu+\theta+\varphi)}{\beta} \\ D &= \frac{pA(\mu+\theta+\varphi)}{\beta} \end{aligned}$$

The slope of the bifurcation curve is positive when $(3EI^2 + 2BI + C) > 0$ and negative when $(3EI^2 + 2BI + C) < 0$

Proof. Recall that the equilibrium condition of (5.3) is the cubic equation $f(I)$, (5.5). We have already shown by proposition 2 that $B < 0$ and $C > 0$ is a necessary condition that $f(I)$ has three positive equilibria using Rolle's theorem. Now consider a bifurcation diagram using β as a control parameter noting that $\dot{f}(I) = 3EI^2 + 2BI + C$. Implicit differentiation of (5.5) with respect to β gives

$$\begin{aligned} \frac{df(I)}{d\beta} &= \dot{f}(I)\frac{dI}{d\beta} \\ &= -\frac{dEI^3}{d\beta} - \frac{dBI^2}{d\beta} - \frac{dCI}{d\beta} - \frac{dD}{d\beta} \\ &= (3EI^2 + 2BI + C)\frac{dI}{d\beta} \\ &= -I^3\frac{dE}{d\beta} - I^2\frac{dB}{d\beta} - I\frac{dC}{d\beta} - \frac{dD}{d\beta} \\ &= -I^3\sigma + I^2(\sigma K) + I\left(\frac{(\gamma+\mu)(\mu+\theta+\varphi)}{\beta^2}\right) + \frac{pA(\mu+\theta+\varphi)}{\beta^2} \\ &= \sigma I^2(K-I) + \frac{(\mu+\theta+\varphi)}{\beta^2}[I(\gamma+\mu) + pA] \end{aligned} \tag{5.6}$$

We see that (5.6) is positive, since $K \geq I$. Thus, the sign of slope of the bifurcation curve, $\frac{dI}{d\beta}$, is determined by the sign of $(3EI^2 + 2BI + C)$. ♣

The slope of the bifurcation of curve I using β as a control parameter is infinitely large when

$$\frac{dI}{d\beta} = \infty$$

Thus from (5.6) the slope becomes infinitely large when

$$3EI^2 + 2BI + C = 0 \tag{5.7}$$

where

$$\begin{aligned} E &= \beta\sigma \\ B &= (\mu + \theta + \sigma\varphi) + \sigma(\gamma + \mu) - \sigma\beta K \\ C &= -p\sigma A - K(\mu + \theta + \sigma\varphi) + \frac{(\gamma + \mu)(\mu + \theta + \varphi)}{\beta} \\ D &= \frac{pA(\mu + \theta + \varphi)}{\beta} \end{aligned}$$

Clearly $E > 0$ for positive parameters. Hence we see that there are two positive roots of (5.7) if $B < 0$, $C > 0$ and $\sqrt{B^2 - 3EC} > 0$;

$$I_{1,2}^{\infty} = \frac{-B \pm \sqrt{B^2 - 3EC}}{3E} \tag{5.8}$$

We also may consider linearizing the system (5.3) so that

$$J = \begin{pmatrix} -2\beta I - (1-\sigma)BV - (\gamma + \mu) + \beta K & -(1-\sigma)\beta I \\ -(\varphi + \sigma\beta V) & -(\mu + \theta + \varphi + \sigma\beta I) \end{pmatrix} \tag{5.9}$$

From

$$\begin{aligned} \beta(1-\sigma)V &= \frac{pA}{I} + \beta(K - I) - (\gamma + \mu) \\ \text{we have} & \\ -\frac{pA}{I} &= +\beta(K - I) - \beta(1-\sigma)V - (\gamma + \mu) \end{aligned}$$

and use it to evaluate the Jacobian at the equilibrium:

$$J\mid_{I^*}=\begin{pmatrix} -\frac{pA}{I}-\beta I & -(1-\sigma)\beta I \\ -(\varphi+\sigma\beta V) & -(\mu+\theta+\varphi+\sigma\beta I)\end{pmatrix} \tag{5.10}$$

where we note that $tr(J\mid_{I^*})<0$.

$$\begin{aligned} det(J) &= \sigma(\beta I)^2+\beta(\mu+\theta+\varphi)+\tfrac{pA}{I}(\mu+\theta+\varphi+\sigma\beta I)-(1-\sigma)\varphi\beta I \\ &\quad -(1-\sigma)\sigma\beta^2 VI \\ &= \beta I[\sigma\beta I+(\mu+\theta+\sigma\varphi)-\beta\sigma(K-I)+(\gamma+\mu)\sigma] \\ &\quad +\tfrac{pA}{I}(\mu+\theta+\varphi)\end{aligned}$$

We simplify the determinant further by using the equilibrium condition, which is

$$\frac{pA}{I}(\mu+\theta+\varphi)+\beta\sigma(K-I)-\beta\sigma V(1-\sigma)-(\mu+\gamma)\sigma=0$$

$$\begin{aligned} det &= \beta I[\sigma\beta I+(\mu+\theta+\sigma\varphi)-\beta\sigma(K-I)+(\gamma+\mu)\sigma] \\ &= \beta[2\sigma\beta I+(\mu+\theta+\sigma\varphi)+(\gamma+\mu)-\sigma\beta K]+\frac{pA}{I}(\mu+\theta+\varphi) \\ &= \beta I[2EI+B]+\frac{pA}{I}(\mu+\theta+\varphi) \\ &= \beta I[2EI+B]+\frac{\beta}{I}[\frac{pA(\mu+\theta+\varphi)}{\beta}] \\ &= \beta I[2EI+B-\frac{D}{I^2}] \\ &= \frac{\beta}{I}[2EI^3+BI^2-D] \\ &= \frac{\beta}{I}[I^2(2EI+B)-D]\end{aligned} \tag{5.11}$$

