Bifurcation analysis and nonstandard finite difference schemes for Kermack and McKendrick type epidemiological models

by

Yibeltal Adane Terefe

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DECLARATION

I, the undersigned, hereby declare that the dissertation submitted herewith for the degree Magister Scientiae to the University of Pretoria contains my own, independent work and has not been submitted for any degree at any other university.

Signature:

Name: Yibeltal Adane Terefe

Date: May 2012

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Abstract

The classical SIR and SIS epidemiological models are extended by considering the number of adequate contacts per infective in unit time as a function of the total population in such a way that this number grows less rapidly as the total population increases. A diffusion term is added to the SIS model and this leads to a reaction–diffusion equation, which governs the spatial spread of the disease. With the parameter $\mathcal{R}_0$ representing the basic reproduction number, it is shown that $\mathcal{R}_0 = 1$ is a forward bifurcation for the SIR and SIS models, with the disease–free equilibrium being globally asymptotic stable when $\mathcal{R}_0$ is less than 1. In the case when $\mathcal{R}_0$ is greater than 1, for both models, the endemic equilibrium is locally asymptotically stable and traveling wave solutions are found for the SIS diffusion model. Nonstandard finite difference (NSFD) schemes that replicate the dynamics of the continuous SIR and SIS models are presented. In particular, for the SIS model, a nonstandard version of the Runge-Kutta method having high order of convergence is investigated. Numerical experiments that support the theory are provided.

On the other hand the SIS model is extended to a Volterra integral equation, for which the existence of multiple endemic equilibria is proved. This fact is confirmed by numerical simulations.

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Chapter 1

Introduction

The application of mathematics to the understanding of infectious disease was initiated by D. Bernoulli (1760) who was interested in evaluating the effectiveness of techniques of "variolation" against smallpox, with the aim of influencing public health policy. Apart from Malthus law, i.e. the exponential growth in population, that was formulated in 1798, the other two main principles in epidemiology were published far later namely, early in the nineties. These are: the mass action principle (W.H.Hamer (1906) and R. Ross (1908)) and the threshold theory (see [33]). Since then, many researchers have been interested in mathematical epidemiology. In the process, compartmental models whereby the host population of parasites is divided into the following classes have been occupying an important place: M (Infants with passive immunity), S (Susceptible individuals), E (Exposed individuals), I (Infected individuals) and R (Recovered individuals). Based on the flow patterns between compartments, several models have been developed with acronyms such as MSEIR, MSEIRS, SEIR, SEIRS, SIR, SIS, etc. (See [28]).

The primary objective of this dissertation is to provide a comprehensive analysis of some of the key issues in the modeling of infectious diseases. The simpler the model is, the more explicit and precise are the results. That is why, we focus on the SIR and SIS Kermack–McKendrick models, which are among the simplest ones. However, these simple models will be investigated under the following extended settings:

(A1) In the SIR and SIS models the number of adequate contacts per infective in unit time is assumed to be a function of the total population in such a way that this number grows less rapidly as the total population increases (see comments at the beginning

of Section 3.2.1 and Section 3.4.1 for the biological relevance of this assumption);

(A2) A diffusion term is added to the SIS model and this leads to a reaction–diffusion equation, which governs the spatial spread of the disease;

(A3) The SIS model is formulated as a Volterra integral equation (of the second kind) or integro–differential equation.

Under these specific settings, our first set of contributions is from the theoretical point of view and can be outlined as follows:

(B1) We establish the well–posedness of each of the models mentioned in (A1), (A2) and (A3) in such a way that the obtained unique solution is biologically meaningful; this includes the boundedness and positivity properties of solutions.

(B2) We give precise stability properties of the equilibria of the systems, including the global asymptotic stability of the disease–free equilibrium. Furthermore, the value 1 of the basic reproduction number $\mathcal{R}_0$ is shown to be a forward bifurcation for the SIR and SIS models in (A1), whereas the possibility of backward bifurcation or co–existence of stable disease–free equilibrium with at lease one stable multiple endemic equilibrium is alluded for the Volterra integral equation formulation.

It should be noted that the continuous model under consideration cannot be completely solved by analytical techniques. Thus, numerical schemes and simulations are of fundamental importance in gaining some useful insights on the solutions of the continuous models. Consequently, the additional, but not the least, objective of this dissertation is to provide reliable numerical schemes. Our second set of contributions is from the constructive point of view and can be outlined as follows:

(C1) We design nonstandard finite difference (NSFD) schemes which replicate the qualitative properties of the continuous models stated in (B) above.

(C2) We propose the nonstandard version of the Runge–Kutta method, which is proved theoretically and computationally to be of order 4.

In order to achieve the theoretical contributions in (B) above, we used the following mathematical tools:

The Banach fixed–point theorem or contraction principle [60] is the main ingredient for the proof of the existence and uniqueness of solutions of each model. This was coupled with techniques such as the integrating factor and the comparison theorem [54] to show the positivity of the solutions. For the SIR and SIS models, Hartman–Grobman Theorem [55] helped to establish the local stability properties, while LaSalle Invariance Principle [35] led to the global asymptotic stability of the disease–free equilibrium. In both cases, a threshold condition defined through the basic reproduction number $\mathcal{R}_0$ is involved. For the SIS diffusion model, the stability property resulted from the spectral theory of the Sturm–Liouville problem corresponding to its linearization.

Regarding our constructive contributions, the main strategies are the following two of Mickens' rules [48], as singled out in [2]:

- The standard denominator of the discrete derivative is replaced by a more complex function.
- Nonlinear terms must be approximated in a nonlocal way.

Given the importance of the NSFD schemes in this dissertation, we elaborate here a bit more on the two rules. To this end, we consider the SIS– diffusion model in its dimensionless form, i.e.,

$$I_t = (1 - I)I + I_{xx}, \tag{1.0.1}$$

which is the Fisher equation. For the model $(1.0.1)$, we propose the NSFD scheme

$$\frac{I_m^{k+1} - I_m^k}{e^{\Delta t} - 1} = (1 - I_m^{k+1})\frac{I_{m+1}^k + I_m^k + I_{m-1}^k}{3} + \frac{I_{m+1}^k - 2I_m^k + I_{m-1}^k}{4\sin^2\frac{\Delta x}{2}}, \tag{1.0.2}$$

where I_m^k represents an approximation of $I(x,t)$ at $x = m\Delta x$ with $m \in \mathbb{Z}$ and $t = k\Delta t$ with $k \in \mathbb{N}$, $\Delta x > 0$ and $\Delta t > 0$ being the space and time step sizes, respectively. Unlike the standard finite difference method

$$\frac{I_m^{k+1} - I_m^k}{\Delta t} = (1 - I_m^k)I_m^k + \frac{I_{m+1}^k - 2I_m^k + I_{m-1}^k}{(\Delta x)^2},$$

the NSFD scheme $(1.0.2)$, which is characterized by the mentioned Mickens' rules, replicates essential properties of the continuous model $(1.0.1)$ such as positivity and boundedness of solutions.

Although the SIR and SIS models are simple, the results on the qualitative analysis summarized under (B) above extend to most compartmental models and have been studied extensively $[6, 7, 8, 14, 17, 18]$. However, the design and analysis of reliable numerical methods such as the NSFD schemes considered here have not yet been sufficiently investigated. Existing works on NSFD schemes in epidemiology include $[3, 4, 21, 24]$. Further discussions and comments as to how our findings fit in the literature will be done within the relevant chapters and/or sections of the dissertation. Some results of the dissertation are published in $[41]$. Some other results are presented at the last two annual congresses of the South Africa Mathematical Society $[39, 40]$.

The rest of the dissertation is organized as follows: Chapter 2 deals with the review of selected basic concepts on dynamical systems defined by ordinary differential and difference equations. These revisions are helpful in the analysis of the SIR and SIS models. The discrete dynamical systems on which we place the emphasis are NSFD schemes. The general rules for their construction are presented in this chapter. Although the chapter deals with preliminaries, we conclude it by proposing a new numerical method of high order, i.e. the nonstandard Runge–Kutta method of order 4.

Chapter 3 is devoted to SIR and SIS models with a general contact rate. It is shown that these models are continuous dynamical systems on a biologically feasible region of the positive cone. It is further shown that the disease–free equilibrium E_0 is globally asymptotically stable whenever the basic reproduction number $\mathcal{R}_0$ is less than 1, while this equilibrium becomes unstable and a unique locally asymptotically stable endemic equilibrium E_∞ is born when $\mathcal{R}_0 > 1$. On the constructive side, NSFD schemes that replicate all these properties of the continuous models are designed and analyzed. From the discussion on commonly used contact rates, we single out the standard incidence formulation in order to provide more illustrative results. Of particular importance is the application to the SIS model of our new NSFD Runge–Kutta method which shows excellent performance.

In Chapter 4, the SIS model is extended to a reaction–diffusion (partial differential) equation that governs the spatial spread of an epidemic. The existence of a unique and biologically meaningful solution is proved by using the Banach fixed point theorem. Necessary and sufficient conditions for the existence of traveling wave solution are investigated. Once again, the chapter ends with the design and analysis of various NSFD schemes that

preserve qualitative properties of the continuous model such as positivity and boundedness of solutions, conservation law and stability of equilibria.

Chapter 5 is an introduction to the extension of the SIS model to Volterra integral equations. The existence of a unique solution being established by the Banach fixed theorem, the main focus of this chapter is on showing the possible existence of multiple endemic equilibrium points when the basic reproduction number is less than 1. This is illustrated numerically as the backward bifurcation phenomenon.

In the last chapter, we gather concluding remarks on our findings and on possible future research directions.

Chapter 2

Dynamical Systems

2.1 Introduction

The mathematical models investigated in this dissertation are all in the framework of dynamical systems defined either by ordinary differential equations, difference equations, partial differential equations or integral equations. In this chapter, we collect the main tools we need for the quantitative and qualitative analysis of continuous (ODE) dynamical systems (Section 2.2) and discrete dynamical systems (Section 2.3). Although, this chapter is concerned with generalities on dynamical systems, the last part of Section 2.3 includes a contribution to higher order nonstandard finite difference schemes.

2.2 Continuous Dynamical Systems

Throughout this section, dynamical systems defined by ordinary differential equations are considered. Our standard reference for such dynamical systems is [55]. We can also mention the thesis [32], where some of the material is presented according to our needs.

2.2.1 Generalities

Consider the following initial–value problem for an autonomous first–order system of differential equations in the time independent variable $t \in [0, \infty)$ and dependent variable

$x \in \mathbb{R}^m$:

$$\dot{x} \equiv \frac{dx}{dt} = f(x), \qquad x(0) = x_0. \tag{2.2.1}$$

Here $f : \mathbb{R}^m \to \mathbb{R}^m$ and $x_0 \in \mathbb{R}^m$ are the given data.

Definition 2.2.1. *The ordinary differential equation in* $(2.2.1)$ *is said to define a dynamical system on a subset* $\Omega \subseteq \mathbb{R}^m$ *if for any* $x_0 \in \Omega$ *there exists a continuous differentiable function* $x(t)$ *on* $(0, \infty)$ *that is continuous on* $[0, \infty)$ *and is the unique solution of the initial value problem* $(2.2.1)$ *such that* $x(t) \in \Omega$ *for all* $t \in [0, \infty)$.

In order to advance conveniently the solution through time t, we introduce the following concept:

Definition 2.2.2. *For a dynamical system on* Ω*, we define its evolution semigroup operator or solution operator to be the map* $\Phi(t) : \Omega \to \Omega$ *such that* $x(t) = \Phi(t)x_0$.

The terminology "semigroup" for the evolution operator Φ is motivated by the following properties:

1. For any $s,\ t > 0,\ \ \Phi(t + s) = \Phi(t)\Phi(s) = \Phi(s)\Phi(t)$,
2. For $t = 0,\ \Phi(0) = I$, the identity operator.

With Definition 2.2.2 in mind, we introduce for $x_0 \in \Omega$, the set

$$\Gamma^+ = \{\Phi(t)x_0 :\ t \in (0, \infty)\} \subset \Omega$$

which is called the (positive or forward) orbit of x_0. The terminology trajectory is also used for orbits.

The existence of dynamical systems is often based on some structural assumptions on the function f. The widely used assumption is contained in the next definition.

Definition 2.2.3. *The function* $f : \mathbb{R}^m \to \mathbb{R}^m$ *is said to be Lipschitz on* $\Omega \subset \mathbb{R}^m$ *with Lipschitz constant* $L \geq 0$ *if*

$$\|f(x) - f(y)\| \leq L\|x - y\|$$

for all $x, y \in \Omega$. *Here* $\|\cdot\|$ *denotes the Euclidean norm in* $\mathbb{R}^m$. *If* f *is Lipschitz on* $\mathbb{R}^m$, *then* f *is said to be globally Lipschitz. If* f *is Lipschitz on every bounded subset* Ω *of* $\mathbb{R}^m$, *then* f *is said to be locally Lipschitz.*

The following existence and uniqueness result is well-known:

Theorem 2.2.4. *Let $f : \mathbb{R}^m \to \mathbb{R}^m$ be globally Lipschitz. Then $(2.2.1)$ defines a dynamical system on $\mathbb{R}^m$.*

In the more realistic case, when f is locally Lipschitz, a global existence result can be obtained under some a priori estimate as stated in the following classical result.

Theorem 2.2.5. *Let $f : \mathbb{R}^m \to \mathbb{R}^m$ be Lipschitz on an $\epsilon-$neighborhood Ω_ϵ of a bounded set $\Omega \subseteq \mathbb{R}^m$. If for any $x_0 \in \Omega$, the solution $x(t)$ of $(2.2.1)$ satisfies $x(t) \in \Omega$ for each time $t \geq 0$ where the solution exists, then $(2.2.1)$ defines a dynamical system on Ω.*

In many instances of the analysis of dynamical systems, we will use the Gronwall inequality that reads as follows:

Lemma 2.2.6. *(Gronwall inequality)*

Let $x(t)$ be a real valued function on $[0, \infty)$ such that

$$x'(t) \leq ax(t) + b, \quad x(0) = x_0$$

for a and b constant. Then for $t \geq 0$,

$$x(t) \leq x_0 e^{at} + \frac{b}{a}(e^{at} - 1), \quad a \neq 0$$

and

$$x(t) \leq x_0 + bt, \quad a = 0.$$

2.2.2 Qualitative Properties

In this subsection, we are interested in the trajectories or orbits initiated at x_0 in any set $\Omega \subset \mathbb{R}^m$ and the action of the evolution semigroup operator $\Phi(t)$ on Ω.

Definition 2.2.7. *For a dynamical system defined by $(2.2.1)$, a set Ω is said to be*

1. *positively invariant (under $\Phi(.)$) if $\Phi(t)\Omega \subseteq \Omega$ for all $t \geq 0$,*
2. *negatively invariant (under $\Phi(.)$) if $\Phi(t)\Omega \supseteq \Omega$ for all $t \geq 0$,*
3. *invariant (under $\Phi(.)$) if it is both positively and negatively invariant, i.e $\Phi(t)U = U$ for all $t \geq 0$.*

Special trajectories play an important role in the qualitative analysis of dynamical systems. The simplest of such trajectories are equilibrium points (or solutions): they do not change with time and turn out to be also the simplest invariant sets.

Definition 2.2.8. *A point $\bar{x} \in \mathbb{R}^m$ is called an equilibrium point of the dynamical system defined by $(2.2.1)$ if $f(\bar{x}) = 0$.*

Remark 2.2.9. *It is clear that $\bar{x} \in \mathbb{R}^m$ is an equilibrium point of $(2.2.1)$ if and only if $\bar{x}$ is a fixed point of the evolution semigroup operator, that is, $\Phi(t)\bar{x} = \bar{x}$. This fact explains why an equilibrium point is also called a fixed point of the dynamical system. Other terms often substituted for equilibrium point are critical point, steady state or rest point.*

Given the simplicity of equilibrium points as invariant sets of the dynamical system, it is natural to wonder how other orbits behave compared to them. This is given in the next definition.

Definition 2.2.10. *Let $\bar{x} \in \mathbb{R}^m$ be an equilibrium point of a dynamical system on Ω defined by $(2.2.1)$. Then $\bar{x}$ is said to be:*

1. *stable if for any $\epsilon > 0$, there exists $\delta = \delta(\epsilon) > 0$ such that if $\|x_0 - \bar{x}\| < \delta$ then $\|x(t) - \bar{x}\| < \epsilon$ for all $t \geq 0$,*

2. *locally attractive, if $\|x(t) - \bar{x}\| \to 0$ as $t \to \infty$ for all $\|x_0 - \bar{x}\|$ sufficiently small,*

3. *locally asymptotically stable if $\bar{x}$ is stable and locally attractive. For an asymptotically stable equilibrium point $\bar{x}$ of $(2.2.1)$, the set of all initial data x_0 such that*

$$\lim_{t\to\infty} \Phi(t)x_0 = \bar{x}$$

   is said to be the basin of attraction of $\bar{x}$,

4. *globally attractive if (2) holds for any $x_0 \in \Omega$ i.e. the basin of attraction of $\bar{x}$ is Ω,*

5. *globally asymptotically stable if (1) and (4) hold,*

6. *unstable if (1) fails to hold.*

The intuitive meaning of the above definition is given in the next remark.

Remark 2.2.11. *An equilibrium point $\bar{x}$ is said to be stable if all nearby solutions stay nearby. It is asymptotically stable if all nearby solutions not only stay nearby, but also tend to $\bar{x}$ or are attracted by $\bar{x}$ as t goes to infinity. On the other hand, if there exist some solutions starting near $\bar{x}$ that move away from it for future time t, then $\bar{x}$ is unstable.*

It is not easy to apply Definition 2.2.10 to check stability and asymptotic stability of an equilibrium solution. The simplest natural way to proceed would have been to replace the system $(2.2.1)$ by its linearized system

$$u' = Ju \tag{2.2.2}$$

near $\bar{x}$, where $J \equiv Jf(\bar{x})$ is the Jacobian of the function f at $\bar{x}$. It is of course assumed that $f : \mathbb{R}^m \to \mathbb{R}^m$ is of class C^1.

Definition 2.2.12. *If the matrix J has no eigenvalues with zero real part, then $\bar{x}$ is called a hyperbolic equilibrium point; otherwise the equilibrium point is called non–hyperbolic.*

The behavior of dynamical systems in the neighborhood of a hyperbolic equilibrium point can be investigated by using the linearization process $(2.2.2)$ as specified in the next theorem.

Theorem 2.2.13. *(Hartman–Grobman Theorem)*

Assume that $f : \mathbb{R}^m \to \mathbb{R}^m$ is of class C^1 and consider a hyperbolic equilibrium point $\bar{x}$ of the dynamical system defined by $(2.2.1)$. Then, there exist $\delta > 0$, a neighborhood $N \subset \mathbb{R}^m$ of the origin and a homeomorphism h from the ball $B = \{x \in \mathbb{R}^n : \|x - \bar{x}\| < \delta\}$ onto N such that (see Fig. 2.1)

$$u(t) := h(x(t)) \text{ solves (2.2.2) if and only if x(t) solves (2.2.1).}$$

Theorem 2.2.13 states that the behavior as $t \to \infty$ of solution $x(t)$ of $(2.2.1)$ near an equilibrium point $\bar{x}$ is the same as the behavior of solution $u(t)$ of its linearization $(2.2.2)$ near the origin. This observation leads us to the following result.