We recall that $D<0$, $E>0$ for all parameters, hence the determinant is positive if $B>0$. Since the trace is negative, we conclude that the steady states are asymptotically stable when $B>0$ by Hurwitz criteria, where B is given in proposition 3

We digress a bit to find an important parameter R_0. At the disease-free equilibrium the Jacobian is given as

$$J_{dfe} = \begin{pmatrix} -\frac{(1-\sigma)\beta\varphi K}{(\mu+\theta+\varphi)} - (\gamma+\mu) + \beta K & 0 \\ -(\varphi + \frac{\sigma\beta\varphi K}{(\mu+\theta+\varphi)}) & -(\mu+\theta+\varphi) \end{pmatrix}$$

where K is a constant, $k = 1$(total population at disease-free equilibrium) The eigenvalues obtained thus are $\lambda_1 = -\frac{(1-\sigma)\beta\varphi K}{(\mu+\theta+\varphi)} - (\gamma+\mu) + \beta$ and $\lambda_2 = -(\mu+\theta+\varphi)$

Clearly $\lambda_2 < 0$ and for asymptotic stability to occur at this fixed point, then we demand that $\lambda_1 < 0$. This implies that a small population of infectives introduced at this fixed point does not result in establishment of the infection or disease, but rather the infection dies out completely. The population returns to the disease-free state, after some time of introduction of an infection.
Conversely, for $\lambda_1 > 0$ a steady endemic equilibria occurs. Introduction of an infection at this stage would sustain the establishment of the infection.

The basic reproductive number is of remarkable importance in disease control. We find that the reproduction number R_0 for the SIS model without vaccination is

$$R_0 = \frac{\beta(A+\Lambda)}{(\mu+\varphi)}$$

When vaccination is present we use the dominant eigenvalue to obtain the value of R_0. This is given as

$$R_0 = \frac{\beta(A+\Lambda)(\mu+\theta+\sigma\varphi)}{(\mu+\varphi)(\mu+\theta+\varphi)}$$

The endemic equilibrium is

$$J = \begin{pmatrix} -2\beta I - (1-\sigma)\beta V - (\gamma+\mu) + \beta K & -(1-\sigma)\beta I \\ -(\varphi + \sigma\beta V) & -(\mu+\theta+\varphi+\sigma\beta I) \end{pmatrix}$$

where $V = \frac{\varphi(K-I)}{(\sigma\beta I+(\mu+\theta+\varphi))}$

We now consider the slope of the bifurcations curve

Using the equilibrium points in (5.5) the determinant of zero indicates the threshold for stability changes:

$$det = \frac{\beta}{I}[2EI^3 + BI^2 - D] = 0 \Leftrightarrow 2EI^3 + BI^2 - D \tag{5.12}$$

When the sign of the slope of bifurcation curve changes, the threshold point is found by equating the left hand side of (5.6) to zero, thus solving for I:

$$3EI^2 + 2BI + C = 0 \Leftrightarrow 2EI^3 + BI^2 - D = 0 \tag{5.13}$$

thus

$$3EI^2 + 2BI + C - (2EI^3 + BI^2 - D) = EI^3 + BI^2 + CI + D = 0 \tag{5.14}$$

which is the equilibrium condition. In summary, using (5.14), we show that when the slope of the bifurcation curve changes, its stability changes too; thus we make the following proposition;

Proposition 4. *The exchange of stability occurs when the slope of the bifurcations curve, β vs I changes.*

5.3.1 When do we get a backward bifurcation

The idea underlying this section is that an infinite slope bifurcation curve signals a backward bifurcation. The slope of the bifurcation curve is infinite when $f(I) = 3EI^2 + 2BI + C = 0$. Thus if $f(I)$ has two positive distinct real roots, we get backward bifurcation. The sufficient conditions for $f(I)$ to have two positive real roots is:

$$f(0) = 0, \quad \frac{-B}{3E} > 0, \quad \text{and} \quad B^2 - 3EC > 0$$

which is equivalent to

$$p < \frac{1}{\sigma\mu\beta A}\Big[\mu(\mu+\gamma)(\mu+\theta+\varphi)-\beta(A+\Lambda)(1+\sigma\varphi)\Big]$$

$$\varphi < \frac{\sigma\beta(A+\Lambda-\sigma\mu(\gamma+\mu)-\mu(\mu+\theta)}{\sigma\mu}$$

and

$$p > \frac{1}{3\sigma^2\mu\beta A}\Big[-3\beta\sigma(A+\Lambda)(\mu+\theta+\varphi)+3\mu\sigma(\mu+\gamma)(\mu+\theta+\varphi)- \mu\Big((\mu+\theta+\varphi)+\sigma(\mu+\gamma)-\frac{\sigma\beta(A+\Lambda}{\mu}\Big)^2\Big]$$