Theorem 2.2.14. *Assume that $f : \mathbb{R}^m \to \mathbb{R}^m$ is of class C^1 and that $\bar{x} \in \mathbb{R}^m$ is a hyperbolic equilibrium point of the dynamical system defined by $(2.2.1)$. Then $\bar{x}$ is asymptotically*

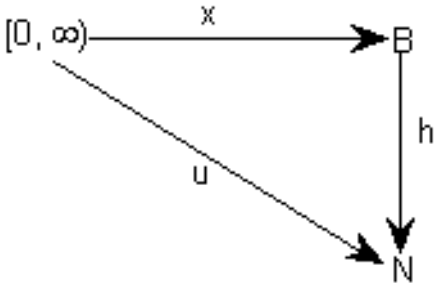


Figure 2.1: Hartman–Grobman Theorem

stable if and only if for the solution $u(t) = e^{tJ}u_0$ *of* $(2.2.2)$ *with* $\|u_0\| = \|x_0 - \bar{x}\|$ *small enough, we have*

$$\lim_{t\to\infty} u(t) = 0. \tag{2.2.3}$$

This is equivalent to

$$Re\lambda < 0, \qquad \forall\lambda \in \sigma(J), \tag{2.2.4}$$

where $\sigma(J)$ *is the set of all eigenvalues of the matrix* J*. The equilibrium point is unstable if and only if there exists at least one* $\lambda \in \sigma(J)$ *such that*

$$Re\lambda > 0, \qquad \text{or} \quad \lim_{t\to\infty} u(t) = \infty. \tag{2.2.5}$$

Remark 2.2.15. *In applications, specifically for epidemiological models, the conditions* $(2.2.4)$ *and* $(2.2.5)$ *are expressed in terms of the so–called basic reproduction number* $\mathcal{R}_0$ *by the fact that* $\mathcal{R}_0 < 1$ *or* $\mathcal{R}_0 > 1$*, respectively. We will be more explicit on the definition, computation and use of* $\mathcal{R}_0$ *later.*

Remark 2.2.16. *For a non–hyperbolic equilibrium point* $\bar{x}$*, Theorem 2.2.13 fails to hold. Moreover, Theorem 2.2.13 motivates the terminology "linear stability" and "linear instability" that we will sometimes use in place of asymptotic stability and instability for a hyperbolic equilibrium point.*

Theorem 2.2.14 suggests that the real parts of the eigenvalues of the Jacobian matrix J play an important role in classifying equilibrium points. This is confirmed in the next definition.

Definition 2.2.17. *An equilibrium point $\bar{x} \in \Omega$ of the dynamical system defined by* $(2.2.1)$ *is*

1. *a saddle point if some, but not all, of the eigenvalues of the associated Jacobian matrix at $\bar{x}$ have positive real parts and the remaining eigenvalues have negative real parts,*

2. *a sink or a stable node, if all eigenvalues have negative real parts,*

3. *a source or an unstable node, if all of the eigenvalues have positive real parts,*

4. *a center, if the eigenvalues are purely imaginary and nonzero numbers.*

In order to include all possible situations with regard to the signs of the real part of the eigenvalues of the matrix J, we assume that J has k eigenvalues with negative real parts and $m-k$ eigenvalues with positive real parts. It is well-known that the (generalized) eigenvectors associated with the k eigenvalues with negative real parts determine a stable subspace denoted by $E^s \subset \mathbb{R}^m$, while the $m-k$ remaining eigenvalues lead to an unstable subspace $E^u \subset \mathbb{R}^m$. With these notations in mind, Theorem 2.2.14 is extended to the so–called stable–unstable manifold theorem. To have a clear vision of this theorem, let us recall the following definition:

Definition 2.2.18. *Suppose that $\bar{x}$ is an equilibrium point of a dynamical system $\Omega \subseteq \mathbb{R}^m$ defined by* $(2.2.1)$. *Then:*

1. *the set $W^s(\bar{x}) = \{x_0 \in \mathbb{R}^m : \Phi(t)x_0 \to \bar{x} \ \text{ as } \ t \to \infty\}$ is called the stable manifold of $\bar{x}$.*

2. *the set $W^s_\epsilon(\bar{x}) = \{x_0 \in W^s(\bar{x}) : \|\Phi(t)x_0 - \bar{x}\| \leq \epsilon \ \ \forall\ t \geq 0 \ \ \}$ is called ϵ–local stable manifold of $\bar{x}$.*

3. *the set $W^u(\bar{x}) = \{x_0 \in \mathbb{R}^m : \Phi(t)x_0 \to \bar{x} \ \text{ as } \ t \to -\infty\}$ is called the unstable manifold of $\bar{x}$.*

4. *the set $W^u_\epsilon(\bar{x}) = \{x_0 \in W^u(\bar{x}) : \|\Phi(t)x_0 - \bar{x}\| \leq \epsilon \ \ \forall\ t \leq 0 \ \ \}$ is called ϵ–local unstable manifold of $\bar{x}$.*

Remark 2.2.19. *The terminology "stable" for the set $W^s(\bar{x})$ is to be understood in the sense of a uniformly stable set defined in [55]. Indeed it is easy to check that the set $W^s(\bar{x})$ is closed and invariant. Thus, for $x_0 \in \mathbb{R}^m$ and $z_0 \in W^s(\bar{x})$, we have*

$$\begin{aligned} \inf_{y_0 \in W^s(\bar{x})} \|\Phi(t)x_0 - y_0\| &\leq \inf_{y_0 \in W^s(\bar{x})} \|\Phi(t)x_0 - \Phi(t)y_0\| \\ &\leq \|\Phi(t)x_0 - \Phi(t)z_0\|. \end{aligned}$$

By uniform continuity of $\Phi(t)$, we know that for each $\epsilon > 0$, $\exists\, \delta > 0$ such that

$$\|x_0 - z_0\| < \delta \Rightarrow \|\Phi(t)x_0 - \Phi(t)z_0\| < \epsilon.$$

Now if

$$\inf_{y_0 \in W^s(\bar{x})} \|x_0 - y_0\| < \frac{\delta}{2},$$

then we have

$$\inf_{y_0 \in W^s(\bar{x})} \|\Phi(t)x_0 - y_0\| < \epsilon.$$

The announced stable–unstable manifold theorem is stated in the following form.

Theorem 2.2.20. *(The stable–unstable manifold theorem)*

Let $\bar{x} \in \mathbb{R}^m$ be an equilibrium point of a dynamical system on Ω defined by $(2.2.1)$. Then there exists a k-dimensional differentiable manifold W^s which is positively invariant and is tangent to the stable subspace E^s at the equilibrium point $\bar{x}$. Furthermore, there exists an $m-k$ dimensional unstable manifold W^u which is negatively invariant and tangent to the unstable subspace E^u at $\bar{x}$.

As mentioned in Remark 2.2.16, the linearization approach we used so far works when the equilibrium point is hyperbolic. Otherwise, we can use the Lyapunov direct method which we outline below.

Definition 2.2.21. *Assume that Equation $(2.2.1)$ defines a dynamical system on an open subset $\Omega \subset \mathbb{R}^m$ and $\bar{x} \in \Omega$ is an equilibrium point. A function $V \in C^1(\Omega, \mathbb{R})$ is called a Lyapunov function of the system $(2.2.1)$ for $\bar{x}$ on a neighborhood $B \subset \Omega$ of $\bar{x}$ provided that*

$$\dot{V}(x) := \lim_{h \to 0} \frac{V(x + hf(x)) - V(x)}{h} = \nabla V(x).f(x) \leq 0, \quad \forall x \in B, \tag{2.2.6}$$

where $\dot{V}(x)$ is the directional derivative of V in the direction of f. If in addition, $V(\bar{x}) = 0$ and $V(x) > 0$ for all $x \in B\backslash\{\bar{x}\}$, then V is said to be a positive definite Lyapunov function at $\bar{x}$.

When there is no risk of confusion about the equilibrium point $\bar{x}$ and its neighborhood B, we will simply use the expression Lyapunov function V for B.

If $x = x(t)$ is a solution of Equation $(2.2.1)$, then by the chain rule, from Equation $(2.2.6)$, we get

$$\frac{d}{dt}V(x(t)) = \dot{V}(x(t)), \tag{2.2.7}$$

which motivates the fact that $\dot{V}$ is often called the derivative of V along trajectories. It is also because of the relation $(2.2.7)$ that one can expect to have information about the behavior of V along trajectories without prior knowledge of the solutions. The Lyapunov method is exploited to check the stability/instability of an equilibrium solution as we specify below.

Theorem 2.2.22. *Let V be a positive definite Lyapunov function of the dynamical system $(2.2.1)$ on a neighborhood B of an equilibrium point $\bar{x}$. Then $\bar{x}$ is stable. If, in addition, $\dot{V}(x) < 0 \quad \forall\, x \in B\backslash\{\bar{x}\}$, then $\bar{x}$ is asymptotically stable; while $\bar{x}$ is unstable if $\dot{V}(x) > 0, \quad \forall\, x \in B\backslash\{\bar{x}\}$.*

The asymptotic stability of an equilibrium point stated in Theorem 2.2.22, constitutes the simplest final state of a dynamical system. Other types of final states are specified in the next definition.

Definition 2.2.23. *Let $(2.2.1)$ define a dynamical system on Ω. For $x_0 \in \Omega$ the set of all points $z \in \mathbb{R}^m$ such that*

$$\lim_{n\to\infty} \Phi(t_n)x_0 = z$$

for some sequence $0 < t_n \to \infty$ is called the $\omega-$ limit set of x_0. This set is denoted by $\omega(x_0)$:

$$\omega(x_0) = \{z \in \mathbb{R}^m : \exists\, t_n > 0 \ \text{ such that } \ \Phi(t_n)x_0 \to z \quad \text{as} \quad n \to \infty\}.$$

Similarly, the $\alpha-$ limit set of x_0 denoted by $\alpha(x_0)$ is given by

$$\alpha(x_0) = \{z \in \mathbb{R}^m : \exists\, t_n < 0 \quad \text{such that} \quad \Phi(t_n)x_0 \to z \quad \text{for} \quad n \to \infty\}.$$

The critical issue with the Lyapunov function is that it is not easy to construct. However, when it is available, it has the advantage of easily leading to some global properties of an equilibrium point, particularly in the case of dissipative systems defined below.

Definition 2.2.24. *A dynamical system $\Omega \subset \mathbb{R}^m$ is said to be dissipative if there exists a bounded, positively invariant set U with the property that for any bounded set $B \subseteq \mathbb{R}^m$, there exists a time $t^* = t^*(U, B) \geq 0$ such that $\Phi(t)B \subseteq U$ for all $t > t^*$. The set U is called an absorbing set.*

The said global stability result is the LaSalle invariance principle that reads as follows:

Theorem 2.2.25. [35] *(LaSalle Theorem)*

Let $\bar{x}$ be an equilibrium point of a dissipative dynamical system on Ω defined by $(2.2.1)$. Let V be a positive definite Lyapunov function for $\bar{x}$ on the set Ω. Furthermore, let $\mathcal{E} = \{x \in \bar{\Omega} : \dot{V}(x) = 0\}$. If $\mathcal{M}$ is the largest invariant set of $\mathcal{E}$ such that $\mathcal{M} \subset \Omega$, then $\bar{x}$ is globally asymptotically stable on Ω if and only if it is globally asymptotically stable for the system restricted to $\mathcal{M}$.

Two–dimensional dynamical systems enjoy some interesting properties. Two of such properties that we will use are stated in the next two theorems.

Theorem 2.2.26. [59]*(Bendixson's Criterion)*

Consider a dynamical system on $\mathbb{R}^2$ defined by

$$\dot{x} = f(x, y); \qquad \dot{y} = g(x, y).$$

If on a simply connected region $D \subset \mathbb{R}^2$, the divergence

$$\frac{\partial f}{\partial x} + \frac{\partial g}{\partial y}$$

is not identically zero and does not change sign, then this dynamical system has no closed orbits lying entirely in D.

Theorem 2.2.27. [59] $(Poincaré - Bendixson)$

Consider a dynamical system in $\mathbb{R}^2$ and let M be a positively invariant compact region on $\mathbb{R}^2$ containing a finite number of equilibrium points. Let $p \in M$ and consider $\omega(p)$. Then one of the following possibilities holds:

1. *The set* $\omega(p)$ *is an equilibrium point;*

2. *The set* $\omega(p)$ *is a closed orbit;*

3. *The set* $\omega(p)$ *consists of equilibrium points* $p_1,\ p_2,\ \ldots,\ p_n$ *and orbit* γ *with* $\alpha(\gamma) = p_i$ *and* $\omega(\gamma) = p_j$*, for* $i \neq j$ *and* $i,\ j = 1, 2, 3, ..., n$*. In the particular case when there are only two equilibria* p_1 *and* p_2 *in* $\omega(p)$*, there exists at most one orbit* $\gamma \subset \omega(p)$ *such that* $\alpha(\gamma) = p_1$ *and* $\omega(\gamma) = p_2$*.*

Bifurcation of equilibria is the last qualitative property of dynamical systems that we outline now.

Consider a dynamical system $(2.2.1)$ that depends on a parameter μ:

$$\dot{x} = f(x, \mu), \quad x \in \mathbb{R}^m, \ \ \mu \in \mathbb{R}. \tag{2.2.8}$$

Here the function f is as smooth as needed so that Taylor expansions can be considered. The equilibria of $(2.2.8)$ are all vectors $(\bar{x}, \mu_0) \in \mathbb{R}^m \times \mathbb{R}$ such that

$$f(\bar{x}, \mu_0) = 0. \tag{2.2.9}$$

Intuitively, Fred–Brauer and Castillo–Chavez [7] define a bifurcation as a point in the parameter space where equilibria appear, disappear, or change stability.

The general definition of a bifurcation point is given below.

Definition 2.2.28. [60] *An equilibrium point* $(\bar{x}, \mu_0)$ *for* $(2.2.8)$ *or simply the point* μ_0 *is called a bifurcation point for* $(2.2.8)$ *if for each* $k \in \mathbb{N}$ *there exist two distinct solutions* (x_k, μ_k) *and* (y_k, μ_k) *to Equation* $(2.2.9)$ *such that the corresponding sequences both converge to* $(\bar{x}, \mu_0)$*.*

Definition 2.2.28 does not reflecting directly the issue of our interest. To be more specific, we make some restrictions on the dynamical system $(2.2.8)$ on balls:

$$\dot{x} \ = \ f(x, \mu_0), \ \text{ on } \ B(\bar{x}, \delta) \tag{2.2.10}$$

and

$$\dot{x} \ = \ f(x, \mu) \ \text{ on } \ B(\bar{x}, \epsilon_1) \times (\mu_0 - \epsilon_2, \mu_0 + \epsilon_2) =: U_{\epsilon_1, \epsilon_2}(\bar{x}, \mu_0). \tag{2.2.11}$$

Definition 2.2.29. [59] *An equilibrium point* $(\bar{x}, \mu_0)$ *is said to undergo a bifurcation at* $\mu = \mu_0$ *if there exist* $\delta > 0$, $\epsilon_1 > 0$ *and* $\epsilon_2 > 0$ *such that the equilibrium point* $(\bar{x}, \mu_0)$ *for* $(2.2.11)$ *is not qualitatively the same as the equilibrium point* $\bar{x}$ *for* $(2.2.10)$.

An alternative formulation of Definition 2.2.29 is as follows. The number $\mu = \mu_0$ is said to be a bifurcation value for $(2.2.8)$ if there exists an equilibrium point $(\bar{x}, \mu_0)$ of $(2.2.8)$ with the following property: $\exists\ \delta > 0$, $\exists\ \epsilon_1 > 0$ and $\exists\ \epsilon_2 > 0$ such that the equilibrium point $(\bar{x}, \mu_0)$ for $(2.2.11)$ on $U_{\epsilon_1,\,\epsilon_2}(x_0, \mu_0)$ is not qualitatively the same as the equilibrium point $\bar{x}$ for $(2.2.10)$ on $B(\bar{x}, \delta)$.

The next two definitions constitute some classifications of bifurcation points.

Definition 2.2.30. *A bifurcation point* μ_0 *at which an equilibrium point* $(\bar{x}, \mu_0)$ *undergoes a bifurcation is called a transcritical bifurcation if the three conditions below hold:*

1. *at least two curves* $x = x(\mu)$ *of equilibrium points exist in the* $\mu - x$ *space for* $\mu < \mu_0$ *and* $\mu > \mu_0$*;*
2. *the curves of the equilibrium point branch at* $\mu = \mu_0$ *or intersect at the point* $(\bar{x}, \mu_0)$*;*
3. *the stability of an equilibrium point along a given curve changes on passing through* $\mu = \mu_0$.

Definition 2.2.31. *A bifurcation point* μ_0 *is called a pitchfork bifurcation if:*

1. $\bar{x}$ *is the only equilibrium point on one side of* $\mu = \mu_0$*, this means, for* $\mu < \mu_0$ *or* $\mu > \mu_0$*;*
2. *two curves* $x = x(\mu)$ *of equilibrium points are created on the other side of* $\mu = \mu_0$.

We have two types of pitchfork bifurcations.

Definition 2.2.32. *A pitchfork bifurcation at* μ_0 *is said to be supercritical or forward if the condition (2) in Definition 2.2.31 occurs for* $\mu > \mu_0$*. It is called subcritical or backward if the condition (2) in Definition 2.2.31 occurs for* $\mu < \mu_0$.

Definition 2.2.33. *A bifurcation point* μ_0 *is a fold bifurcation point or saddle–node bifurcation if there exists an equilibrium point* $(\bar{x}, \mu_0)$ *with the property that for all* $\delta > 0$*, there exists* $\epsilon > 0$ *such that for* $|\mu - \mu_0| < \epsilon$

Type of Bifurcation	*Conditions*
saddle–node	$\frac{\partial f}{\partial \mu}(\bar{x},\mu_0) \neq 0, \quad \frac{\partial^2 f}{\partial x^2}(\bar{x},\mu_0)) \neq 0$
transcritical	$\frac{\partial f}{\partial \mu}(\bar{x},\mu_0) = 0, \quad \frac{\partial^2 f}{\partial x \partial \mu}(\bar{x},\mu_0) \neq 0, \quad \frac{\partial^2 f}{\partial x^2}(\bar{x},\mu_0) \neq 0$
pitchfork	$\frac{\partial f}{\partial \mu}(\bar{x},\mu_0) = 0, \quad \frac{\partial^2 f}{\partial x^2}(\bar{x},\mu_0) = 0, \quad \frac{\partial^2 f}{\partial x \partial \mu}(\bar{x},\mu_0) \neq 0, \quad \frac{\partial^3 f}{\partial x^3}(\bar{x},\mu_0) \neq 0$

Table 2.1: Types of bifurcations and corresponding existence conditions.

1. $B(\bar{x},\delta)$ *has no equilibrium point for* $\mu < \mu_0$

2. $B(\bar{x},\delta)$ *has two solutions for* $\mu > \mu_0$.

In the scalar case, i.e. $m = 1$ in $(2.2.8)$, sufficient conditions for existence and type of bifurcations at $\mu = \mu_0$ for the equilibrium point $(\bar{x},\mu_0)$ are known $[59]$ and are summarized in Table 2.1 . The situation for higher dimensions is more difficult. Some sufficient conditions based on the asymptotic expansions

$$x(\epsilon) = \epsilon\eta + \mathcal{O}(\epsilon^2), \qquad \mu(\epsilon) = \mu_0 + \mathcal{O}(\epsilon), \qquad 0 < \epsilon << 1, \tag{2.2.12}$$

are stated in the following result:

Theorem 2.2.34. $[55]$ *Assume that* $(\bar{x},\mu) \in \mathbb{R}^m \times \mathbb{R}$ *is an equilibrium solution of* $(2.2.8)$ *for each* $\mu \in \mathbb{R}$. *Let the Jacobian matrix* $Jf(\bar{x},\mu)$ *be singular at* $\mu = \mu_0$. *Assume further that the null space of the linear operator* $Jf(\bar{x},\mu_0)$ *has dimension one, its basis being given by a vector* $\eta \in \mathbb{R}^m$ *such that the range of* $Jf(\bar{x},\mu_0)$ *does not contain the vector* $\frac{d}{d\mu}[df(\bar{x},\mu)]|_{\mu=\mu_0}.\eta$. *Then there exists an equilibrium solution of* $(2.2.8)$ *of the form* $(2.2.12)$ *and* $\mu = \mu_0$ *is a transcritical bifurcation if* $\frac{d\mu}{d\epsilon}(\mu_0) \neq 0$, *whereas it is a pitchfork bifurcation whenever* $\frac{d\mu}{d\epsilon}(\mu_0) = 0$ *and* $\frac{d^2\mu}{d^2\epsilon}(\mu_0) \neq 0$.

2.3 Discrete Dynamical Systems

In this section dynamical systems generated by vector–valued mappings are presented. The definitions and properties for discrete dynamical systems are in some sense analogous to those of continuous dynamical systems on the understanding that the continuous variable $t \in [0,\infty)$ is replaced by the discrete variable $n \in \mathbb{N}$. We shall focus on the main tools that we need. Our main references for this section are $[32,\ 34,\ 55]$.

2.3.1 Generalities

Let $F : \mathbb{R}^m \to \mathbb{R}^m$. Consider a sequence $\{x_n\}_{n=0}^{\infty}$ defined recursively from $x_0 \in \mathbb{R}^m$ by

$$x_{n+1} = F(x_n). \tag{2.3.1}$$

Definition 2.3.1. *Equation* $(2.3.1)$ *defines a discrete dynamical system on* $\Omega \subseteq \mathbb{R}^m$ *if, for every* $x_0 \in \Omega$, *the sequence* $\{x_n\}_{n=0}^{\infty}$ *remains in* Ω.

Remark 2.3.2. *Generalized discrete dynamical systems, whereby the explicit relation* $(2.3.1)$ *is replaced by the implicit relation*

$$G(x_n,\ x_{n+1}) = 0,$$

can be defined. But we will not deal with them in this work.

Definition 2.3.3. *Given a discrete dynamical system defined on a set* $\Omega \subseteq \mathbb{R}^m$, *its evolution semigroup operator is the map* $\Phi^n : \Omega \to \Omega$ *such that* $x_n = \Phi^n x_0$ *for all* $n = 0,\ 1,\ 2,\ 3,\ \cdots$

The evolution semigroup operator has the following properties:

1. Semigroup property: $x_{n+m} = \Phi^n x_m = \Phi^m x_n = \Phi^{n+m} x_0,$ for all $m,\ n = 0,\ 1,\ 2,\ 3,\ \cdots$
2. Identity Property: $\Phi^0 \equiv I$ is the identity operator.

The discrete Gronwall inequality reads as follows:

Theorem 2.3.4. $[55]$*(Gronwall inequality)*

Let a positive sequence $\{x_n\}_{n=0}^{N}$ *satisfy*

$$x_{n+1} \leq cx_n + d, \qquad n = 0,\ 1, 2,\ \ldots,\ N-1,$$

for some constants $c > 0$ *and* d. *Then*

$$x_n \leq \frac{d}{1-c}(1-c^n) + x_0 c^n, \qquad n = 0,\ 1,\ \ldots,\ N, \quad \textit{if} \quad c \neq 1$$

and

$$x_n \leq nd + x_0, \qquad n = 0,\ 1,\ \ldots,\ N, \qquad \textit{if} \quad c = 1.$$

2.3.2 Qualitative Properties

Definition 2.3.5. *Let Φ^n be the evolution semigroup operator of a discrete dynamical system on Ω. A subset $U \subset \Omega \subseteq \mathbb{R}^m$ is said to be*

1. *positively invariant if $\Phi^n U \subseteq U$ for all $n \geq 0$.*
2. *negatively invariant if $\Phi^n U \supseteq U$ for all $n \geq 0$.*
3. *invariant if U is both positively and negatively invariant. This means $\Phi^n U = U$ for all $n \geq 0$.*

Definition 2.3.6. *A vector $\bar{x} \in \Omega \subset \mathbb{R}^m$ is said to be a fixed point of a discrete dynamical system on Ω defined by Equation $(2.3.1)$ if $F(\bar{x}) = \bar{x}$ or equivalently if $\Phi^n \bar{x} = \bar{x}$ for all $n \geq 0$.*

Definition 2.3.7. *Let $\bar{x} \in \Omega \subset \mathbb{R}^m$ be a fixed point of a discrete dynamical system $(2.3.1)$ on Ω. Then $\bar{x}$ is said to be*

1. *stable if, for any $\epsilon > 0$, there exists $\delta = \delta(\epsilon) > 0$ such that $x_0 \in \Omega$,*

$$\|x_0 - \bar{x}\| < \delta$$

implies

$$\|x_n - \bar{x}\| < \epsilon \qquad \text{for all} \qquad n \geq 0.$$

2. *(locally) asymptotically stable if (1) holds and in addition there exists a constant $b > 0$ such that, $x_0 \in \Omega$, $\|x_0 - \bar{x}\| < b$ implies*

$$\lim_{n \to \infty} \|x_n - \bar{x}\| = 0.$$

3. *globally asymptotically stable (on Ω) if (1) holds and*

$$\lim_{n \to \infty} \|x_n - \bar{x}\| = 0 \qquad \text{for any} \qquad x_0 \in \Omega.$$

4. *unstable if (1) fails to hold.*

To determine the stability property of a fixed point $\bar{x}$, we assume that the map F is of class C^1 and we denote by $J = DF(\bar{x})$, the Jacobian matrix of F at $\bar{x}$. Then,

$$y_{n+1} = Jy_n, \qquad n = 0,\ 1,\ 2,\ 3,\ \cdots \tag{2.3.2}$$

is the linearization of $(2.3.1)$ around $\bar{x}$ where $y_n = x_n - \bar{x}$. The stability properties of this linear system is determined by the eigenvalues of the Jacobian matrix J. Hence, the stability property of $\bar{x}$ for the original system would be an easy task if it is related to the stability property of the fixed point $\bar{y} = 0$ for the linear system $(2.3.2)$.

Definition 2.3.8. *A fixed point $\bar{x}$ of the discrete dynamical system given by Equation $(2.3.1)$ is said to be hyperbolic if the Jacobian matrix J has no eigenvalue of unit modulus. Otherwise the fixed point is called non–hyperbolic.*

Remark 2.3.9. *The map F in $(2.3.1)$ is said to be hyperbolic if all fixed points are hyperbolic.*

Theorem 2.3.10. *(Hartman–Grobman Theorem)*

Let $F : \mathbb{R}^m \to \mathbb{R}^m$ of class C^1 have a hyperbolic fixed point $\bar{x}$. Then there exist $\delta > 0$, a neighborhood $N \subset \mathbb{R}^m$ of the origin and a homeomorphism $h : B(\bar{x}, \delta) \to N$ such that

$$h(F(x_0)) = Jh(x_0) \quad \text{for all} \quad x_0 \in B(\bar{x}, \delta).$$

Consequently, by setting $y_n = h(x_n)$ for all $n \geq 0$, the mapping $(2.3.1)$ in the neighborhood $B(\bar{x}, \delta)$ of $\bar{x}$ is equivalent to the mapping $(2.3.2)$ in the neighborhood N of the origin (see Fig 2.2).

In practice, Theorem 2.3.10 is used as stated in the next result.

Theorem 2.3.11. *Let F be a continuously differentiable function defined on a set $\Omega \subseteq \mathbb{R}^m$, and let $\bar{x} \in \Omega$ be a hyperbolic fixed point of $(2.3.1)$.*

1. *Then $\bar{x}$ is asymptotically stable if and only if for*

$$y_n = J^n y_0,$$

with $\|y_0\| := \|x_0 - \bar{x}\|$ small enough, we have

$$\lim_{n\to\infty} y_n = 0,$$

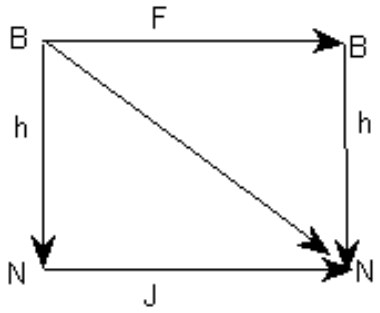


Figure 2.2: Hartman–Grobman Theorem for discrete systems.

or equivalently, all the eigenvalues of the Jacobian matrix J have modulus less than one.

2. *The fixed point $\bar{x}$ is unstable if there exists at least one eigenvalue of the Jacobian matrix J with modulus greater than one, or*

$$\lim_{n\to\infty} \|y_n\| = \infty.$$

If the fixed point $\bar{x}$ is non–hyperbolic, the matrix J has at least one eigenvalue with modulus equal to one. Then Theorem 2.3.11 does not apply: $\bar{x}$ may be either stable, asymptotically stable or unstable. To overcome this difficulty, we can use the Lyapunov function in conjunction with LaSalle invariance principle as for continuous dynamical systems.

Definition 2.3.12. [44] *Let $\bar{x}$ be a fixed point of dynamical system $(2.3.1)$ defined on $\Omega \subset \mathbb{R}^m$. A function $V \in C^1(\Omega, \mathbb{R})$ is said to be Lyapunov a function for $\bar{x}$ on some neighborhood $B \subset \Omega$ if*

1. *the function V satisfies $V(\bar{x}) \leq V(x)$ for all $x \in B$.*

2. *the inequality $V(F(x)) \leq V(x)$ holds for all $x \in B$.*

In addition, if $V(\bar{x}) = 0$ and $V(x) > 0$ for all $x \in B\backslash\{\bar{x}\}$ then V is said to be positive definite function at $\bar{x}$.

Once a Lyapunov function is determined, it becomes possible to check stability properties of a fixed point as specified below.

Theorem 2.3.13. [44] *(Lyapunov's Stability Theorem)*

If there exists a Lyapunov function $V(x)$ for the fixed point $\bar{x}$ on the ball $B(\bar{x}, \delta)$, then the fixed point $\bar{x}$ is stable. If $V(F(x)) < V(x)$ for every point $x \in B(\bar{x}, \delta)\backslash\{\bar{x}\}$, then $\bar{x}$ is asymptotically stable. But if $V(F(x)) > V(x)$ for all $x \in B(\bar{x}, \delta)\backslash\{\bar{x}\}$, then $\bar{x}$ is unstable.

It is important to notice that Theorem 2.3.13 guarantees the local asymptotic stability of a fixed point. Much more is needed for the global asymptotic stability. The following concept plays an important role in this regard.

Definition 2.3.14. *A discrete dynamical system on Ω is said to be dissipative if there exists a compact, positively invariant set $U \subset \mathbb{R}^m$ with the property that for any bounded set $B \subseteq \Omega$, there exists an integer $n^* = n^*(U, B) \geq 0$ such that $\Phi^n B \subseteq U$ for all $n > n^*$. The set U is called an absorbing set. In the case when B is replaced by each point $x_0 \in \Omega$, the dynamical system is said to be point dissipative.*

Theorem 2.3.15. [4] *Suppose $\bar{x}$ is a fixed point of the dynamical system on Ω given by $(2.3.1)$. Assume that the system $(2.3.1)$ is point dissipative. Assume further that there exists a continuous function $V : \overline{\Omega} \to \mathbb{R}$ such that*

1. *the function V is bounded from below on Ω;*
2. *the inequality $V(F(x)) \leq V(x)$ holds for all $x \in \Omega$;*
3. *The fixed point $\bar{x}$ is globally asymptotically stable when the system $(2.3.1)$ is restricted to the set $\mathcal{M}$, which is the largest invariant set contained in*

$$\mathcal{E} = \{x \in \Omega : V(F(x)) = V(x)\}.$$

Then, the fixed point $\bar{x}$ is globally asymptotically stable on the whole set Ω.

Remark 2.3.16. *Theorem 2.3.15 is a version of LaSalle Invariance Principle* [36]. *The function V is some kind of Lyapunov function, though the lower bound required for $V(x)$ is not specifically $V(\bar{x})$ as stated in part (1) of Definition 2.3.12 . The substance of the invariance principle is contained in part (3) of Theorem 2.3.15.*

2.3.3 Nonstandard Finite Difference Schemes

Most of the discrete schemes that we will consider in this dissertation are nonstandard finite difference (NSFD) schemes. The NSFD method was introduced more than two decades ago by R.Mickens as a powerful approach that replicates the dynamics of the continuous dynamical systems, apart from guaranteeing the convergence of the discrete solution to the exact solutions.

A comprehensive reference on the NSFD schemes is [48]. The method was subsequently developed by Anguelov and Lubuma [2] who gave its mathematical foundation. Further references can be found in [42]. The definition below is taken from this fundamental reference [2].

Definition 2.3.17. *A difference equation*

$$D_{\Delta t}x_n = F_{\Delta t}(f,\ x_n) \tag{2.3.3}$$

that produces a sequence $\{x_n\}_{n=0}^{\infty}$ *of approximate solutions to the differential equation* $(2.2.1)$ *at the times* $t_n = n\Delta t$*, is called a nonstandard finite difference scheme if at least one of the following conditions is satisfied:*

- *In the first order discrete derivative* $D_{\triangle t}x_n \simeq x'(t_n)$*, the classical denominator* $h = \triangle t$ *is replaced by a nonnegative function* $\phi : (0,\infty) \to (0,\infty)$ *satisfying*

$$\phi(h) = h + \mathcal{O}(h^2). \tag{2.3.4}$$

  For instance $\phi(h) = 1 - e^{-h}$ *or* $\phi(h) = \frac{e^{\lambda h}-1}{\lambda}$ *where* λ *is a constant in* $(2.2.1)$.

- *In the expression* $F_{\triangle t}(f, x_n)$*, nonlinear terms are approximated in a non–local way. For instance a term like* $x^2(t_n)$ *is approximated by* $x_{n+1}x_n$ *instead of* x_n^2.

Remark 2.3.18. *Mickens* [48] *puts the following criteria to identify nonstandard schemes apart from the requirements in Definition 2.3.17:*

1. *The order of the discrete derivative should be equal to the order of the corresponding derivative of the differential equation,*

2. *Special conditions that hold for the solutions of the differential equations should also hold for the solutions of the finite difference scheme,*

3. *The scheme should not introduce extraneous or spurious solutions.*

The additional requirements made by Mickens are particular cases of the following more general concepts introduced in [2].

Definition 2.3.19. *Assume that the solution of* $(2.2.1)$ *satisfies a property* P*. The difference Equation* $(2.3.3)$ *is said to be qualitatively stable or dynamically consistent with respect to the property* P *if for all step sizes* $h > 0$*, the discrete solution for* $(2.3.3)$ *satisfies property* P*.*

A minimal property P that is desirable for any scheme is described as follows:

Definition 2.3.20. *A difference scheme* $(2.3.3)$ *for approximating* $(2.2.1)$ *is said to be elementary stable if, for any value of step size* h*, its fixed points are exactly the equilibrium points of the differential system* $(2.2.1)$ *and these fixed points for the difference scheme have the same linear stability/instability properties as for the differential system.*

A typical situation when a scheme is dynamically consistent with respect to any property is contained in the next definition.

Definition 2.3.21. *The numerical method* $(2.3.3)$ *to approximate* $(2.2.1)$ *is called an exact scheme whenever the difference equation* $(2.3.3)$ *and the differential equation* $(2.2.1)$ *have the same general solutions at the discrete time* $t = t_n$*. In particular, with* $x(t)$ *being the solution of the initial value problem* $(2.2.1)$*, we have* $x_n = x(t_n)$*.*

The nonstandard version of the classical θ method has been extensively studied in literature (see $[32,\ 43]$). These NSFD schemes, which are of order 1 for $\theta \neq \frac{1}{2}$ and of order 2 for $\theta = \frac{1}{2}$, will be used in the next chapters. Here, we want to develop NSFD Runge–Kutta methods as higher order schemes.

The classical explicit k - stage Runge–Kutta method for the solution of $(2.2.1)$ is defined by $([34])$

$$x_{n+1} = x_n + h\sum_{i=1}^{k} b_i K_i, \tag{2.3.5}$$

where

$$K_i = f\left(x_n + h\sum_{j=1}^{i-1} a_{ij}K_j\right), \quad i = 1, 2, ..., k, \qquad b_j = \sum_{i=1}^{j-1} a_{ij}\ , \tag{2.3.6}$$

$(a_{ij})_{1\leq i,\, j\leq k}$ is a lower triangular matrix with zero diagonal and

$$\sum_{j=1}^{k} b_j = 1. \tag{2.3.7}$$

The condition $(2.3.7)$ is necessary and sufficient for the Runge–Kutta method to be consistent and in fact convergent, with the local truncation error T_{n+1} being given by

$$T_{n+1} := x(t_{n+1}) - x(t_n) - h\sum_{i=1}^{k} b_i K_i = \mathcal{O}(h^2), \tag{2.3.8}$$

where the exact solution $x(t_n)$ is used in the definition of K_i given in $(2.3.6)$.

The interest in the explicit k–stage Runge–Kutta method, with $1 \leq k \leq 4$, arises from the following result, which is more precise than $(2.3.8)$.