Figure 5.1: Backward bifurcation with $A = 10$, $p = 0.01$, $\gamma = 0.12$, $\varphi = 0.6$, $\theta = 0.1$, $\Lambda = 0.03$, $\mu = 0.02$ and $\beta = 1$

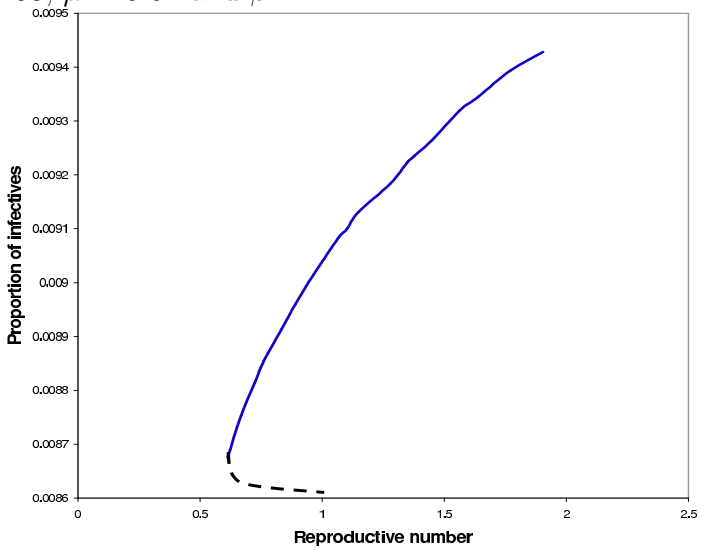


Figure 5.1 shows the backward bifurcation obtained for the parameters give. We note that varying the immigration rate may have an effect of decreasing or increasing R_0. If the immigration level is significantly high, then the bifurcation point is vastly reduced that elimination of an already established disease is odious.

5.4 Conclusion

The SIS model with vaccination has been analyzed for disease control purposes. We see that merely reducing the replacement number to below 1 does not seem

to eradicate the disease. In severe cases, perhaps the disease may fail to be controlled totally. The exhibition of a backward bifurcation may mean that, in order to control the disease, we need a vaccination rate, φ that far exceeds the vaccination reproduction number.

Chapter 6

Backward bifurcation in Progression age enhanced model with super-infection

6.1 Introduction

It was a physician, Lt. Col. A. G. Mckendrick who first introduced age structure into the dynamics of a one sex-population(1926). Since then several age structured linear and nonlinear continuous models have been studied such as in [15]. These assume that a population can be described as a function of two variables : age a and time t. However in recent years, these continuous epidemiological models have been used to study progression age bifurcations. The model we will study has an additional component of super-infection, and the model may exhibit backward bifurcation as in [13]. We aim to produce criteria which give rise to backward bifurcation also known as subcritical bifurcation (Chapter 3, S. Wiggins). Super-infection is seen as an important factor in giving rise to backward bifurcation. We therefore study it in this chapter and perhaps try to show how it influences the dynamics of the system. In the wake of reemergence of infections such as *tuberculosis*, superinfection and coinfection have received a lot of attention.

We begin by briefly describing a few processes. Conceivably, an infected individual is subject to further contacts with infectious individuals. It depends on the type of disease whether, in a mathematical model, these may be ignored or may be included. This concept is called *super-infection*. Super-infection is the concurrent or subsequent multiple infection of a host with the same parasite, may it be with identical or different strains. *Co infection* occurs when a host contracts several infections. For instance, an HIV-infected individual with a severely compromised immune system can become co-infected with an opportunistic infection. In case of tuberculosis, a co-infection may lead to re-activation of TB in latently infected individuals. Of special modelling interest are:

- dynamic interplay between processed of super-infection and co-infection;
- significance of age structure in the population of hosts

Superinfection is also conceived to be important for slowly progressing microparasitic diseases like the viral diseases HIV and hepatitis A, B and C and the bacterial disease cholera, typhoid and tuberculosis also known as TB. Apart from having an initial phase in which the infectious agent develops rapidly in the human host, the scenarios of progression seem to be somewhat different in diseases. In HIV the fast initial phase is followed usually by a long phase of low virus titers which is eventually followed in many or most cases by AIDS. We note that In sub-saharan Africa, there is prevalence of HIV-1 which leads to fully blown AIDS, whereas HIV-2, dominant in west Africa does not lead to fully blown AIDS. In TB, asymptotically infected individuals of the infected individuals are passive carriers for a long time until, possibly, their infectivity is activated. In HIV, super-infection can lead to the rapid progression of AIDS, while in TB could play a part in activating careers.

We will briefly discuss the phenomenon of multiple endemic equilibria. In particular in the subcritical (or subthreshold) [7] case when the basic replacement ratio is smaller than one, has recently attracted a lot of attention in mathematical epidemiology. [13] From a control point of view, in order to eradicate a well-established infectious disease, it is not sufficient to lower the basic reproduction number R_0 below one, but below another threshold value called the transmission threshold (sub-threshold in other models), consists of lowering the disease

prevalence into the domain of attraction of the disease-free equilibrium. It is the aim of this chapter to strengthen the case for super-infection to cause multiple endemic equilibria.