Theorem 2.3.22. $[34]$ *An explicit k–stage ($k \leq 4$) Runge–Kutta method is of order k in the sense that*

$$T_{n+1} = \mathcal{O}(h^{k+1}). \tag{2.3.9}$$

In order to test the efficiency of a numerical scheme, it is normal to take a test model. For this, consider the explicit k–stage ($k \leq 4$) Runge–Kutta method. We apply it to the model differential system

$$x' = Jx, \qquad x(0) = x_0, \tag{2.3.10}$$

where J is a diagonalizable $m \times m$ matrix with eigenvalues λ_l having negative real parts:

$$Q^{-1}JQ = \Lambda := diag(\lambda_1, \lambda_2, ..., \lambda_m). \tag{2.3.11}$$

Under this assumption, the solution

$$x(t) = e^{tJ}x_0, \tag{2.3.12}$$

of $(2.3.10)$ has the asymptotic behavior

$$\lim_{t\to\infty} \|x(t)\| = 0. \tag{2.3.13}$$

It can be shown that the Runge–Kutta method applied to $(2.3.10)$ reads as

$$x_{n+1} = R(\Delta t J)x_n, \tag{2.3.14}$$

with the matrix function

$$R(\Delta tJ) := Q\ diag[R(\lambda_l \Delta t)]Q^{-1}, \tag{2.3.15}$$

where (see [34])

$$R(\lambda_l \Delta t) = \sum_{j=0}^{k} \frac{1}{j!}(\lambda_l \Delta t)^j. \tag{2.3.16}$$

Hence, (x_n) replicates the property $(2.3.13)$ or $x_n \to 0$ as $n \to \infty$ if and only if

$$|R(\lambda_l \Delta t)| < 1 \quad \forall l. \tag{2.3.17}$$

Definition 2.3.23. [32] *The Runge–Kutta method* $(2.3.5) - (2.3.6)$ *is said to be absolutely stable for a given* $\lambda \Delta t,\ Re\lambda < 0$, *if* $|R(\lambda \Delta t)| < 1$.

The argument that led to Definition 2.3.23 suggests that we modify the k–stage Runge–Kutta method $(2.3.5) - (2.3.6)$ into the NS Runge–Kutta method through the following steps.

Consider a function $\varphi : \mathbb{R} \to \mathbb{R}_+$ such that $0 < \varphi(z) < 1$ for $z > 0$ and

$$\varphi(z) = z + \mathcal{O}(z^{k+1}). \tag{2.3.18}$$

For instance, we can take

$$\varphi(z) = \frac{z}{1 + c\ z^k},$$

where c is a positive constant.

We consider the function

$$\phi(h) = \frac{\varphi(qh)}{q},$$

where $q \geq |\lambda|$ and λ traces all the eigenvalues of all the Jacobian matrices at the fixed points for $(2.2.1)$. Our NS Runge–Kutta method is given by

$$x_{n+1} = x_n + \phi(h) \sum_{i=1}^{k} b_i K_i, \tag{2.3.19}$$

where

$$K_i = f\left(x_n + \phi(h) \sum_{j=1}^{i-1} a_{ij} K_j\right), \quad i = 1, 2, ..., k\ .$$

Theorem 2.3.24. *Assume that* $1 \leq k \leq 4$. *Then the NS Runge–Kutta method* $(2.3.19)$ *is of order* k. *Furthermore, this scheme replicates the asymptotic behavior of the model equation* $(2.3.10)$ *in the following sense: For any* $h > 0$, *the discrete solution* $x_n \to 0$ *if* $Re\lambda_l < 0 \quad \forall \lambda_l$ *whereas* $\|x_n\| \to \infty$ *if there exists at least one eigenvalue* λ_l *with* $Re\lambda_l > 0$.

Proof: The order of the method results from the relation $(2.3.18)$. The convergence/divergence as $n \to \infty$ is based on the analogous of the representations $(2.3.14)$ and $(2.3.16)$:

$$x_{n+1} = R\left(\lambda\phi(h)\right) x_n \quad \text{and} \quad R\left(\lambda\phi(h)\right) = \sum_{j=0}^{k} \frac{(\lambda\phi(h))^j}{j!}.$$

Chapter 3

Classical SIR and SIS Models

3.1 Introduction

In this chapter, we deal with the simplest well–known compartmental mathematical models for transmission of diseases in a population. These are the SIR and SIS models. However, we consider these models with an extended contact rate.

The SIR models is considered in Section 3.2. After presenting the model formulation in Section 3.2.1, the study is organized in the main directions given below.

- Quantitative analysis (Section 3.2.2): we prove the well–posedness of the problem,
- Qualitative analysis (Section 3.2.2): we investigate the stability of equilibria, including the global asymptotic stability of the disease–free equilibrium,
- Constructive analysis (Section 3.2.3): we design nonstandard finite difference schemes that are dynamically consistent with the properties of the continuous model.

The study of the SIS model in Section 3.3 is shortened, given the similarities with the presentation of the SIR model.

The last part (Section 3.4) of the chapter reports on frequently used contact rates with emphasis on illustrations including bifurcation diagrams and numerical experiments. In particular, the nonstandard Runge–Kutta method is presented for the first time to the best of our knowledge and tested to be a higher order scheme (Section 3.4.4).

3.2 SIR Model with General Contact Rate

3.2.1 Model Formulation

In the mathematical formulation of a model for the transmission of a disease, the number $C(N) = N\beta(N) \geq 0$ of contacts made by an average infective in unit time plays an important role. Experience has shown that this number of contacts tends:

1. to grow less rapidly as the population size N increases and/or
2. to saturate or stabilize as the population size N becomes large.

Therefore, following [8], we assume in the first instance that

$$C'(N) \geq 0 \quad \text{and} \quad \beta'(N) \leq 0. \tag{3.2.1}$$

The second condition in $(3.2.1)$ implies that $C'(N)$ is bounded in the following specific manner:

$$C'(N) \leq \beta(N) \leq \sup_N \beta(N).$$

Thus

$$C(N) \leq aN + b, \qquad a > 0, \qquad b \geq 0. \tag{3.2.2}$$

The general conditions in $(3.2.1)$ are sufficient for the analysis in this section. However, in order to comply strictly with the requirement in items (1) and (2) above, the functions $C(N)$ and $\beta(N)$ in $(3.2.1)$ will be chosen such that the additional conditions below are met. Either

$$\lim_{N\to\infty} \beta(N) = 0, \tag{3.2.3}$$

in which case the property in (1) holds; or

$$C(N) \text{ is bounded}, \tag{3.2.4}$$

which guarantees both the less rapidly increasing and saturation properties.

The basic SIR model for the spread of diseases is well–known and goes back to Kermack–McKendrick [33]. However, we present it here with an extended contact rate $C(N)$ as introduced above.

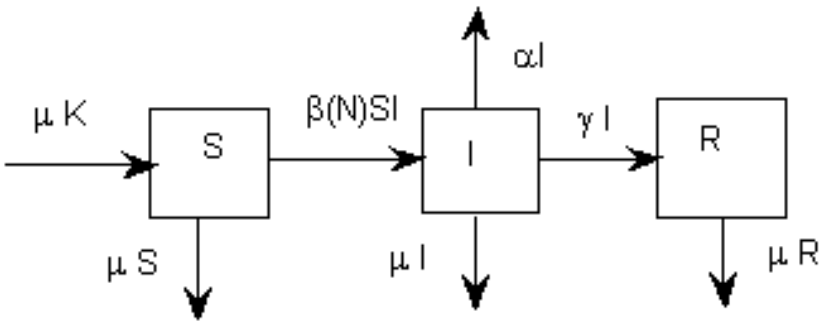


Figure 3.1: Flow chart for SIR model.

The total population N is divided into three disjoint classes: individuals S who are susceptible to infection, infective individuals I and individuals R who are recovered from infection. In all classes, individuals die naturally at the rate $\mu > 0$, while in I the disease induces additional death at the rate $\alpha \geq 0$. Infective individuals are recovered at the rate $\gamma > 0$. Susceptible individuals are recruited at the rate μK with $K > 0$ being the carrying capacity.

With the flow diagram of the SIR model given in Fig 3.1, the SIR model with general contact rate reads as follows:

$$S' = \mu K - \beta(N)SI - \mu S \tag{3.2.5}$$

$$I' = \beta(N)SI - (\alpha + \mu + \gamma)I \tag{3.2.6}$$

$$R' = \gamma I - \mu R. \tag{3.2.7}$$

The term $\beta(N)SI$ represents the average number of new cases per unit time. The system $(3.2.5) - (3.2.7)$ is appended with the following initial conditions:

$$S(0) = S_0, \quad I(0) = I_0, \quad \text{and} \quad R(0) = R_0. \tag{3.2.8}$$

3.2.2 Quantitative and Qualitative Analysis

Our first concern is the well–posedness of the initial value problem $(3.2.5) - (3.2.8)$ in a manner that is biologically feasible. To this end, we are interested in nonnegative solutions,

assuming that the initial conditions are nonnegative.

By adding $(3.2.5) - (3.2.7)$, we get

$$N' = \mu(K - N) - \alpha I, \tag{3.2.9}$$

$$\text{where} \quad N(t) = S(t) + I(t) + R(t). \tag{3.2.10}$$

From Equation $(3.2.9)$, we have the following conservation law:

$$\mu K - (\mu + \alpha)N \leq N' \leq \mu K - \mu N. \tag{3.2.11}$$

By Gronwall Inequality (Lemma 2.2.6) applied from above and below to Equation $(3.2.11)$, we have for $t \geq 0$

$$N(t) \leq K + (N_0 - K)e^{-\mu t}$$

and

$$N(t) \geq \frac{\mu K}{\alpha + \mu}\left(1 - e^{-(\alpha+\mu)t}\right) + N_0 e^{-(\alpha+\mu)t}.$$

Thus for $0 \leq N_0 \leq K$, we have

$$0 \leq N(t) \leq K. \tag{3.2.12}$$

Therefore, the compact set

$$\Omega = \{(S, I, R) \in \mathbb{R}^3_+ : \ 0 \leq S + I + R \leq K\} \tag{3.2.13}$$

constitutes the biologically feasible region for the model $(3.2.5) - (3.2.8)$. The well–posedness result reads as follows.

Theorem 3.2.1. *The SIR model* $(3.2.5) - (3.2.7)$ *defines a dynamical system on* Ω.

Proof: We will apply Theorem 2.2.5. It is clear that the right–hand side of $(3.2.5) - (3.2.7)$ is locally Lipschitz. We now show that for $S_0 \geq 0, \quad I_0 \geq 0$ and $R_0 \geq 0$, any solution of $(3.2.5) - (3.2.7)$ is such that $S(t) \geq 0, \quad I(t) \geq 0$ and $R(t) \geq 0$. We restrict ourselves to the component $S(t)$ of the solution, the situation being similar for the other components $I(t)$ and $R(t)$.

Equation $(3.2.5)$ is a first order linear equation in $S(t)$ that can be written as

$$S' + (\beta(N)I + \mu)\, S = \mu K \tag{3.2.14}$$

and has integrating factor

$$\rho(t) = e^{\int_0^t P(u)du}, \quad \text{where} \quad P = \beta(N)I + \mu.$$

Thus, Equation $(3.2.14)$ is equivalent to

$$(\rho S)' = \rho\mu K.$$

If we take the integral of both sides on the closed interval $[0, t]$, we obtain

$$\rho(t)S(t) = \rho(0)S(0) + \mu K \int_0^t \rho(u)du.$$

Hence,

$$S(t) = e^{-\int_0^t P(u)du}\left(S(0) + \mu K \int_0^t \rho(u)du\right) \geq 0, \qquad \text{because} \quad \rho(0) = 1 \ \text{ and } \ S_0 \geq 0.$$

In view of $(3.2.10)$ and $(3.2.12)$, any solution corresponding to the initial value $(S_0, I_0, R_0) \in \Omega$ satisfies the a priori bound $(S(t), I(t), R(t)) \in \Omega$. Consequently, Theorem 2.2.5 applies and guarantees that to any (S_0, I_0, R_0) in Ω, there exists a corresponding unique global solution of $(3.2.5)-(3.2.7)$ that remains in Ω. □

Equation $(3.2.6)$ of infective individuals can be written as

$$I' = (\alpha + \mu + \gamma)\left[\mathcal{R}_0 \frac{C(N)}{C(K)}\frac{S}{N} - 1\right] I, \tag{3.2.15}$$

$$\text{where} \qquad \mathcal{R}_0 = \frac{C(K)}{\alpha + \mu + \gamma}. \tag{3.2.16}$$

A close look at $(3.2.15)$ shows two interesting cases based on the values of $\mathcal{R}_0$. Firstly, if $\mathcal{R}_0 < 1$, it follows from $(3.2.15)$ and $(3.2.1)$ that, for the solution of $(3.2.5) - (3.2.7)$ as in Theorem 3.2.1, we have

$$I' \leq 0,$$

so that I is decreasing. Hence, the disease will die out.

Secondly, if $\mathcal{R}_0 > 1$ and provided that there are sufficiently enough susceptible individuals $S(t)$, we have

$$I'(t) \geq 0$$

so that I is increasing. Thus, there will be an epidemic situation. Indeed if $S(t) \in \left(\frac{K}{\mathcal{R}_0}, K\right)$, then we have from $(3.2.15)$

$$\begin{aligned} \mathcal{R}_0 \frac{C(N)}{C(K)} \frac{S}{N} - 1 &> \mathcal{R}_0 \frac{C(N)}{C(K)} \frac{\frac{K}{\mathcal{R}_0}}{N} - 1 \\ &= \frac{\beta(N)}{\beta(K)} - 1 \\ &\geq 0, \qquad \text{because } \beta \text{ is decreasing (see (3.2.1)).} \end{aligned}$$

The number $\mathcal{R}_0$ given in $(3.2.16)$ plays an important role in the study of the epidemiological model $(3.2.5) - (3.2.7)$. It is the so–called basic reproduction number defined as follows:

Definition 3.2.2. $[1, 16]$ *The basic reproduction number is the average number of secondary cases produced by a single infected individual in a completely susceptible population.*

Remark 3.2.3. *The expression* $(3.2.16)$ *for* $\mathcal{R}_0$ *is in line with Definition 3.2.2. Indeed, the average number of susceptible individuals that one infective will infect for the duration*

$$\frac{1}{\alpha + \mu + \gamma}$$

of its life in the infective class is

$$\textit{(period of infection in the infective class)} \times \textit{(contact rate)}. \tag{3.2.17}$$

Formula $(3.2.16)$ *or* $(3.2.17)$ *is a byproduct of the so–called next generation matrix method* $[18]$*, which is used for the calculation of* $\mathcal{R}_0$ *for more general epidemiological models.*

The relevance of $\mathcal{R}_0$, mentioned above in the qualitative analysis of the model $(3.2.5) - (3.2.7)$ is made more explicit in the rest of this chapter.

In what follows, it will be convenient from time to time to consider the system $(3.2.5) - (3.2.7)$ in the equivalent form $(3.2.5)$, $(3.2.6)$ and $(3.2.9)$. In this case, the region Ω becomes

$$\Omega^* = \{(S, I, N) \in \mathbb{R}^3_+ : \ 0 \leq N - S - I \quad \text{and} \quad N \leq K\}.$$

But in order to simplify notation, we will sometimes write Ω instead of Ω^*. It is in this specific context that equilibria of $(3.2.5) - (3.2.7)$ are investigated as solutions of the system:

$$\mu K - \beta(N) S I - \mu S = 0, \tag{3.2.18}$$

$$\beta(N) S I - (\alpha + \mu + \gamma) I = 0, \tag{3.2.19}$$

$$\mu(K - N) - \alpha I = 0. \tag{3.2.20}$$

From equation $(3.2.19)$, we have either $I = 0$ or $\beta(N)S - (\alpha + \mu + \gamma) = 0$.

If $I = 0$, then from $(3.2.18)$ and $(3.2.20)$, we get $S = K$ and $N = K$, respectively. Hence,

$$E_0 := (K, 0, K) \quad \text{for} \quad (3.2.5) - (3.2.6) \quad \text{and} \quad (3.2.9)$$

or equivalently

$$E_0 = (K, 0, 0) \quad \text{for} \quad (3.2.5) - (3.2.7)$$

is the disease–free equilibrium (DFE) point of the SIR model.

Proposition 3.2.4. *The disease–free equilibrium point E_0 is hyperbolic if $\mathcal{R}_0 \neq 1$.*

Proof: To show that E_0 is a hyperbolic equilibrium point, we use the Jacobian matrix of $(3.2.5) - (3.2.6)$ and $(3.2.9)$:

$$J(S, I, N) = \begin{pmatrix} -\beta(N)I - \mu & -\beta(N)S & -\beta'(N)SI \\ \beta(N)I & \beta(N)S - (\alpha + \mu + \gamma) & \beta'(N)SI \\ 0 & -\alpha & -\mu \end{pmatrix}. \tag{3.2.21}$$

Then

$$J(E_0) = \begin{pmatrix} -\mu & -C(K) & 0 \\ 0 & C(K) - (\alpha + \mu + \gamma) & 0 \\ 0 & -\alpha & -\mu \end{pmatrix}.$$

To find the eigenvalues r of $J(E_0)$, we solve the equation $det[rI - J(E_0)] = 0$, where I is the 3×3 identity matrix. This equation can be written as

$$\begin{vmatrix} r + \mu & C(K) & 0 \\ 0 & r - (C(K) - (\alpha + \mu + \gamma)) & 0 \\ 0 & \alpha & r + \mu \end{vmatrix} = 0$$

or

$$(r+\mu)^2(r-(C(K)-(\alpha+\mu+\gamma)))=0.$$

Hence, $r_1=-\mu$ (with multiplicity 2) and $r_2=C(K)-(\alpha+\mu+\gamma)$ are real eigenvalues which are not equal to zero if $C(K)-(\alpha+\mu+\gamma)\neq 0$. Thus, by Definition 2.2.13, E_0 is a hyperbolic equilibrium point in this case. □

Theorem 3.2.5. *The disease–free equilibrium point E_0 is locally asymptotically stable (LAS) if $\mathcal{R}_0<1$ and unstable if $\mathcal{R}_0>1$.*

Proof: Since the equilibrium E_0 is hyperbolic (see Proposition 3.2.4), we can apply Hartman–Grobman linearization theorem (see Theorem 2.2.13) and Theorem 2.2.14.

From the proof of Proposition 3.2.4, the eigenvalue $r_1=-\mu$ of the Jacobian matrix $J(E_0)$ is negative. The other eigenvalue $r_2=C(K)-(\alpha+\mu+\gamma)$ satisfies $r_2<0$ if and only if $\mathcal{R}_0<1$. This proves the theorem. □

In terms of the celebrated threshold theory of Kermack and McKendrick (see [1]), the epidemiological implication of Theorem 3.2.5 is that a small influx of infected individuals into the community would not result in a major epidemic provided $\mathcal{R}_0<1$. On the other hand, the disease will be established in the community if $\mathcal{R}_0>1$. To ensure disease elimination is independent of the initial size of the sub–populations of the model $(3.2.5)-(3.2.7)$, it is necessary to investigate when the DFE is globally asymptotically stable (GAS) in Ω. This is considered below.

Theorem 3.2.6. *The disease–free equilibrium E_0 is globally asymptotically stable (GAS) if $\mathcal{R}_0<1$.*

Proof: We will apply LaSalle invariance principle in Theorem 2.2.25, observing that the dynamical system under consideration is dissipative (see Theorem 3.2.1).

On the compact region Ω^* introduced earlier, we consider the function

$$V:\Omega^*\subset\mathbb{R}^3\to\mathbb{R},\qquad V(S,I,N)=I,$$

which clearly satisfies the properties $V(E_0)=0$ and $V(E)>0$ for $E_0\neq E\in\Omega^*$. Let $E=(S,I,N)\in\Omega^*$. By definition of the derivative of V in the direction of the vector that

is defined by the right–hand $f(S,I,N)$ side of $(3.2.5), (3.2.6)$ and $(3.2.9)$, we have

$$\begin{aligned}
\dot{V} &= \nabla V.f(S,I,N), \\
&= (0,1,0).f(S,I,N), \\
&= [\beta(N)S - (\alpha+\mu+\gamma)]I, \quad \text{by (3.2.6)} \\
&\leq [\beta(N)N - (\alpha+\mu+\gamma)]I, \quad \text{because} \quad S \leq N \\
&= [C(N) - (\alpha+\mu+\gamma)]I, \quad \text{since} \quad \beta(N)N = C(N) \\
&\leq [C(K) - (\alpha+\mu+\gamma)]I, \quad \text{because } C \text{ is increasing} \\
&= (\alpha+\mu+\gamma)(\mathcal{R}_0 - 1)I, \quad \text{by definition in (3.2.16).}
\end{aligned}$$

$$\text{Thus} \quad \dot{V} \leq 0 \quad \text{on} \quad \Omega^* \quad \text{if} \quad \mathcal{R}_0 \leq 1.$$

Hence, V is a positive definite Lyapunov function for E_0 on Ω^*. Furthermore, when $(S,I,N) \equiv (S(t),I(t),N(t)) \in \Omega^*$ is a solution of $(3.2.5) - (3.2.6)$ and $(3.2.9)$ and $\mathcal{R}_0 < 1$, we have from $\dot{V} = I'$, $I(t) = 0, \ \forall t$ if $I'(t) = 0, \ \forall t$ and $V'(t) < 0 \ \forall t$ if $I(t) > 0 \ \forall t$.

Next in accordance to Theorem 2.2.25, we consider the set

$$\mathcal{E} = \{(S,I,N) \in \Omega^* : \dot{V}(S,I,N) = 0\}.$$

We claim that $\{E_0\}$ is the largest invariant set that is contained in $\mathcal{E}$. Indeed let $\mathcal{A} \subset \mathcal{E}$ be an invariant set. Take $(S_0,I_0,N_0) \in \mathcal{A}$. Then $(S(t),I(t),N(t)) = \Phi(t)(S_0,I_0,N_0) \in \mathcal{A}$, because $\mathcal{A}$ is invariant. Furthermore, $(S(t),I(t),N(t)) \in \mathcal{E}$ for $t \geq 0$ since $\mathcal{A} \subset \mathcal{E}$. Thus, $\dot{V}(S(t),I(t),N(t)) = \dot{I}(t) = 0$. In view of the condition $\mathcal{R}_0 < 1$, the first part of this proof implies that $I(t) = 0$ for every $t \geq 0$. Therefore, $S(t) = N(t) = K, \ \forall t$. This shows that $(S_0,I_0,N_0) = (K,0,K)$ and thus $\mathcal{A} \subset \{E_0\}$.

Since for the dynamical system $(3.2.5), \ (3.2.6)$ and $(3.2.9)$ restricted to $\{E_0\}$, the equilibrium point E_0 is the only GAS, we infer from Theorem 2.2.25 that E_0 is GAS on Ω^* for the dynamical system $(3.2.5), \ (3.2.6)$ and $(3.2.9)$. □

The fact stated in Theorem 3.2.4 that the disease–free equilibrium is unstable when $\mathcal{R}_0 > 1$ is made more precise in the next result.

Theorem 3.2.7. *Assume that $\mathcal{R}_0 > 1$. Then, there exists a unique additional equilibrium point $E_\infty = (S_\infty, I_\infty, N_\infty)$, $I_\infty > 0$ called "endemic equilibrium". This endemic equilibrium (EE) point is LAS.*

Proof: Consider Equation $(3.2.19)$ with $I > 0$. Then we have $N > 0$, $\beta(N) > 0$ and

$$\beta(N)S = (\alpha + \mu + \gamma), \tag{3.2.22}$$

which transforms Equation $(3.2.18)$ into

$$(\alpha + \mu + \gamma)I = \mu K - \frac{\mu(\alpha + \mu + \gamma)}{\beta(N)}. \tag{3.2.23}$$

If we substitute the resulting expression of I into Equation $(3.2.20)$, we get

$$K - N - \alpha\left(\frac{K}{\alpha + \mu + \gamma} - \frac{1}{\beta(N)}\right) = 0,$$

which is equivalent to

$$f(N) := K\beta(N) - C(N) - \alpha\left(\frac{K\beta(N)}{\alpha + \mu + \gamma} - 1\right) = 0. \tag{3.2.24}$$

It should be noted that the function $f(N)$ is decreasing on $(0, \infty)$ since

$$\begin{aligned} f'(N) &= K\beta'(N) - C'(N) - \frac{\alpha K\beta'(N)}{\alpha + \mu + \gamma} \\ &= K\beta'(N)\left(1 - \frac{\alpha}{\alpha + \mu + \gamma}\right) - C'(N) \\ &< 0, \end{aligned}$$

by the properties of β and C in $(3.2.1)$.

At $N = \frac{\mu K}{\alpha+\mu}$, we have after computation, $f\left(\frac{\mu K}{\alpha+\mu}\right) = K\beta\left(\frac{\mu K}{\alpha+\mu}\right)\left(\frac{\alpha\gamma}{(\alpha+\mu)(\alpha+\mu+\gamma)}\right) + \alpha > 0$. At $N = K$, $f(K) = -\alpha\left(\frac{K\beta(K)}{\alpha+\mu+\gamma} - 1\right) < 0$, because $\mathcal{R}_0 > 1$. Since the function $f(N)$ is continuous and decreasing on the interval $[\frac{\mu K}{\alpha+\mu}, K]$, we infer from the intermediate value theorem that there exists a unique $N_\infty \in (\frac{\mu K}{\alpha+\mu}, K)$ such that $f(N_\infty) = 0$. Given the fact that f is injective on $(0, \infty)$, the number N_∞ is actually the unique root of f in the interval $(0, K)$. Plugging the value $N = N_\infty$ into $(2.4.22)$ and $(2.4.23)$, we obtain in view of the expression $\mathcal{R}_0$ in $(2.4.16)$ the following susceptible and infective coordinates of the endemic equilibrium $E_\infty = (S_\infty, I_\infty, N_\infty)$:

$$S_\infty = \frac{\beta(K)K}{\beta(N_\infty)\mathcal{R}_0}, \qquad I_\infty = \frac{\mu}{\beta(K)\beta(N_\infty)}\left[\mathcal{R}_0\beta(N_\infty) - \beta(K)\right]. \tag{3.2.25}$$

The second part of the proof is the stability property of the endemic equilibrium E_∞. For this we use Theorem 2.2.14 and the Jacobian matrix given in $(3.2.21)$ at the point E_∞:

$$J(E_\infty) = \begin{pmatrix} -\beta(N_\infty)I_\infty - \mu & -\beta(N_\infty)S_\infty & -\beta'(N_\infty)S_\infty I_\infty \\ \beta(N_\infty)I_\infty & 0 & \beta'(N_\infty)S_\infty I_\infty \\ 0 & -\alpha & -\mu \end{pmatrix}$$

The eigenvalues of the matrix $J(E_\infty)$ are the roots r of the characteristic equation

$$det(rI - J(E_\infty)) = \begin{vmatrix} r + (\beta(N_\infty)I_\infty + \mu) & \beta(N_\infty)S_\infty & \beta'(N_\infty)S_\infty I_\infty \\ -\beta(N_\infty)I_\infty & r & -\beta'(N_\infty)S_\infty I_\infty \\ 0 & \alpha & r + \mu \end{vmatrix} = 0.$$

We can write this equation as

$$r^3 + a_2 r^2 + a_1 r + a_0 = 0,$$

where

$$\begin{aligned} a_2 &= 2\mu + \beta(N_\infty)I_\infty, \\ a_1 &= \mu\left[\mu + \beta(N_\infty)I_\infty\right] + \left[\alpha\beta'(N_\infty) + \beta^2(N_\infty)\right] S_\infty I_\infty, \\ \text{and} \quad a_0 &= \mu\left[\alpha\beta'(N_\infty) + \beta^2(N_\infty)\right] S_\infty I_\infty. \end{aligned}$$

It is clear that $a_2 > 0$. It is also true that $a_1 > 0$ and $a_0 > 0$ in view of the decreasing property of $\beta(N)$ stated in $(3.2.1)$ and,

$$\begin{aligned} \alpha\beta'(N_\infty) + \beta^2(N_\infty) &= \alpha\left(\frac{C'(N_\infty)N_\infty - C(N_\infty)}{N_\infty^2}\right) + \frac{C^2(N_\infty)}{N_\infty^2} \\ &= \frac{C^2(N_\infty) - \alpha C(N_\infty) + \alpha C'(N_\infty)N_\infty}{N_\infty^2} \\ &\geq \frac{C(N_\infty)\left[C(N_\infty) - \alpha\right]}{N_\infty^2} \\ &> 0, \end{aligned}$$

because by using Equation $(3.2.22)$, we have

$$C(N_\infty) = \beta(N_\infty)N_\infty \geq \beta(N_\infty)S_\infty = \alpha + \mu + \gamma > \alpha.$$

On the other hand, we have

$$\begin{aligned} a_2 a_1 &= [2\mu + \beta(N_\infty) I_\infty] \left[\mu(\mu + \beta(N_\infty) I_\infty) + [\alpha\beta'(N_\infty) + \beta^2(N_\infty)] S_\infty I_\infty\right] \\ &> \mu \left[\alpha\beta'(N_\infty) + \beta^2(N_\infty)\right] S_\infty I_\infty \\ &= a_0. \end{aligned}$$

By the Routh–Hurwitz condition [23], we conclude that all the eigenvalues of $J(E_\infty)$ have negative real parts. Thus, the endemic equilibrium E_∞ is locally asymptotically stable by Theorem 2.2.14. □

Remark 3.2.8. *A remark is in order regarding the explicit expression of the endemic equilibrium E_∞ under the condition $\mathcal{R}_0 > 1$ in Theorem 3.2.7. Assume that there is no death induced by the disease, i.e. $\alpha = 0$. Then we have*

$$E_\infty = (S_\infty, I_\infty, N_\infty) = \left[\frac{\mu+\gamma}{\beta}, \frac{\mu}{\mu+\gamma}\left(K - \frac{\mu+\gamma}{\beta}\right), K\right],$$

which readily follows from (3.2.20), (3.2.19) and (3.2.18) respectively. However, no such explicit expression for E_∞ is available in the general case when $\alpha > 0$. Nevertheless, the proof of Theorem 3.2.7 permits us to apply a constructive method for approximating E_∞. More precisely, the bisection method applies and works as follows [53]:

For $n = 0$, we consider the initial interval $I_0 = [a_0, b_0]$, where $a_0 = 0$ and $b_0 = K$.

At the iteration $n \geq 1$, we introduce the mid–point

$$c_n = \frac{a_{n-1} + b_{n-1}}{2}$$

and consider the interval $I_n = [a_n, b_n]$ given by

$$\begin{aligned} a_n &= c_n \quad \text{and} \quad b_n = b_{n-1} \quad \text{if} \quad f(a_{n-1}) f(c_n) > 0, \\ a_n &= a_{n-1} \quad \text{and} \quad b_n = c_n \quad \text{if} \quad f(a_{n-1}) f(c_n) < 0. \end{aligned}$$

In this way, we have constructed by mathematical induction a nested sequence

$$I_0 \supset I_1 \supset \ldots \supset I_n \supset \ldots$$

of nonempty closed intervals, each of which contains the endemic equilibrium coordinate N_∞, and such that

$$\max\{N_\infty - a_n,\ b_n - N_\infty\} \leq \frac{K}{2^n}. \tag{3.2.26}$$

In view of $(3.2.26)$, a_n, c_n *and* b_n *are approximations of* N_∞ *at the* n^{th} *iteration. The bisection iteration terminates at the* n^{th} *step for which,* $\frac{K}{2^n} < \epsilon$ *where* $\epsilon > 0$ *is a fixed tolerance. Once an approximation of* N_∞ *is obtained, we find an approximation of* S_∞ *and* I_∞ *by using the formula* $(3.2.25)$.

Remark 3.2.9. *If* $\mathcal{R}_0 = 1$ *then from Equation* $(3.2.24)$, *we observe that* $N = K$ *is the unique zero of the function* $f(N)$, *which implies, in view of* $(3.2.25)$, *that the endemic equilibrium collapses to disease–free equilibrium.*

Theorem 3.2.5 and Theorem 3.2.7 illustrate the statement in Remark 2.2.15 regarding the basic reproduction number $\mathcal{R}_0$. Combining these two theorems , we have, in view of Definition 2.2.32, established the following result.

Theorem 3.2.10. *For the SIR model* $(3.2.5) - (3.2.7)$, *the value* $\mathcal{R}_0 = 1$ *is a forward bifurcation point.*

3.2.3 NSFD Schemes

In this section, we design numerical schemes that are dynamically consistent with the properties of the SIR model $(3.2.5) - (3.2.7)$. Given the well-known power of the nonstandard finite difference schemes in replicating the properties of dynamical systems, we use this approach, the generalities of which were presented in Section 2.3.

Following the strategy proposed in $[49]$, it is instructive to start with the conservation law $(3.2.11)$, which we recall here for convenience:

$$\mu K - (\alpha + \mu)N \leq N' \leq \mu K - \mu N.$$

Assume that N takes the value $N_0 \leq K$ at the time $t = 0$. Application of Gronwall inequality (Lemma 2.2.6) to the conservation law yields

$$\frac{\mu K}{\alpha + \mu} + \left(N_0 - \frac{\mu K}{\alpha + \mu}\right) e^{-(\alpha+\mu)t} \leq N(t) \leq K + (N_0 - K)e^{-\mu t}$$

for any $t \geq 0$. At the discrete time $t = t_{n+1} = (n + 1)\Delta t$ defined in Section 2.4.2, the previous double inequality becomes

$$\frac{\mu K}{\alpha + \mu} + \left(N_0 - \frac{\mu K}{\alpha + \mu}\right) e^{-(\alpha+\mu)t_{n+1}} \leq N(t_{n+1}) \leq K + (N_0 - K)e^{-\mu t_{n+1}}. \qquad (3.2.27)$$

By using the semi–group property of the evolution operator for differential equations, Equation $(3.2.27)$ can be written as

$$\frac{\mu K}{\alpha+\mu}+\left(N(t_n)-\frac{\mu K}{\alpha+\mu}\right)e^{-(\alpha+\mu)\Delta t}\leq N(t_{n+1})\leq K+(N(t_n)-K)e^{-\mu\Delta t}.$$

Subtracting $N(t_n)$ from all sides, we have

$$\left[\frac{\mu K}{\alpha+\mu}-N(t_n)\right]\left(1-e^{-(\alpha+\mu)\Delta t}\right)\leq N(t_{n+1})-N(t_n)\leq [K-N(t_n)]\left(1-e^{-\mu\Delta t}\right). \tag{3.2.28}$$

Observe that

$$\frac{1}{1-e^{-(\alpha+\mu)\Delta t}}\leq\frac{1}{1-e^{-\mu\Delta t}}.$$

Hence Equation $(3.2.28)$ implies that

$$\frac{\mu K}{\alpha+\mu}-N(t_n)\leq\frac{N(t_{n+1})-N(t_n)}{1-e^{-(\alpha+\mu)\Delta t}}\leq\frac{N(t_{n+1})-N(t_n)}{1-e^{-\mu\Delta t}}\leq K-N(t_n). \tag{3.2.29}$$

On setting $N_n:=N(t_n)$, Equation $(3.2.29)$ provides two types of exact schemes, which we investigate now. The first exact scheme is

$$\frac{\mu K}{\alpha+\mu}-N_n\leq\frac{N_{n+1}-N_n}{1-e^{-\mu\Delta t}}\leq K-N_n, \tag{3.2.30}$$

which is written in the more convenient form

$$\frac{\mu^2 K}{\alpha+\mu}-\mu N_n\leq\frac{N_{n+1}-N_n}{\frac{1-e^{-\mu\Delta t}}{\mu}}\leq\mu K-\mu N_n. \tag{3.2.31}$$

The second exact scheme is

$$\frac{\mu K}{\alpha+\mu}-N_n\leq\frac{N_{n+1}-N_n}{1-e^{-(\alpha+\mu)\Delta t}}\leq K-N_n,$$

or equivalently,

$$\mu K-(\alpha+\mu)N_n\leq\frac{N_{n+1}-N_n}{\frac{1-e^{-(\alpha+\mu)\Delta t}}{\alpha+\mu}}\leq(\alpha+\mu)K-\mu N_n. \tag{3.2.32}$$

Apart from the forward Euler type schemes $(3.2.31)$ and $(3.2.32)$, we have their backward counterparts

$$\frac{\mu^2 K}{\alpha+\mu}-\mu N_{n+1}\leq\frac{N_{n+1}-N_n}{\frac{e^{\mu\Delta t}-1}{\mu}}\leq\mu K-\mu N_{n+1} \tag{3.2.33}$$

and

$$\mu K - (\alpha+\mu)N_{n+1} \leq \frac{N_{n+1}-N_n}{\frac{e^{(\alpha+\mu)\Delta t}-1}{\alpha+\mu}} \leq (\alpha+\mu)K - \mu N_{n+1}. \tag{3.2.34}$$

To obtain $(3.2.33)$, we proceed as follows from Equation $(3.2.30)$ which leads successively to:

$$\frac{\mu K}{\alpha+\mu}(1-e^{-\mu\Delta t}) - N_n(1-e^{-\mu\Delta t}) \leq N_{n+1}-N_n \leq K(1-e^{-\mu\Delta t}) - N_n(1-e^{-\mu\Delta t})$$

by multiplying with $(1-e^{-\mu\Delta t})$;

$$\frac{\mu K}{\alpha+\mu}(e^{\mu\Delta t}-1) - N_n(e^{\mu\Delta t}-1) \leq e^{\mu\Delta t}N_{n+1} - e^{\mu\Delta t}N_n \leq K(e^{\mu\Delta t}-1) - N_n(e^{\mu\Delta t}-1)$$

by multiplying with $e^{\mu\Delta t}$;

$$\frac{\mu K}{\alpha+\mu}(e^{\mu\Delta t}-1) - N_{n+1}(e^{\mu\Delta t}-1) \leq N_{n+1}-N_n \leq K(e^{\mu\Delta t}-1) - N_{n+1}(e^{\mu\Delta t}-1)$$

by adding N_{n+1} to all sides and simplifying.

Equation $(3.2.34)$ is obtained in a similar manner.