We assume that super-infection speeds up the progression of a latent individual to active infectiousness. We assume that super-infection is a primary infection itself, and is a randomized event. We split the latency stage into the progressive and quiescent stages. With a certain rate η_1, the individual passes from the progressive latent stage to the infectious stage or, with a rate ρ, drops to the quiescent stage. Super-infection lifts the individual back into the progressive stage. In order to give the term disease-progression a meaning, we assign a class age a, to both progressing and quiescent exposed individuals, namely the time after infection that has been spent in the progressive stage. We model the progression by a linear transport equation, i.e., a first order linear partial differential equation, with a nonlinear boundary condition. Since in the progressive stage, the exposed individuals increase their class age, while it is on hold in the quiescent stage, we call a the progression age.

Further to explain the effect of superinfection on progression age, we need to consider the per capita rate of infection, k, and the rate of super-infection, $\tilde{k}$. These two parameters are not independent because they are compound parameters which include common contact rates while the probabilities that a contact actually leads to an infection may be different. We write $\tilde{k} = \psi k$. The factor ψ describes how an individual's susceptibility at a secondary infection relates to the susceptibility at the primary infection. If $\psi < 1$, the primary infection protects against secondary infections, while it facilitates super-infection if $\psi > 1$. As it turns out $\psi > 1$ is required for multiple endemic equilibria to occur, i.e., it is necessary that super-infection is facilitated by the primary infection. We let the transmission rate η_1 be a step function

$$\eta_1 = \begin{cases} 0 & \text{on} \quad [0, a^+) \\ \eta_1 & \text{on} \quad (a^+, \infty) \end{cases}$$

We aim to show that there is a backward bifurcation of endemic equilibria in k if

$$\psi\left(\frac{\rho}{\rho+\mu+\eta}+\rho a^{+}\right)>1$$

6.2 The model

We consider a disease spreading in a population with the total population size at time t given by $N(t)$. The population is divided into various compartments, with $S(t)$ and $I(t)$ denoting the susceptible and infected classes respectively. It is assumed that a susceptible individual, once in contact with an infected individual either becomes infectious right away and enters the infective class (with probability p) or becomes exposed and enters an exposed class (with probability $q = 1 - p$) where it is infected but not infectious, i.e., the disease is latent. To model the effect of super-infection we subdivide the latent stage, and accordingly the exposed class, into a latent stage where the disease progresses and a latent stage where the disease development is on hold; that is the *progressive latent stage* and the *quiescent latent stage* respectively. A freshly exposed individual first enters the progressive exposed class from which, at a certain rate ρ, it can drop to the quiescent stage. In the quiescent individuals can be re-infected (super-infection) and reenter the progressive exposed class. Individuals that stay in the exposed class long enough become infectious hence enter the infectious class, I, at a rate ρ_1. We keep track of the class age of progressing exposed individuals and let a denote the time after infection that an exposed individual has spent in the progressive stage. Thus we call a the progressive age. The transmission rates ρ_1 and ρ as well as the super-infection rate depend on class age a. $E_1(a,t)$, as a function of a, is the class-age density of exposed individuals in the progressive latent stage at time t, while $E_2(a,t)$ is the density of the individuals in the quiescent stage. We will include vital dynamics in this model hence individuals die from the disease at a per capita rate γ, susceptibles are imported into the population at a rate Λ, and there is a constant natural death rate μ.

We then have the system of equations as

$$\begin{aligned}
\dot{S}(t) &= \Lambda - k\frac{SI}{N} - \mu S \\
\dot{I}(t) &= pk\frac{SI}{N} + \int_0^\infty \eta_1(a)E_1 da - (\mu+\gamma)I \\
(\partial_t + \partial_a)E_1(a,t) &= -\rho(a)E_1 + \tilde{k}(a)\frac{E_2 I}{N} - \eta_1(a)E_1 - \mu E_1 \qquad (6.1) \\
E_1(0,t) &= qk\frac{SI}{N} \\
\partial_t E_2(a,t) &= \rho(a,t)E_1 - \tilde{k}(a)\frac{E_2 I}{N} - \mu E_2
\end{aligned}$$

where we used the following parameters:

We will assume that

Parameter	Symbol
per capita recruitment rate into the population	Λ
per capita natural death rate	μ
disease-induced mortality rate	γ
probability of a susceptible transferring to the infective class -	
after contact with an infective	p
probability of a susceptible transferring to progressive -	
exposed class after contact with an infective	q
effective per capita infection rate for susceptibles	k
per capita super-infection rate for individuals in the -	
quiescent exposed	
class with progression age a	$\tilde{k}(a)$
per capita rate of transmission from the exposed to -	
quiescent exposed stage	$\rho(a)$
per capita rate of transmission from the progressive exposed -	
to the infective stage	$\eta_1(a)$

Table 6.1: Table of notation in progression age model

$$\begin{aligned}
\eta_1(\cdot), \rho(\cdot), \tilde{k}(\cdot) &\in L^\infty(0,\infty) \\
\rho(\cdot)\tilde{k}(\cdot) &\quad \text{are uniformly continuous} \qquad (6.2) \\
p + q &= 1
\end{aligned}$$

We make further the assumption that all the parameters of the model are non-negative and $\mu > 0$. The equations in (6.2) have the initial conditions :

$$S(0) = S_0, I(0) = I_0, E_1(a,0) = E_1^0(a), E_2(a,0) = E_2^0(a)$$

Adding all the equations of (2) we see that

$$\dot{N}(t) = \Lambda - \mu N - \gamma I$$

with initial condition $N(0) = N_0$.