In summary, we have the following result:

Theorem 3.2.11. *Explicit exact schemes of* $(3.2.11)$ *are given by Equations* $(3.2.31)$ *and* $(3.2.32)$*, whereas Equations* $(3.2.33)$ *and* $(3.2.34)$ *represent implicit exact schemes.*

Remark 3.2.12. *The exact schemes given in Theorem 3.2.11 are not in contradiction with the conservation law* $(3.2.11)$ *since we also have the "less" sharp conservation law*

$$\frac{\mu}{\alpha+\mu}(\mu K - (\alpha+\mu)N) \leq N' \leq (\alpha+\mu)K - \mu N.$$

Let us denote by $\phi = \phi(\Delta t)$ the different denominator functions of the discrete derivative in the exact schemes presented above. For all these schemes, the denominator satisfies the asymptotic property

$$\phi(\Delta t) = h + \mathcal{O}(h^2), \quad \text{where} \quad h = \Delta t. \tag{3.2.35}$$

This fact explains why we will, in what follows, replace the traditional denominator h by any function $\phi(h)$ that meets the requirement $(3.2.35)$. Such a function being fixed, we

consider for the SIR model $(3.2.5) - (3.2.7)$, the following NSFD scheme:

$$\frac{S_{n+1} - S_n}{\phi(h)} = \mu K - \frac{C(N_n)}{S_{n+1} + I_n + R_n} I_n S_{n+1} - \mu S_{n+1} \tag{3.2.36}$$

$$\frac{I_{n+1} - I_n}{\phi(h)} = \frac{C(N_n)}{S_{n+1} + I_n + R_n} I_n S_{n+1} - (\alpha + \mu + \gamma) I_{n+1} \tag{3.2.37}$$

$$\frac{R_{n+1} - R_n}{\phi(h)} = \gamma I_{n+1} - \mu R_{n+1}, \tag{3.2.38}$$

where $N_n = S_n + I_n + R_n$.

By adding $(3.2.36) - (3.2.38)$, we get the equation

$$\frac{N_{n+1} - N_n}{\phi(h)} = \mu(K - N_{n+1}) - \alpha I_{n+1}. \tag{3.2.39}$$

Remark 3.2.13. *The function $C(N)$ is generally implicit in N, which makes sense to approximate it by $C(N_n)$. In the case when $C(N)$ is explicit (as in many applications), it might be useful to approximate it by $C(N_{n+1})$. This will be considered later on in the discussion of the specific examples presented in the frequently used contact rates, Section 3.4.*

Proposition 3.2.14. *Assume that $S_n \geq 0,\ I_n \geq 0$ and $R_n \geq 0$ are given. Then Equation $(3.2.36)$ admits a unique solution $S_{n+1} \geq 0$ given explicitly in $(3.2.43)$ below.*

Proof: Assume that $S_n \geq 0,\ I_n \geq 0$ and $R_n \geq 0$ are given. Then Equation $(3.2.36)$ is equivalent to the following quadratic equation in S_{n+1}:

$$AS_{n+1}^2 + BS_{n+1} + D = 0.$$

Here

$$A = 1 + \mu\phi > 0, \tag{3.2.40}$$

$$B = (1 + \mu\phi)(I_n + R_n) + C(N_n)\phi I_n - (S_n + \mu\phi K), \tag{3.2.41}$$

and

$$D = -(S_n + \mu\phi K)(I_n + R_n) < 0. \tag{3.2.42}$$

Hence,

$$S_{n+1} = \frac{-B + \sqrt{B^2 - 4AD}}{2A} \geq 0 \tag{3.2.43}$$

is the only nonnegative solution. □

From the computational point of view, it is better to write the NSFD scheme $(3.2.36)-(3.2.39)$ in the following form, S_{n+1} being given by $(3.2.43)$,

$$I_{n+1} = \frac{\left(\frac{C(N_n)}{S_{n+1}+I_n+R_n}\phi S_{n+1}+1\right)I_n}{1+(\alpha+\mu+\gamma)\phi} \tag{3.2.44}$$

$$R_{n+1} = \frac{R_n+\gamma\phi I_{n+1}}{1+\mu\phi} \tag{3.2.45}$$

$$N_{n+1} = \frac{N_n+(\mu K-\alpha I_{n+1})\phi}{1+\mu\phi}. \tag{3.2.46}$$

From now on, we want to show that the NSFD scheme $(3.2.36)-(3.2.38)$ is dynamically consistent with the properties of the continuous SIR model $(3.2.5)-(3.2.7)$. The first set of properties is contained in Propositions 3.2.15 – 3.2.17 which are summarized in Corollary 3.2.18.

Proposition 3.2.15. *The NSFD scheme* $(3.2.36)-(3.2.37)$ *preserves the positivity property.*

Proof: We use the principle of mathematical induction. Assume that we have $S_0 \geq 0,\ I_0 \geq 0$ and $R_0 \geq 0$. Then $S_1 \geq 0$ by Proposition 3.2.14 (cf $(3.2.43)$). This incorporated in $(3.2.44)$ gives $I_1 \geq 0$, which in turn leads to $R_1 \geq 0$ if plugged in $(3.2.45)$.

Assume that we have $S_n \geq 0,\ I_n \geq 0$ and $R_n \geq 0$. Then the same argument of using the following Gauss–Seidel cycle in the formulae $(3.2.43)-(3.2.45)$ applies:

$$(S_n \geq 0, I_n \geq 0) \to (S_{n+1} \geq 0, I_n \geq 0) \to (I_{n+1} \geq 0, R_n \geq 0) \to R_{n+1} \geq 0.$$

This proves the claim for $n+1$. □

Proposition 3.2.16. *The NSFD scheme* $(3.2.36)-(3.2.37)$ *replicates the conservation law* $(3.2.11)$ *in the following specific form:*

$$\mu K-(\alpha+\mu)N_{n+1} \leq \frac{N_{n+1}-N_n}{\phi(h)} \leq \mu K-\mu N_{n+1}.$$

Proof: This is a direct consequence of $(3.2.39)$ and of Proposition 3.2.15, where $N_n \geq 0$. □

Proposition 3.2.17. *The NSFD scheme* $(3.2.36)-(3.2.37)$ *is dynamically consistent with respect to the boundedness property, i.e.* $0 \leq N_n \leq K$ *for any* n *whenever* $0 \leq N_0 \leq K$.

Proof: From Proposition 3.2.16, we have

$$\frac{N_n}{1+(\alpha+\mu)\phi}+\frac{\mu\phi K}{1+(\alpha+\mu)\phi}\leq N_{n+1}\leq\frac{N_n}{1+\mu\phi}+\frac{\mu K\phi}{1+\mu\phi}.$$

By using the discrete Gronwall inequality (Theorem 2.3.4) from the right and the left side, we obtain

$$N_n\leq K+(N_0-K)(1+\mu\phi)^{-n})$$

and

$$N_n\geq N_0[1+(\alpha+\mu)\phi]^{-n}+\left(1-[1+(\alpha+\mu)\phi]^{-n}\right)\frac{\mu K}{\alpha+\mu},$$

respectively. The combination of the above two inequalities leads to $0\leq N_n\leq K$ if $0\leq N_0\leq K$. □

At this point in time, Propositions 3.2.15, 3.2.16 and 3.2.17 can be summarized as follows:

Corollary 3.2.18. *The NSFD scheme* $(3.2.36)-(3.2.37)$ *defines a discrete dynamical system on the same biologically feasible domain as for the continuous model:*

$$\Omega=\{(S,I,R)\in\mathbb{R}^3_+:\ 0\leq S+I+R=N\leq K\}.$$

Furthermore, the system is dissipative.

The second set of properties is related to the fixed points of the NSFD scheme $(3.2.36)-(3.2.39)$ and to their stability.

Proposition 3.2.19. *The NSFD scheme* $(3.2.36)-(3.2.37)$ *has no ghost or spurious equilibria. In other words, the disease–free equilibrium* $E_0=(K,0,0)$ *of the continuous model* $(3.2.5)-(3.2.7)$ *is the only fixed point of the discrete system* $(3.2.36)-(3.2.38)$ *whenever* $\mathcal{R}_0\leq 1$*, whereas, the endemic equilibrium* $E_\infty=(S_\infty,I_\infty,R_\infty)$ *is the only additional fixed–point of the NSFD scheme for* $\mathcal{R}_0>1$*.*

Proof: It is convenient to use the NSFD scheme $(3.2.36)-(3.2.39)$ in the equivalent

form $(3.2.43) - (3.2.46)$ so that we can find the fixed–points of the system

$$\frac{-B + \sqrt{B^2 - 4AD}}{2A} = S, \tag{3.2.47}$$

$$\frac{(\frac{C(N)}{S+I+R}\phi S + 1)I}{1 + (\alpha + \mu + \gamma)\phi} = I, \tag{3.2.48}$$

$$\frac{R + \gamma\phi I}{1 + \mu\phi} = R, \tag{3.2.49}$$

$$\frac{N + (\mu K - \alpha I)\phi}{1 + \mu\phi} = N. \tag{3.2.50}$$

Equation $(3.2.48)$ holds if and only if

$$I = 0 \text{ or } C(N)S = N(\alpha + \mu + \gamma). \tag{3.2.51}$$

If $I = 0$, then from $(3.2.47)$ and $(3.2.49)$ we get $S = K$ and $R = 0$, respectively. Hence, $E_0 = (K, 0, 0)$ is a fixed point of the NSFD scheme.

If the second condition holds in $(3.2.51)$ with $I > 0$, then $(3.2.51)$ with $(3.2.16)$ give

$$S = \frac{NC(K)}{C(N)\mathcal{R}_0}. \tag{3.2.52}$$

From Equation $(3.2.50)$ and Equation $(3.2.49)$, we obtain

$$I = \frac{\mu}{\alpha}(K - N) \quad \text{and} \quad R = \frac{\gamma}{\alpha}(K - N). \tag{3.2.53}$$

From Equations $(3.2.52)$ and $(3.2.53)$, we get

$$\frac{NC(K)}{C(N)\mathcal{R}_0} + \frac{\mu}{\alpha}(K - N) + \frac{\gamma}{\alpha}(K - N) = N. \tag{3.2.54}$$

If we simplified $(3.2.54)$, it gives an implicit equation for $N \in [0, K]$:

$$\alpha C(K) + (\mu + \gamma)K\mathcal{R}_0\beta(N) = (\alpha + \mu + \gamma)\mathcal{R}_0 C(N),$$

$$\text{or} \quad f(N) := \alpha C(K) + (\mu + \gamma)K\mathcal{R}_0\beta(N) - (\alpha + \mu + \gamma)\mathcal{R}_0 C(N) = 0. \tag{3.2.55}$$

If $\mathcal{R}_0 > 1$, it follows from the proof of Theorem 3.2.7 that there exists a unique zero N_∞ of $(3.2.55)$ in the interval $(0, K)$, which helps us to find S_∞, I_∞ and R_∞ from $(3.2.52)$ and $(3.2.53)$, respectively. Hence, $E_\infty = (S_\infty, I_\infty, R_\infty)$ is the only fixed point of the NSFD scheme.

If $\mathcal{R}_0 < 1$, then from $(3.2.55)$, $f(K) = \alpha\ C(K)(1-\mathcal{R}_0) > 0$, which implies that $f(N) > 0$ for all $N \in (0, K]$, because f is decreasing on $(0, K]$. Thus, f has no root in $(0, K)$ and the disease–free equilibrium point is the only fixed–point in this case.

If $\mathcal{R}_0 = 1$, then $N = K$ is the unique zero of $(3.2.55)$. Thus, from $(3.2.52)$ and $(3.2.53)$, we have $I = 0$, $R = 0$ and $S = K$, respectively. □

Proposition 3.2.20. *The disease–free fixed point $E_0 = (K, 0, 0)$ of equations $(3.2.36) - (3.2.37)$ is a hyperbolic fixed point if $\mathcal{R}_0 \neq 1$.*

Proof: The Jacobian matrix of the system under consideration at E_0 is

$$J(E_0) = \begin{pmatrix} \frac{1}{1+\mu\phi} & \frac{-C(K)\phi}{1+\mu\phi} & 0 \\ 0 & \frac{C(K)\phi+1}{1+(\alpha+\mu+\gamma)\phi} & 0 \\ 0 & \frac{\gamma\phi}{1+\mu\phi}\left(\frac{C(K)\phi+1}{1+(\alpha+\mu+\gamma)\phi}\right) & \frac{1}{1+\mu\phi} \end{pmatrix}. \tag{3.2.56}$$

Since,

$$C(K) = \mathcal{R}_0(\alpha+\mu+\gamma),$$

the characteristic equation can be written as

$$det(rI - J) = \left(r - \frac{1}{1+\mu\phi}\right)^2 \left(r - \frac{1+\mathcal{R}_0(\alpha+\mu+\gamma)\phi}{1+(\alpha+\mu+\gamma)\phi}\right) = 0.$$

This shows that

$$r_1 = \frac{1}{1+\mu\phi} \tag{3.2.57}$$

is an eigenvalue of $J(E_0)$ (with multiplicity two) and

$$r_2 = \frac{1+\mathcal{R}_0(\alpha+\mu+\gamma)\phi}{1+(\alpha+\mu+\gamma)\phi} \tag{3.2.58}$$

is a simple eigenvalue. By using Definition 2.3.8, and the assumption $\mathcal{R}_0 \neq 1$, E_0 is hyperbolic fixed point. □

The stability property of E_0 reads as follows.

Theorem 3.2.21. *For $\mathcal{R}_0 < 1$, the disease–free fixed point $E_0 = (K, 0, 0)$ is locally asymptotically stable and unstable for $\mathcal{R}_0 > 1$.*

Proof: Since the fixed–point E_0 is hyperbolic and in view of the expressions $(3.2.57)$ and $(3.2.58)$, the theorem is a direct consequence of the linearization theorem of Hartman–Grobman (Theorem 2.3.10) in its practical form given in Theorem 2.3.11. □

Actually, we have more than the local asymptotic stability of E_0, as stated in the next theorem.

Theorem 3.2.22. *For $\mathcal{R}_0 < 1$, the disease–free fixed point E_0 is globally asymptotically stable.*

Proof: We know from Theorem 3.2.21 that E_0 is stable for $\mathcal{R}_0 < 1$. Thus, the task ahead of us is to prove that E_0 is globally attractive. From Equation $(3.2.44)$, we have

$$\begin{aligned} I_{n+1} &= \frac{\left(\frac{C(N_n)}{S_{n+1}+I_n+R_n}\phi S_{n+1}+1\right) I_n}{1+(\alpha+\mu+\gamma)\phi}, \\ &\leq \frac{(C(K)\phi+1)I_n}{1+(\alpha+\mu+\gamma)\phi}, \\ &= \frac{(\mathcal{R}_0(\alpha+\mu+\gamma)\phi+1)\, I_n}{1+(\alpha+\mu+\gamma)\phi}, \quad \text{by definition of } \mathcal{R}_0. \end{aligned}$$

Thus, $I_{n+1} \leq DI_n$, where

$$D = \frac{\mathcal{R}_0(\alpha+\mu+\gamma)\phi+1}{1+(\alpha+\mu+\gamma)\phi}.$$

Since $0 < D < 1$ for $\mathcal{R}_0 < 1$, the sequence $(I_n)_{n\geq 0}$ tends to zero for any initial value $0 \leq I_0 \leq N_0 \leq K$. Using this convergence in $(3.2.45)$, we deduce that the sequence $(R_n)_{n\geq 0}$ converges equally to zero for any initial value $0 \leq R_0 \leq N_0 \leq K$. Finally , we consider Equation $(3.2.43)$, with Equations $(3.2.41) - (3.2.42)$, to conclude that the sequence $(S_n)_{n\geq 0}$ converges to K for any initial value $0 \leq S_0 \leq N_0 \leq K$. Hence, the theorem is proved. □

Remark 3.2.23. *Along the lines of the proof of Theorem 3.2.22, one reads the discrete counterpart of LaSalle Invariance Principle (Theorem 2.2.31 and Theorem 2.3.15).*

Indeed, the function

$$V(E) \equiv V(S,I,R) := I$$

defined on the compact set Ω is a Lyapunov function for the discrete dynamical system $(3.2.43) - (3.2.45)$, which satisfies the conditions in Theorem 2.3.15. Thus, E_0 is indeed globally asymptotically stable.

To study the stability of the unique endemic fixed point, E_∞, we need the following notation:

Let a function $\varphi : \mathbb{R} \to \mathbb{R}$ satisfy $(3.2.35)$ such that

$$0 < \varphi(h) < 1 \quad \text{for} \quad h > 0. \tag{3.2.59}$$

Let $r_1,\ r_2$ and r_3 be the eigenvalues of the Jacobian matrices in $(3.2.21)$ at the disease-free equilibrium and endemic equilibrium. Let us define a denominator function

$$\phi(h) = \frac{\varphi(qh)}{q}, \quad \text{where} \quad q = max\{|r_1|, |r_2|, |r_3|\}. \tag{3.2.60}$$

Then we have the following result:

Theorem 3.2.24. *For $\mathcal{R}_0 > 1$, the $NSFD$ scheme $(3.2.36) - (3.2.37)$ is elementary stable whenever $\phi(h)$ is chosen according to $(3.2.59)$ and $(3.2.60)$.*

Proof: To prove this theorem, we apply the technique in [4]. By Definition 2.3.20 of elementary stability of a discrete scheme, we have to prove the following two facts:

1. The NSFD scheme $(3.2.36) - (3.2.37)$ has only E_0 and E_∞ as fixed points.
2. These fixed points preserve the stability of the continuous system when applied to its linearized system.