Disease-free equilibrium In the disease-free equilibrium population, the equation of $N(t)$ becomes $\dot{N}(t) = \Lambda - \mu N$. Solving this, we get
$\dot{N}(t) = \Lambda - \mu N$
$\dot{N}(t) - \Lambda + \mu N = 0$
using the integrating factor: $exp^{\int \mu dt} = e^{\mu t}$,
$\dot{N}e^{\mu t} + \mu N e^{\mu t} = \Lambda e^{\mu t}$
$\frac{d}{dt}\left[Ne^{-\mu t}\right] = \Lambda e^{\mu t}$
$-N(0) + Ne^{\mu t} = \int \Lambda e^{\mu s} ds$,
$N(t)e^{-\mu t} = \frac{\Lambda}{\mu} e^{\mu} t + C + N(0)$, where C is a constant.

$$\text{hence} \quad N(t) = \frac{\Lambda}{\mu}\left(1 - e^{\mu t}\right) + N(0)e^{-\mu t} \tag{6.3}$$

and hence $\lim_{t\to\infty} N(t) = \frac{\Lambda}{\mu}$.

We introduce the following quantities which are

$$\pi(a) = e^{-} \int_0^a \rho(\sigma) d\sigma$$

$$\pi_1(a) = e^{-} \int_0^a \eta_1(\sigma) d\sigma \tag{6.4}$$

The quantity $\pi(a)\pi_1(a)$ gives the probability of remaining in the progressive exposed stage till stage a, provided that the individual survives to that age.

6.3 Equilibria

Setting the system (6.2) to zero, and normalizing the system we get:

$$\begin{aligned} 0 &= \mu - ks^*i^* - \mu s + \gamma i^* \\ 0 &= pks^*i^* + \int_0^\infty \eta_1(a)e_1^*(a)da - (\mu+\gamma)i^* \\ \frac{d}{da}e_1^* &= -\rho(a)e_1^* + \tilde{k}(a)e_2^*i^* - \eta_1(a)e_1^* - \mu e_1^* \\ e_1^*(0) &= qks^*i^* \\ 0 &= \rho(a,t)e_1^* - \tilde{k}(a)e_2^*i^* - \mu e_2^* \end{aligned} \tag{6.5}$$

where $s^* = \frac{S^*}{N^*}, i^* = \frac{I^*}{N^*}, e_1^* = \frac{E_1^*}{N^*}, e_2^* = \frac{E_2^*}{N^*}$
We note that

$$s^* + i^* + \int_0^\infty e_1^*(a)da + \int_0^\infty e_2^*(a)da = 1 \tag{6.6}$$

Each solution $\varepsilon^* = (s^*, i^*, e_1^*, e_2^*)$ of (6.6) gives an equilibrium of the system (6.2).

The system (6.6) at disease-free equilibrium has the solution $\varepsilon^0 = (1, 0, 0, 0)$, where $S^* = \frac{\Lambda}{\mu}$, $I^* = E_1^* = E_2^* = 0$. To find the endemic equilibria, $I^* \neq 0$, and using the last equation we get

$$e_2^*(a) = \frac{\rho(a)e_1^*(a)}{\tilde{k}(a)i^* + \mu} \tag{6.7}$$

and using the first equation, s^* becomes:

$$s^* = \frac{\mu + \gamma i^*}{ki^* + \mu} \tag{6.8}$$

We note that $s^* \leq 1$ if and only if $\gamma \leq k$. Exploring $\gamma > k$, we see that the model (6.2) only has disease-free equilibrium. Substituting (6.7) and (6.8)in the third equation, we get

$$\begin{aligned} \frac{d}{da}e_1^* &= -\rho(a)e_1^* + \tilde{k}(a)i^*\frac{\rho(a)e_1^*(a)}{\tilde{k}(a)i^* + \mu} - \eta_1(a)e_1^* - \mu e_1^* \\ e^*(0) &= qks^*i^* \end{aligned} \tag{6.9}$$

$$\frac{d}{da}e_1^* = \Bigg[-\rho(a) + \tilde{k}(a)i^* \frac{\rho(a)}{\tilde{k}(a)i^* + \mu} - \eta_1(a) - \mu \Bigg] e_1^*$$

The integrating factor is

$$e^{\int [-\rho(a) + \tilde{k}(a)i^* \frac{\rho(a)}{\tilde{k}(a)i^* + \mu} - \eta_1(a) - \mu] da}$$

$$= e^{\int -\rho(\sigma) d\sigma} \cdot e^{\int \frac{\tilde{k}(\sigma)\rho(\sigma)}{\tilde{k}(\sigma)i^* + \mu} d\sigma} \cdot e^{-\int \eta_1(\sigma) d\sigma} \cdot e^{-\int \mu d\sigma}$$

so

$$\frac{d}{da}\left[e_1^* \left\{ e^{-\mu a} \pi(a) \pi_1(a) e^{\int \frac{\tilde{k}(\sigma)\rho(\sigma)}{\tilde{k}(\sigma)i^* + \mu} d\sigma} \right\} \right] = 0$$

hence

$$e_1^*(a) = e^{-\mu a} \pi(a) \pi_1(a) e^{\int_0^\infty \frac{\tilde{k}(\sigma)\rho(\sigma)i^*}{\tilde{k}(\sigma)i^* + \mu} d\sigma} \cdot qks^*i^* \tag{6.10}$$

This implies an estimate from below on $e_1^*(a)$:

$$e_1^*(a) > qks^*i^* e^{-\mu a} \pi(a) \pi_1(a)$$

and integrating with respect to a

$$\int_0^\infty e_1^*(a) da > ks^*i^*q \int_0^\infty e^{-\mu a} \pi(a) \pi_1(a) da$$

Let

$$\alpha = q \int_0^\infty e^{-\mu a} \pi(a) \pi_1(a) da \tag{6.11}$$

then we see that $\mu\alpha < q \leq 1$. $\mu\alpha$ is interpreted as the probability of dying from natural causes while being in the progressive latent stage provided that there is no super-infection [11]. From (6.3), (6.8) and the above inequality we get

$$i^* \leq \frac{k(1 - \mu\alpha) - (\gamma + \mu)}{k(1 + \gamma\mu)}$$

Thus we have the resultant theorem

Theorem 3. *If* $k \leq \frac{(\nu+\mu)}{1-\mu\alpha}$ *then the system(6.2) does not have endemic equilibria*

This is rather clear and thus to study endemic equilibria, we assume $k > \frac{(\nu+\mu)}{1-\mu\alpha}$.

e_1^* is an increasing function from (6.10), therefore the equilibrium proportion of progressing exposed individuals increases as the proportion of infective individuals increases [11]. Solving for i^* in (6.6) we get

$$\begin{aligned} 0 &= pks^*i^* + \int_0^\infty \eta_1(a)qks^*i^*e^{-\mu a}\pi_1(a)e^{-\int_0^a \frac{\rho(\sigma)\mu}{k(\sigma)i^*+\mu}d\sigma}da - (\gamma+\mu)i^* \\ \text{then} \\ 1 &= \frac{pks^*}{(\gamma+\mu)} + \frac{qks^*}{(\gamma+\mu)}\int_0^\infty \eta_1(a)qks^*e^{-\mu a}\pi_1(a)e^{-\int_0^a \frac{\rho(\sigma)\mu}{k(\sigma)i^*\mu}d\sigma}da \end{aligned} \tag{6.12}$$

Let

$$\varphi(i^*) = \int_0^\infty \eta_1(a)qks^*e^{-\mu a}\pi_1(a)e^{-\int_0^a \frac{\rho(\sigma)\mu}{k(\sigma)i^*+\mu}d\sigma}da \tag{6.13}$$

then integrating by parts, we clearly see that

$$\varphi(i^*) = 1 - \mu\int_0^\infty \left(1 + \frac{\rho(a)}{\tilde{k}(\sigma)i^*+\mu}\right)e^{-\mu a}\pi_1(a)e^{-\int_0^a \frac{\rho(\sigma)\mu}{k(\sigma)i^*+\mu}d\sigma}da \tag{6.14}$$

We then make a note that regarding the integral from (6.13) and (6.14), we see that

Proposition 5. *For all* $0 \leq i^* \leq 1$ *we have that*

$$\varphi(i^*) < 1$$

$\varphi(i^*)$ *is also an increasing function of* i^*

Using (6.8), we see that the i^*th component of each equilibrium $\varepsilon^* = (s^*, i^*, e_1^*, e_2^*)$ is a solution to i in the following equation obtained from (6.12)

$$\frac{pks^*}{(\gamma+\mu)} + \frac{qks^*}{(\gamma+\mu)}\varphi(i) = \frac{ki+\mu}{\mu+\gamma i} \tag{6.15}$$

with the other components of $\varphi(i^*)$ in equations (6.8) and (6.9). We want to use Rolle's theorem, thus assign the left and right hand sides of (6.15) to functions $f(i)$ and $g(i)$ respectively. We then have

$$\begin{aligned} f(i) &= \frac{pks^*}{(\gamma+\mu)} + \frac{qks^*}{(\gamma+\mu)}\varphi(i) \\ g(i) &= \frac{ki+\mu}{\mu+\gamma i} \end{aligned} \tag{6.16}$$

The existence and number of equilibria depends on the number of times the graphs of these functions intersect or meet.

We have seen in earlier models that the basic reproductive number $R_0 = 1$ is a threshold point and thus the existence and number of equilibria depend on it. Replacing $R_0 = 1$ on the left hand side of (6.12), with $s^* = 1$;

$$R_0 = \frac{pk}{(\gamma+\mu)} + \frac{qk}{(\gamma+\mu)} \int_0^\infty \eta_1(a) qk e^{-\mu a} \pi_1(a) e^{-\int_0^a \frac{\rho(\sigma)\mu}{k(\sigma)i^*+\mu} d\sigma} da \tag{6.17}$$