Part 1 is covered by Proposition 3.2.19. Regarding part 2, it is convenient to write the $(3.2.5) - (3.2.6)$ and $(3.2.9)$ in matrix form. To this end , we introduce the vector notation $X = (S, I, N)$. Then our system $(3.2.5) - (3.2.6)$ and $(3.2.9)$ reads as

$$\dot{X} = A(X)X + F, \tag{3.2.61}$$

where

$$A(X) = \begin{pmatrix} -\beta(N)I - \mu & 0 & 0 \\ \beta(N)I & -(\alpha + \mu + \gamma) & 0 \\ 0 & -\alpha & -\mu \end{pmatrix}$$

and

$$F = \begin{pmatrix} \mu K \\ 0 \\ \mu K \end{pmatrix}.$$

Likewise with $X_{n+1} = (S_{n+1}, I_{n+1}, N_{n+1})$, the NSFD scheme $(3.2.36) - (3.2.37)$ and $(3.2.39)$ can be written as

$$\frac{X_{n+1} - X_n}{\phi} = B(S_{n+1}, S_n, I_n, N_n)X_{n+1} + F, \tag{3.2.62}$$

where

$$B(S_{n+1}, S_n, I_n, N_n) = \begin{pmatrix} -\frac{C(N_n)I_n}{S_{n+1}+S_n+R_n} - \mu & 0 & 0 \\ \frac{C(N_n)I_n}{S_{n+1}+S_n+R_n} & -(\alpha+\mu+\gamma) & 0 \\ 0 & -\alpha & -\mu \end{pmatrix}.$$

The linear approximation of the continuous model about the endemic equilibrium point E_∞ is

$$\dot{Y} = J(E_\infty)Y, \quad Y = X - E_\infty, \tag{3.2.63}$$

where $J(E_\infty)$ is the corresponding Jacobian matrix at E_∞ given in Equation $(3.2.21)$. The $NSFD$ scheme $(3.2.62)$ applied to $(2.4.63)$ yields

$$\frac{Y_{n+1} - Y_n}{\phi} = J(E_\infty)Y_{n+1}, \quad \text{with} \quad Y_n = X_n - E_\infty, \tag{3.2.64}$$

or equivalently,

$$Y_{n+1} = (I - \phi J(E_\infty))^{-1} Y_n.$$

Notice that here $(I - \phi J(E_\infty))$ is a non-singular matrix by definition of $\phi(h)$ in $(3.2.60)$. Notice also that the eigenvalues $(r_i)_{i=1}^3$ of $J(E_\infty)$ are complete. Thus, the matrix $J(E_\infty)$ is diagonalizable and we have

$$S^{-1}JS = diag(r_1, r_2, r_3).$$

If we substitute the dependent variables by

$$Z = S^{-1}Y$$

and

$$Z_n = S^{-1}Y_n,$$

then Equations $(3.2.63)$ and $(3.2.64)$ become

$$\dot{Z} = diag(r_1, r_2, r_3)Z$$

and

$$Z_{n+1} = diag(\frac{1}{1-\phi r_1}, \frac{1}{1-\phi r_2}, \frac{1}{1-\phi r_3})Z_n,$$

respectively. Since by Theorem 3.2.7, E_∞ is locally asymptotically stable for $(3.2.63)$, the real parts of the eigenvalues r_1, r_2, and r_3 are negative. Hence for the spectral radius of the matrix $(I-\phi J(E_\infty))^{-1}$, we have:

$$\begin{aligned}
\rho\left((I-\phi J(E_\infty))^{-1}\right) &= \max\{\frac{1}{|1-\phi r_i|} : i = 1,2,3\} \qquad (3.2.65)\\
&= \max\{\frac{1}{\sqrt{1-2\phi(Re r_1)+\phi^2|r_1|^2}}, \frac{1}{\sqrt{1-2\phi(Re r_2)+\phi^2|r_2|^2}},\\
&\quad \frac{1}{\sqrt{1-2\phi(Re r_3)+\phi^2|r_3|^2}}\}\\
&< 1.
\end{aligned}$$

This shows that E_∞ is locally asymptotically stable for the given $NSFD$ scheme.

As for the Jacobian matrix $J(E_0)$ at the disease–free equilibrium, a similar argument to the above shows that

$$\begin{aligned}
\rho((I-\phi J)^{-1}) &= \max\{\frac{1}{1+\phi\mu}, \frac{1}{|1-\phi r_3|}\}\\
&> 1,
\end{aligned}$$

because $|1-\phi r_3| < 1$ and $r_1 = r_2 = -\mu$. (see after Eq (3.2.21)) □

From Theorem 3.2.21 and Theorem 3.2.22, we have the following bifurcation result:

Theorem 3.2.25. *The NSFD model $(3.2.36)-(3.2.37)$ is dynamically consistent with the fact that the value $\mathcal{R}_0 = 1$ of the basic reproduction number is a forward bifurcation.*

3.3 SIS Model with General Contact Rate

In this section, we consider a second type of basic deterministic model for infectious diseases which are spread by direct contact in a population. That is the SIS model which is among the simplest models for diseases in which an infection does not confer immunity. The total population is divided into two disjoint classes: susceptible individuals S to infection and infective individuals I. Infective individuals return to susceptible class after an infective period. The results presented here and in the next sections for the SIS model are published in [41].

3.3.1 Quantitative and Qualitative Analysis

The SIS model with demographic effects and with disease induced death is given by

$$S' = \mu K - \beta(N)SI - \mu S + \gamma I \tag{3.3.1}$$

$$I' = \beta(N)SI - (\alpha + \mu + \gamma)I. \tag{3.3.2}$$

The flow chart of the SIS model is given in Fig 3.2. The parameters used have the same meaning as in Section 3.2. For convenience, we recall that

- μ is the natural death rate;
- α is the death rate induced by the disease;
- $C(N) = N\beta(N)$ is the average contact rate by an infective;
- γ is a rate that infective individuals return to susceptible class;
- K is the carrying capacity of the environment;
- N is the total population at time t : $N(t) = S(t) + I(t)$.

The qualitative properties of the SIS model are summarized in the following theorem.

Theorem 3.3.1. *1. The SIS model* $(3.3.1) - (3.3.2)$ *is a dynamical system on*

$$\Omega = \{(S, I) \in \mathbb{R}^2_+ : \ 0 \leq S + I = N \leq K\}.$$

2. The basic reproduction number is $\mathcal{R}_0 = \frac{C(K)}{\alpha+\mu+\gamma}$.

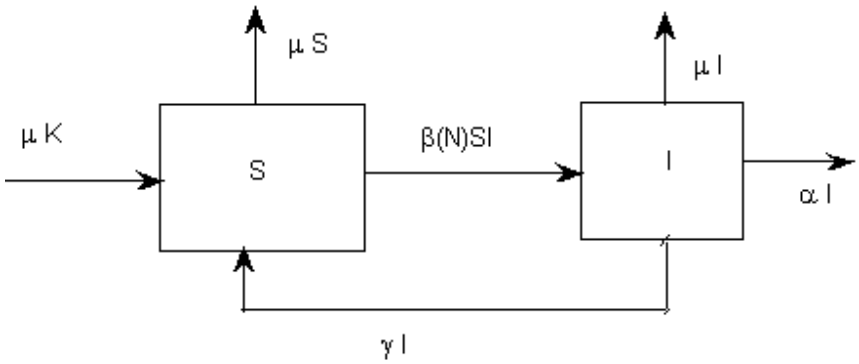


Figure 3.2: Flow chart for SIS model.

3. *If* $\mathcal{R}_0 < 1$, *the disease-free equilibrium* $E_0 = (K, 0)$ *is globally asymptotically stable.*

4. *If* $\mathcal{R}_0 > 1$, E_0 *is unstable and there exists a unique endemic equilibrium* $E_\infty = (S_\infty, I_\infty)$, *which is locally asymptotically stable.*

5. *The following conservation law holds:*

$$\mu K - (\alpha + \mu)N \leq N' \leq \mu(K - N). \tag{3.3.3}$$

Proof: This theorem is proved in a similar manner to the proofs of the corresponding theorems in Section 3.2.

Remark 3.3.2. *For SIS model* $(3.3.1) - (3.3.2)$, $\mathcal{R}_0 = 1$ *is a forward bifurcation point.*

Remark 3.3.3. *In addition to the reasoning in Section 3.2, the local asymptotic stability of the endemic equilibrium of the SIS model can be obtained by the following alternative procedure. Indeed, the relevant Jacobian matrix,*

$$J(E_\infty) = \begin{pmatrix} \beta(N_\infty)(N_\infty - 2I_\infty) - (\mu + \alpha + \gamma) & \big(\beta'(N_\infty)(N_\infty - I_\infty) + \beta(N_\infty)\big)I_\infty \\ -\alpha & -\mu \end{pmatrix},$$

reduces to

$$J(E_\infty) = \begin{pmatrix} -\beta(N_\infty)I_\infty & \big(\beta'(N_\infty)(N_\infty - I_\infty) + \beta(N_\infty)\big)I_\infty \\ -\alpha & -\mu \end{pmatrix},$$

because $\beta(N_\infty)(N_\infty - I_\infty) - (\mu + \alpha + \delta) = 0$, *by the defining relation of an equilibrium point. Clearly, the trace of* $J(E_\infty)$ *is negative. For the two eigenvalues to be negative, the determinant should be positive; we need to have*

$$\beta'(N_\infty)(N_\infty - I_\infty) + \beta(N_\infty) > 0,$$

which is true because

$$\begin{aligned} \beta'(N_\infty)(N_\infty - I_\infty) + \beta(N_\infty) &> \beta'(N_\infty)N_\infty + \beta(N_\infty) \\ &= (\beta(N)N)'|_{N=N_\infty} \\ &= C'(N_\infty) \\ &\geq 0. \end{aligned}$$

Therefore, the endemic equilibrium point is locally asymptotically stable.

Remark 3.3.4. *Analogous to Remark 3.2.7, when* $\mathcal{R}_0 > 1$ *and* $\alpha = 0$, *the endemic equilibrium is explicitly given by* $E_\infty = (K - \frac{(\mu+\gamma)}{\beta}, K)$.

3.3.2 NSFD Schemes

In this subsection, we design dynamically consistent NSFD schemes for the classical SIS model with general contact rate. The continuous and discrete conservation laws for the SIS model $(3.3.1) - (3.3.2)$ are exactly the same as the conservation laws $(3.2.11)$ as well as $(3.2.31)$ and $(3.2.33)$, though the variables have different meanings. Therefore, following the procedure that led to the NSFD scheme $(3.2.35) - (3.2.37)$ for the SIR model, we consider for the SIS model the scheme

$$\frac{S_{n+1} - S_n}{\phi} = \mu K - \frac{C(N_n)}{S_{n+1} + I_n} S_{n+1} I_n - \mu S_{n+1} + \gamma I_n \tag{3.3.4}$$

$$\frac{I_{n+1} - I_n}{\phi} = \frac{C(N_n)}{S_{n+1} + I_n} S_{n+1} I_n - (\alpha + \mu) I_{n+1} - \gamma I_n. \tag{3.3.5}$$

However, we have to approximate the linear term $(\alpha + \mu + \gamma)I$ in a nonlocal way in order to obtain the essential equation

$$\frac{N_{n+1} - N_n}{\phi} = \mu(K - N_{n+1}) - \alpha I_{n+1}, \tag{3.3.6}$$

that leads to the conservation law

$$\mu K - (\alpha + \mu)N_{n+1} \leq \frac{N_{n+1} - N_n}{\phi} \leq \mu(K - N_{n+1}). \tag{3.3.7}$$

It should also be noted that the denominator function $\phi = \phi(h)$ is chosen in accordance with $(3.2.35)$.

Of course for computation reasons, we use the following Gauss-Seidel equivalent formulation of $(3.3.4) - (3.3.6)$, which is the analogue of $(3.2.43) - (3.2.46)$:

$$S_{n+1} = \frac{-B + \sqrt{B^2 - 4AD}}{2A}, \tag{3.3.8}$$

$$I_{n+1} = \frac{\left(\frac{C(N_n)}{S_{n+1}+I_n}\phi S_{n+1} + (1 - \gamma\phi)\right) I_n}{1 + (\alpha + \mu)\phi}, \tag{3.3.9}$$

$$N_{n+1} = \frac{N_n + (\mu K - \alpha I_{n+1})\phi}{1 + \mu\phi}, \tag{3.3.10}$$

where,

$$A = 1 + \mu\phi, \tag{3.3.11}$$

$$B = [1 + (C(N_n) + \mu - \gamma)\,\phi]\, I_n - (S_n + \mu\phi K), \tag{3.3.12}$$

$$\text{and} \qquad D = -(S_n + \mu\phi K + \gamma\phi I_n)I_n. \tag{3.3.13}$$

The power of the NSFD scheme $(3.3.4) - (3.3.5)$ is stated in the next theorem, the proof of which can be reproduced from the SIR model word–for–word (see Corollary 3.2.18, Theorem 3.2.22, and Theorem 3.2.24):

Theorem 3.3.5. *1. The NSFD scheme is a dynamical system on*

$$\Omega = \{(S, I) \in \mathbb{R}^2_+ : 0 \leq S + I = N \leq K\}.$$

2. The discrete dynamical system defined by the NSFD scheme $(2.5.4) - (2.5.5)$ has a forward bifurcation at the point $\mathcal{R}_0 = 1$. That is

- *If $\mathcal{R}_0 < 1$, the disease free fixed point $E_0 = (K, 0)$ is globally asymptotically stable.*
- *If $\mathcal{R}_0 > 1$, E_0 is an unstable fixed point and $E_\infty = (S_\infty, I_\infty)$ is the unique endemic fixed point and it is locally asymptotically stable.*

3. For $\mathcal{R}_0 > 1$, the NSFD scheme $(3.3.4) - (3.3.5)$ is elementary stable.

3.4 Frequently Used Contact Rates

3.4.1 Generalities

The extended formulation of the contact rate $C(N)$ considered in the previous sections is motivated by the most frequently used contact rates on which we discuss below. This also gives us the opportunity to comment further on the general conditions $(3.2.1)$, $(3.2.3)$ and $(3.2.4)$.

The first formulation goes back to the beginning of the 20^{th} century and is due to Hamer and R. Ross. It is known as the "mass action principle or incidence "and it reads as follows:

Mass action principle: *The rate of spread of infection is proportional to the product of the susceptible population S and the infectious population I, the constant of proportionality being $\lambda > 0$:*

$$C(N) = \lambda N \quad , \; i.e. \;\; \beta(N) = \lambda. \tag{3.4.1}$$

(The letters $\lambda,\ b,\ etc.$ represent here and below various positive constants.)

Following the comments in $[28]$, it might seem plausible that the population density, and hence the contact rate, would increase with the population size. But the daily contact patterns of people are often similar in large and small communities, cities and regions. For human diseases and also for animal diseases such as mice in a mouse–room or animals in a herd, the contact rate seems to be weakly dependent on the population size. As reported by several studies $[28]$, the simple mass action principle is not appropriate since it translates the above–mentioned naive perception of having the contact rate increasing indefinitely with the population size.

To address the shortcoming of the mass action principle, the standard incidence formulation was introduced $[47]$ on the basis of the following more realistic assumptions:

Standard incidence: *The contact rate grows less rapidly as the population size increases. More precisely, we take*

$$C(N) = \lambda \;\; i.e \;\; \beta(N) = \frac{\lambda}{N}. \tag{3.4.2}$$

The interaction between the infectious and the susceptible populations is naturally a complex and highly nonlinear process. Several researchers have chosen standard incidence based

formulations which involve much stronger nonlinearities than λSI. We quote here three of these formulations:

- The **Michaelis–Menten type of interaction** corresponds to the contact rate

$$C(N) = \frac{\lambda N}{1 + bN}, \qquad b > 0. \tag{3.4.3}$$

  The formula in Equation $(3.4.3)$, which arises in pharmacology to model the basic enzyme reaction $[51]$, was used for the first time in epidemiology by Dietz $[20]$.

- For **population that mixes randomly**, Heesterbeek et al. $[27]$ suggested the contact rate

$$C(N) = \frac{\lambda N}{1 + bN + \sqrt{1 + 2bN}}, \qquad b > 0. \tag{3.4.4}$$

- **Rational power incidence** is our final example for the transmission of disease in cities of moderate size where the contact rate was tested to be a rational power of the population $[8]$:

$$C(N) = \lambda N^a, \tag{3.4.5}$$

  for a very small number $0 < a < 1$.

It should be noted that all these commonly used contact rates meet the general requirements in $(3.2.1)$. As mentioned earlier, the mass action incidence follows neither the less rapidly grow property $(3.2.3)$ nor the saturation property $(3.2.4)$. On the contrary, both properties are satisfied by the standard, the Michaelis–Menten and the saturated contact incidences. Finally the rational power incidence fails to have saturation property though the contact rate grows less rapidly as the population size increases.

For convenience, the different contact rates $C(N)$ are summarized in Table 3.1 along with the corresponding incidence rates and basic reproduction number, $\mathcal{R}_0$.

Remark 3.4.1. *The use of different contact rates naturally raises the question of comparing the models and identifying the best ones. The question can be answered by testing the models on real data and experiment, an aspect that is beyond the scope of this dissertation. Our interest in this dissertation is to provide the qualitative behavior of the contact rate*

Type of contact rate	$C(N)$	$\beta(N)SI$	$\mathcal{R}_0$
Mass action incidence	λN	λSI	$\frac{\lambda K}{\alpha+\mu+\gamma}$
Rational power incidence	λN^a	$\lambda N^{a-1}SI$	$\frac{\lambda K^a}{\alpha+\mu+\gamma}$
Standard incidence	λ	$\frac{\lambda SI}{N}$	$\frac{\lambda}{\alpha+\mu+\gamma}$
Michaelis–Menten reaction	$\frac{\lambda N}{1+bN}$	$\frac{\lambda SI}{1+bN}$	$\frac{\lambda K}{(1+bK)(\alpha+\mu+\gamma)}$
Saturated contact incidence	$\frac{\lambda N}{1+bN+\sqrt{1+2bN}}$	$\frac{\lambda SI}{1+bN+\sqrt{1+2bN}}$	$\frac{\lambda K}{(1+bK+\sqrt{1+2bK})(\alpha+\mu+\gamma)}$

Table 3.1: Some types of contact rates.

$C(N)$ with respect to its growth in comparison to the increase of N. In particular, consider two models with contact rates $C_1(N)$ and $C_2(N)$ satisfying $(3.2.1)$ and $(3.2.3)$. If it can be shown that

$$\lim_{N\to\infty}\frac{\beta_1(N)}{\beta_2(N)}=0,$$

then the model with $C_1(N)$ has its contact rate growing much less rapidly than N compared to the other model which has also $C_2(N)$ growing less rapidly than N. An illustration of this situation is given by the standard incidence and rational power incidence, respectively.

Remark 3.4.2. *In some cases, it is necessary to express the contact rates as a function of the susceptible population S and/or the infective population I. For instance, if the number of infective individuals is very high in the population, then the exposure to the disease agent is virtually certain $[39]$. Examples of contact rates of this type include the following:*

- *Michaelis – Menten type incidence rates $[15,\ 47]$:*

$$C(S)=\frac{\lambda}{S+c}\quad or\quad C(I)=\frac{\lambda}{I+c}.$$

- *Ratio–dependent type incidence rate $[21]$:*

$$C(S,I)=\frac{\lambda}{bS+I}.$$

- *Beddington–DeAngelis type incidence rate $[13]$:*

$$C(S,I)=\frac{\lambda}{aS+bI+c},\quad where\ \ a,\ b,\ c>0.$$

- *Nonlinear incidence rates of the form* [37]*:*

$$C(S,I) = \lambda I^{p-1} S^{q-1},$$

where $p \geq 1,\ q \geq 1$.

3.4.2 Illustrations for the SIR Model

This section is meant to illustrate theoretically, graphically and numerically the results we obtained for the SIR model. We deal mainly with the SIR model with standard incidence i.e. with contact rate given in $(3.4.2)$:

$$S' = \mu K - \frac{\lambda IS}{N} - \mu S \tag{3.4.6}$$

$$I' = \frac{\lambda IS}{N} - (\alpha + \mu + \gamma)I \tag{3.4.7}$$

$$R' = \gamma I - \mu R. \tag{3.4.8}$$

By adding $(3.4.6) - (3.4.8)$, we obtain the Equation $(3.2.9)$. It should be noted that the system of equations $(3.4.6) - (3.4.8)$ is equivalent to the system of equations $(3.4.6)$, $(3.4.7)$ and $(3.2.9)$.