We note that $\frac{1}{\gamma+\mu}$ is the average time spent in the infectious stage, so $\frac{k}{\gamma+\mu}$ is the average number of individuals an infectious individual can infect. So R_0 (6.17) gives the average number of secondary cases resulting from an infective individual. R_0 does not depend on the super-infection rate $\tilde{k}$, and this shows that super-infection does not result in additional infections. Integrating by parts, clearly we see that

$$R_0 = \frac{k}{\gamma+\mu}(1 - \mu\alpha - \beta)$$

where

$$\beta = q \int_0^\infty \rho(a) e^{-\mu a} \pi_1(a) \pi(a) da$$

We purposefully let α be replaced by β so that we may interpret β. This has been interpreted as the probability of dropping to the quiescent latent stage in Thieme's earlier paper [Thieme, 2002]. It is well known that in simpler models, for $R_0 < 1$ the disease-free equilibrium is stable, thus the condition we set for the non existence of the endemic state is

$$R_1 = \frac{k}{\gamma+\mu}(1 - \mu\alpha) \leq 1 \tag{6.18}$$

and note that $R_0 < R_1$. R_1 is the average number of individuals infected by an infectious individual in a susceptible population that do not die during the progressive latent stage. We will also recall that $\mu\alpha$ is the probability of dying

whilst in the progressive latent stage.
We use the following terminology in a bid to handle the number of endemic equilibria; Let $\varepsilon^* = (s^*, i^*, e_1^*, e_2^*)$, $\varepsilon^{**} = (s^{**}, i^{**}, e_1^{**}, e_2^{**})$ be two equilibria of the system (1). We also demand that $\varepsilon^* \leq \varepsilon^{**}$ if $i^* \leq i^{**}$. In other words, we order the equilibria according to the values of their proportions of the infective individuals in them. We also assume that is *simple* equilibrium if

$$\frac{qk}{\gamma+\mu}\dot{\varphi}(i^*) \neq \frac{k-\gamma)\mu}{(\gamma i^+\mu)^2} \tag{6.19}$$

Geometrically this means that the two functions $f(i)$ and $g(i)$ are different at the equilibrium point ε^*, and therefore, intersect at ε^*. This means therefore that the difference between $f(i)$ and $g(i)$ changes sign. If ε^* and ε^{**} are simple, then $\varepsilon^* \neq \varepsilon^{**}$ by theory of linear algebra. This means that the functions $f(i)$ and $g(i)$ have a common tangent at the equilibrium point ε^* and their graphs either touch or intersect at that point.

By [12, Theorem 2] we develop the following theorem

Theorem 4. *1. If $R_1 < 1$, then there are no endemic equilibria*

2. If $R_0 < 1$ and (6.2) has endemic equilibria which are simple, then there is an even number of endemic equilibria

3. If $R_0 > 1$ the endemic equilibria has at least one equilibrium. If there are several equilibria which are all simple, then their number is odd.

proof: Part (1) follows from the discussion above. The function $f(i)$ is increasing and is concave down. $f(0) = 1$ and $f(1) = \frac{(k+\mu)}{\gamma+\mu}$. The function $g(i)$ is also an increasing function but its concavity may be changing. $g(0) = R_0$ and $g(1) < \frac{k}{\gamma+\mu}$, by proposition ()and $p + q = 1$. So $g(1) < f(1)$. Consequently, if $R_0 < 1$ then $g(0) < f(0)$ and there are either no intersections or an even number of intersections of the two graphs. If $g(0) > f(0)$ then there is at least one intersection of the graphs, or an odd number of them. ♣

We also need to establish the uniqueness criteria for the endemic equilibrium. Derivating (6.13) we get

$$\dot{\varphi}(i^*) = \int_0^\infty \eta_1(a) q k s^* e^{-\mu a} \pi_1(a) e^{-\int_0^a \frac{\rho(\sigma)\mu}{\tilde{k}(\sigma)i^*+\mu} d\sigma} \left(\frac{\tilde{k}(\sigma)\rho(\sigma)}{(\tilde{k}(\sigma)i^*+\mu)^2} d\sigma \right) da \tag{6.20}$$

Assume that there are two endemic equilibria, then by Rolle's theorem there exists some $i \in (0,1)$ such that

$$\dot{g}(i) = \dot{f}(i)$$

Then

$$\dot{g}(i) < \frac{qk}{(\gamma+\mu)\mu} \int_0^\infty \eta_1(a) q k s^* e^{-\mu a} \pi_1(a) e^{-\int_0^a \frac{\rho(\sigma)\mu}{\tilde{k}(\sigma)i^*+\mu} d\sigma} \left(\int_0^\infty \tilde{k}(\sigma)\rho(\sigma) d\sigma \right) da$$

We will recall that for the existence of equilibria it is necessary that $k > \gamma$, hence

$$\dot{f}(i) > \frac{(k+\gamma)\mu}{(\gamma+\mu)^2}$$

6.3.1 Existence of endemic equilibria when $R_0 < 1$. Backward bifurcation

We introduce the infection rate k as the bifurcation parameter in this section as R_0 is not a good parameter to use in order to establish bifurcation behavior. We assume that there is no coupling between the infection rate k and the super-infection rate $\tilde{k}$. Solving for k(making k subject of equation) in (6.15) we get

$$k = \frac{\mu(\mu+\gamma)}{p(\mu+\gamma i^*) + q(\mu+\gamma i^*)\varphi(i^*) - (\mu+\gamma)i^*} \tag{6.21}$$

where $k = k(i^*)$. Derivating $k(i^*)$ with respect to i^*, and going through long expressions not shown here, we get

$$\dot{k}(i^*) = \frac{\mu(\mu+\gamma)(p\gamma + q\gamma\varphi(i^*) + q(\mu+\gamma i^*)\dot{\varphi}(i^*) - (\gamma+\mu))}{(p(\mu+\gamma i^*) + q(\mu+\gamma i^*)\varphi(i^*) - (\mu+\gamma)i^*)^2} \tag{6.22}$$

The bifurcation at the disease free equilibrium, where $i^* = 0$ is supercritical if and only if $\dot{k}(i^*) > 0$ and subcritical if and only if $\dot{k}(i^*) < 0$. This condition is well in accordance with [9, p.15]. At $i^* = 0$

$$\dot{k}(0) = p\gamma + q\gamma\varphi(0) + q\mu\dot{\varphi}(0) - (\gamma+\mu)$$

Thus, the disease free equilibrium is subcritical if and only if

$$\begin{aligned}(p\gamma + q\gamma\varphi(0) + q\mu\dot{\varphi}(0) - (\gamma+\mu)) &> 0 \\ q\gamma\varphi(0) + q\mu\dot{\varphi}(0) &> -p\gamma + (\gamma + \mu(p+q)) \\ \rightarrow q\gamma\varphi(0) + q\mu\dot{\varphi}(0) &> \mu + q\gamma \end{aligned} \tag{6.23}$$

We then have the resultant proposition

Proposition 6. *The system exhibits a backward bifurcation if and only if*

$$q\dot{\varphi}(0) - q\gamma \int_0^\infty \left(\frac{\mu(1+\rho(a))}{\mu}\right) e^{-\mu a}\pi(a)\pi_1(a)\pi(a)da > 1 \tag{6.24}$$

where we may have

$$\dot{\varphi}(0) = \frac{1}{\mu}\int_0^* \eta_1(a)e^{-\mu a}\pi(a)\pi_1(a)\pi(a)\int_0^a \rho(\sigma)\tilde{k}(\sigma)d(\sigma)da \tag{6.25}$$

The model thus exhibits a backward bifurcation if there is a set of parameters such that (6.24) is satisfied. We now show the existence of a backward bifurcation by use of an example in the next section.

6.3.2 Example

We assume that $\tilde{k}(a) = k\psi(a)$. We consider a non fatal disease, that is $\gamma = 0$. The infectives are assumed to enter the latent stage alone, $q = 1$ and $p = 0$. The condition for the backward bifurcation is $\dot{\varphi}(0) > 1$. We then have

$$\dot{\varphi}(0) = \frac{1}{\mu}\int_0^* \eta_1(a)e^{-\mu a}\pi(a)\pi_1(a)\pi(a)\int_0^a \rho(\sigma)\tilde{k}\psi(\sigma)d(\sigma)da > 1$$

(6.22) evaluated at $i^* = 0$, we get $k = \frac{\mu}{\varphi(0)}$ hence

$$\dot{\varphi}(0) = \int_0^* \eta_1(a)e^{-\mu a}\pi(a)\pi_1(a)\pi(a)\left(\int_0^a \rho(\sigma)\varphi(\sigma)d(\sigma) - 1\right)da > 0 \tag{6.26}$$

Since there is some latency period, we do not expect individuals in the latency stage to become infectious immediately after infection, thus we let $\eta_1 = 0$ for

small $a > 0$. Let a^+ be the largest a such that $\eta_1 = 0$ almost everywhere on $[0, a)$, then a^+ is finite unless $\eta_1 = 0$ almost everywhere on $[0, a)$. Parameter $a^+$is the threshold progression age for activation at which progressing exposed individuals enter the infectious class. We remark that if $a^+ \in [0, \infty)$, then $\eta_1 = 0$ depends on class-age in a crucial way. With all these assumptions we then say

Theorem 5. *The endemic equilibria exhibits backward bifurcation in k if $p = 0$, $\gamma = 0$, $a^+ \in (0, \infty)$ and*

$$\int_0^* \rho(\sigma)\psi(\sigma)d(\sigma) > 1$$

6.4 Discussion

The phenomenon of multiple endemic equilibria, in particular in the subthreshold (or subcritical) case where the replacement ratio R is less than one, has recently attracted a lot of attention in mathematical epidemiology. From a control point of view, it means therefore that in order to eradicate a well-established disease, it does not suffice to lower R_0 below one, but rather below another threshold value which is the *transmission threshold*. In [9] this falls in the region of what is described as the *subthreshold*. We note that backward bifurcations of endemic equilibria occurs as a result of the incorporation of several groups of susceptibles, infectives (*as shown in chapter 3*), or both (*as shown in chapter 4*)with different susceptibilities and or infective rates to the disease. Replacing the standard or mass action incidence by a power law also leads to backward bifurcation.

6.5 Conclusion

We have shown that in progressive age enhanced models backward bifurcations do exist and we use a simple example to sustain this claim. We however considered a simpler case where the disease is non fatal. If the disease is fatal the model becomes very complex. In this chapter we do not explore numerical analysis due to time constraints. We have however shown that this model exhibits backward bifurcation. The wellposedness of the model and uniqueness of solution has been considered in similar models in [15] and [16] It is our desire to further pursue the numerical analysis and consider the case where there is disease mortality.

In the chapters we managed to show several factors that influence backward bifurcation and forward bifurcation using various bifurcation techniques. We notice that factors that influence backward bifurcations are vast and in each model we can only consider a few factors. We considered numerical analyses to strengthen the exhibition of backward bifurcations in some epidemiological models, followed by brief discussions in each chapter.

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