Remark 3.4.3. *It is a common practice to present epidemiological models in terms of fractions of the populations in the different compartments. In the current case, introducing the fractions*

$$s = \frac{S}{N}, \quad i = \frac{I}{N} \quad \text{and} \quad r = \frac{R}{N}, \tag{3.4.9}$$

the model $(3.4.6) - (3.4.8)$ *is equivalent to the system*

$$s' = \frac{\mu K}{N} - \frac{\mu K}{N} s - (\lambda - \alpha) si \tag{3.4.10}$$

$$i' = \lambda si - (\alpha + \gamma + \frac{\mu K}{N}) i + \alpha i^2 \tag{3.4.11}$$

$$r' = \gamma i - \frac{\mu K}{N} r + \alpha ir, \tag{3.4.12}$$

where $s + i + r = 1$.

Indeed from $(3.4.9)$*, we have*

$$S' = s'N + sN',$$

which in view of $(3.4.6)$ *and* $(3.2.9)$*, yields*

$$\mu K - \frac{\lambda SI}{N} - \mu S = s'N + s(\mu(K - N) - \alpha I).$$

Dividing the two sides by N*, we obtain Equation* $(3.4.10)$*. The other equations* $(3.4.11)$ *and* $(3.4.12)$ *are obtained in a similar manner.*

The presence, in the model $(3.4.10) - (3.4.12)$*, of the unknown function* $N(t)$ *could be a source of difficulty for the actual use of this formulation. To overcome this difficulty, the model* $(3.4.10) - (3.4.12)$ *is coupled with the conservation law* $(3.2.11)$ *which, as shown after this equation, yields*

$$\underline{N}(t) \leq N(t) \leq \overline{N}(t),$$

where the lower and upper solutions are given by

$$\overline{N}(t) = K + (N_0 - K)e^{-\mu t}$$

and

$$\underline{N}(t) = \frac{\mu K}{\alpha + \mu} + \left(N_0 - \frac{\mu K}{\alpha + \mu}\right) e^{-(\alpha+\mu)t},$$

respectively. An exception to the above mentioned difficulty occurs when K *is replaced by the total population* $N(t)$*. In this case, the population* $N(t)$ *is a decreasing function, as a result of* $(3.2.9)$*. Furthermore, the model* $(3.4.10) - (3.4.12)$ *reduces to the following equations which can be fully studied without any problem:*

$$s' = \mu - \mu s - (\lambda - \alpha)si \tag{3.4.13}$$

$$i' = \lambda si - (\alpha + \mu + \gamma)i + \alpha i^2 \tag{3.4.14}$$

$$r' = \gamma i - \mu r + \alpha ir. \tag{3.4.15}$$

Since the contact rate in the Equations $(3.4.6) - (3.4.8)$ satisfies the condition given in Equation $(3.2.1)$, the results obtained in Section 3.2 hold and can be summarized as follows:

Theorem 3.4.4. *The SIR model* $(3.4.6) - (3.4.8)$ *is a dynamical system on the biologically feasible region*

$$\Omega = \{(S, I, R) \in \mathbb{R}^3_+ : \ 0 \leq S + I + R = N \leq K\}.$$

The basic reproduction number and the disease–free equilibrium point are

$$\mathcal{R}_0 = \frac{\lambda}{\alpha + \mu + \gamma} \qquad \textit{and} \quad E_0 \equiv (S^*, I^*, R^*) = (K, 0, 0),$$

respectively.

The value 1 of the parameter $\mathcal{R}_0$ is a forward bifurcation point. More precisely, E_0 is the unique equilibrium point whenever $\mathcal{R}_0 < 1$ and this equilibrium point is globally asymptotically stable. When $\mathcal{R}_0 > 1$, a unique locally asymptotically stable endemic equilibrium point E_∞ is obtained:

$$E_\infty \equiv (S_\infty, I_\infty, R_\infty) = \left(\frac{(\mu+\gamma)K}{\lambda - \alpha}, \frac{\mu K(\mathcal{R}_0 - 1)}{\lambda - \alpha}, \frac{\gamma K(\mathcal{R}_0 - 1)}{\lambda - \alpha} \right).$$

Theorem 3.4.4 is illustrated in Figures 3.3–3.6 where the bifurcation diagrams are given. In all these examples, we take $K = 1000$, $\mu = \gamma = 0.2$, and $\alpha = 0.1$ so that λ is the parameter that make $\mathcal{R}_0$ varies. The bifurcation diagrams corresponding to the mass action

(a) standard incidence (b) mass action

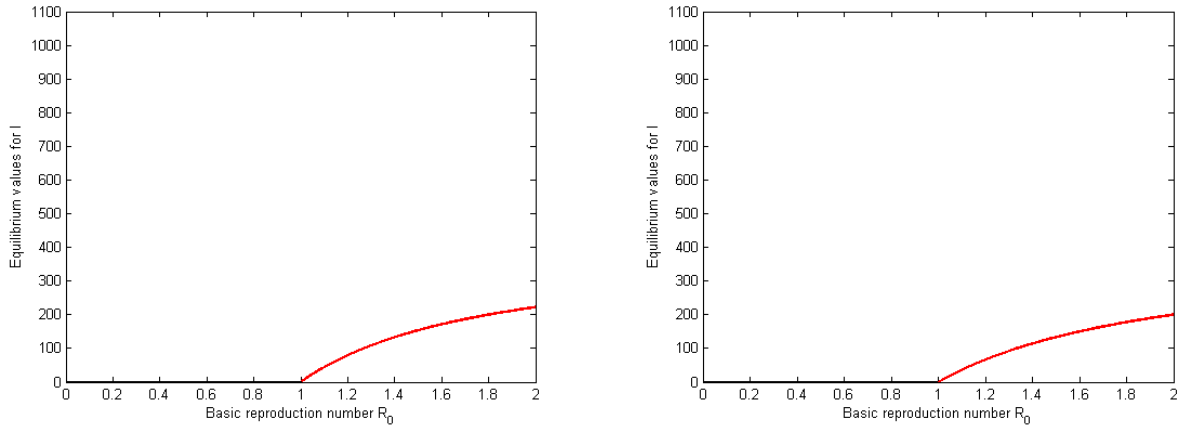


Figure 3.3: Bifurcation diagrams: I versus $\mathcal{R}_0$.

incidence are also given (Theorem 3.2.10). The similarity of these bifurcation diagrams reinforces what we said in Remark 3.4.1: no conclusion can be made on the quality of the model on the basis of the form of the contact rates unless the models are tested with real data.

For our second series of illustrations, we propose a new example of contact rate:

$$C(N) = \frac{\lambda e^N}{1 + e^N}, \quad i.\,e. \quad \beta(N) = \frac{\lambda e^N}{N(1 + e^N)}, \tag{3.4.16}$$

(a) standard incidence (b) mass action

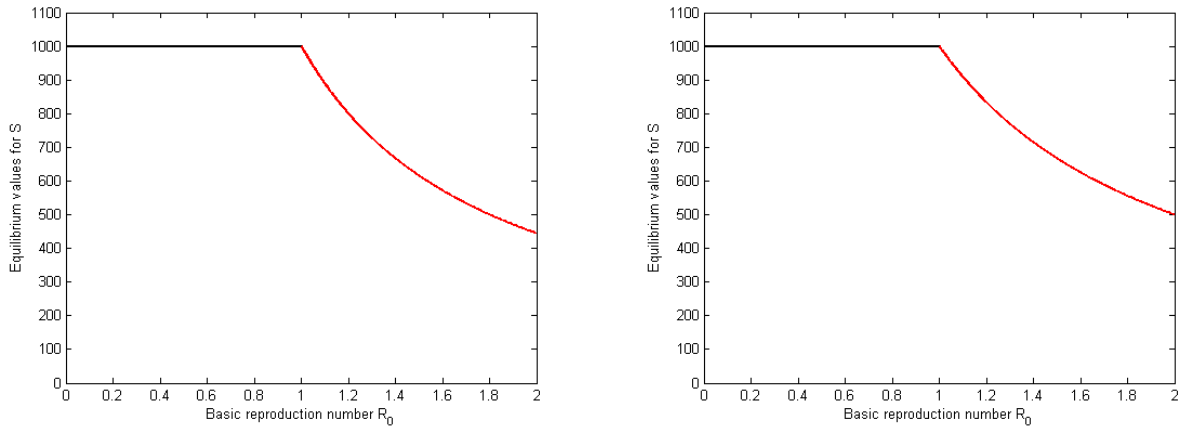


Figure 3.4: Bifurcation diagrams: S versus $\mathcal{R}_0$.

Here, λ is a positive constant. Despite its similarity with the Michaelis–Menten incidence rate, the interest in this example is, as we will see, that the endemic equilibrium E_∞ can not be found explicitly. Our starting point is to establish the following result:

Proposition 3.4.5. *The functions* $C(N)$ *and* $\beta(N)$ *in* $(3.4.16)$ *satisfy the conditions stated in* $(3.2.1)$ *and* $(3.2.4)$.

Proof: The bounded function $C(N) = \frac{\lambda e^N}{1+e^N}$ is clearly increasing since

$$C'(N) = \frac{\lambda\left(e^N(1+e^N) - e^{2N}\right)}{(1+e^N)^2} = \frac{\lambda e^N}{(1+e^N)^2} > 0.$$

On the other hand, for $\beta(N) = \frac{\lambda e^N}{N(1+e^N)}$, we have

$$\begin{aligned}
\beta'(N) &= \frac{\lambda\left(e^N(N(1+e^N)) - e^N(1+e^N+Ne^N)\right)}{(N(1+e^N))^2} \\
&= \frac{\lambda\left(e^N(N+Ne^N) - e^N(1+e^N+Ne^N)\right)}{(N(1+e^N))^2} \\
&= \frac{\lambda e^N\left(N-(1+e^N)\right)}{(N(1+e^N))^2} \\
&< 0.
\end{aligned}$$

This completes the proof. □.

The underlying SIR model for the contact rate $(3.4.16)$ is reproduced here for conve-

(a) standard incidence (b) mass action

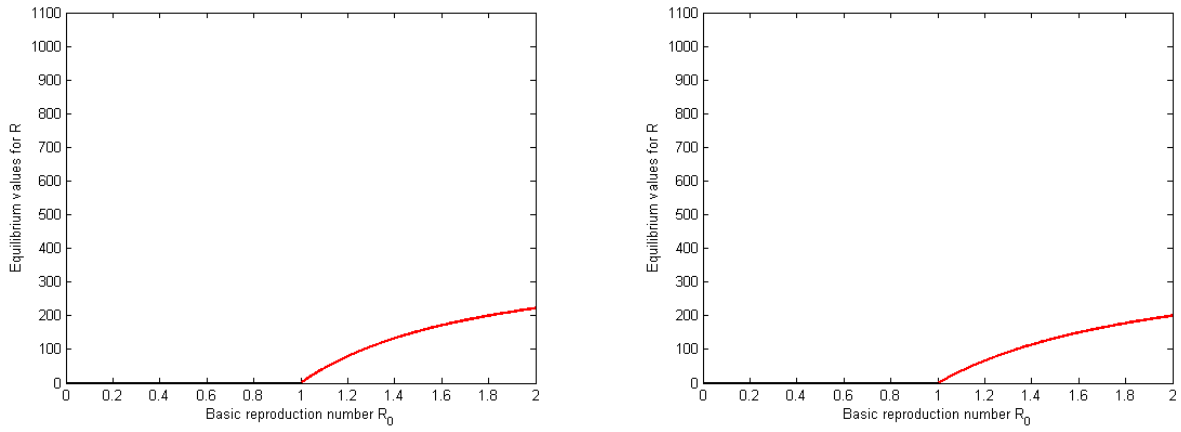


Figure 3.5: Bifurcation diagrams: R versus $\mathcal{R}_0$.

nience and reads as follows:

$$S' = \mu K - \frac{\lambda e^N SI}{N(1+e^N)} - \mu S \tag{3.4.17}$$

$$I' = \frac{\lambda e^N SI}{N(1+e^N)} - (\alpha+\mu+\gamma)I \tag{3.4.18}$$

$$R' = \gamma I - \mu R \tag{3.4.19}$$

$$N' = \mu(K-N) - \alpha I. \tag{3.4.20}$$

In view of equation $(3.2.16)$, the basic reproduction number is

$$\mathcal{R}_0 = \frac{\lambda e^K}{(1+e^K)(\alpha+\mu+\gamma)}.$$

The disease–free equilibrium is

$$E_0 \equiv (S^*, I^*, N^*) = (K, 0, K).$$

However, the endemic equilibrium

$$E_\infty = (S_\infty, I_\infty, N_\infty),$$

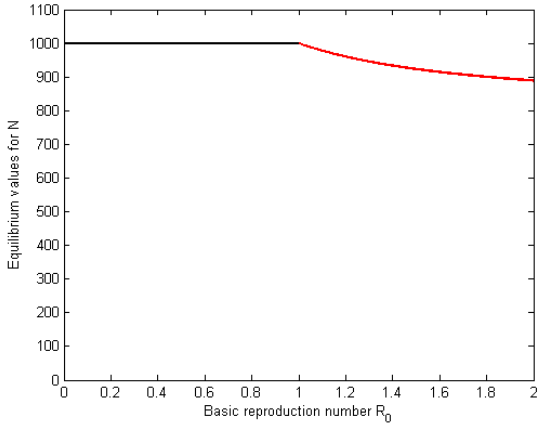
which is born when $\mathcal{R}_0 > 1$ cannot be found explicitly. It is rather given by $(cf\ (3.2.25))$

$$S_\infty = \frac{e^K N_\infty (1+e^{N_\infty})}{\mathcal{R}_0 e^{N_\infty}(1+e^K)}, \quad I_\infty = \frac{\mu}{\lambda}\left(\frac{K\mathcal{R}_0(1+e^K)}{e^K} - \frac{N_\infty(1+e^{N_\infty})}{e^{N_\infty}}\right), \tag{3.4.21}$$

where $N = N_\infty$ is the unique solution of the equation

$$f(N) := \frac{\lambda e^N}{1+e^N}(K-N) - \alpha\left(\frac{\lambda K e^N}{(\alpha+\mu+\gamma)(1+e^N)} - N\right) = 0, \tag{3.4.22}$$

(a) standard incidence



(b) mass action

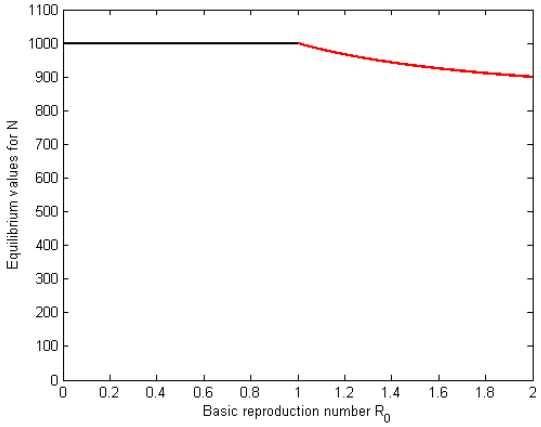


Figure 3.6: Bifurcation diagrams: N versus $\mathcal{R}_0$.

obtained from Equation $(3.2.24)$ in the interval $[0, K]$.

As a consequence of Proposition 3.4.5, the analogue of Theorem 3.4.4 holds for the model $(3.4.17) - (3.4.20)$. However, from $(3.4.22)$, it is clear that N_∞ cannot be found explicitly when $\mathcal{R}_0 > 1$.

In order to approximate N_∞, we use the bisection method presented in Remark 3.2.8 and applied it to Equation $(3.4.22)$ to generate a sequence $(N_\infty^n)_{n\geq 1}$ of approximations. This will then provide E_∞^n via $(3.4.21)$. The result is displayed on Fig 3.7 which gives the approximations

$$S_\infty = 17.1025, \quad I_\infty = 16.2137 \quad R_\infty = 38.3642, \quad \text{and} \quad N_\infty = 71.6804.$$

In this figure, we used the values $K = 1000, \quad \mu = 0.02, \quad \gamma = 0.2, \quad \alpha = 0.1.$

Our next aspect of interest in the process of illustrating the previous results for the SIR model is to consider the NSFD scheme $(3.2.36)-(3.2.38)$ for the SIR model $(3.4.6)-(3.4.8)$, with standard incidence. We have the NSFD scheme:

$$\frac{S_{n+1} - S_n}{\phi(h)} = \mu K - \frac{\lambda I_n S_{n+1}}{S_{n+1} + I_n + R_n} - \mu S_{n+1} \tag{3.4.23}$$

$$\frac{I_{n+1} - I_n}{\phi(h)} = \frac{\lambda I_n S_{n+1}}{S_{n+1} + I_n + R_n} - (\alpha + \mu + \gamma) I_{n+1} \tag{3.4.24}$$

$$\frac{R_{n+1} - R_n}{\phi(h)} = \gamma I_{n+1} - \mu R_{n+1} \tag{3.4.25}$$

$$\frac{N_{n+1} - N_n}{\phi(h)} = \mu(K - N_{n+1}) - \alpha I_{n+1}, \tag{3.4.26}$$

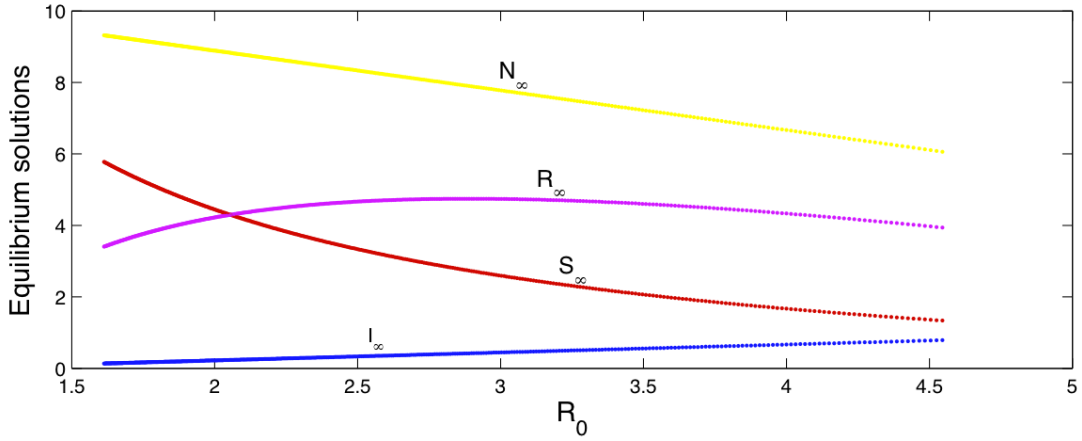


Figure 3.7: Approximation of the endemic equilibrium by the bisection method.

where $\phi(h) = \frac{e^{\mu h}-1}{\mu}$.

For computational purpose, Equations $(3.4.23) - (3.4.26)$ are rearranged into the form $(3.2.43)$ together with $(3.2.44) - (3.2.46)$ that reduces to:

$$I_{n+1} = \frac{[(1+\lambda\phi)S_{n+1} + I_n + R_n]I_n}{(S_{n+1} + I_n + R_n)[1 + (\alpha+\mu+\gamma)\phi]} \tag{3.4.27}$$

$$R_{n+1} = \frac{R_n + \gamma\phi I_{n+1}}{1+\mu\phi} \tag{3.4.28}$$

$$N_{n+1} = \frac{N_n + (\mu K - \alpha I_{n+1})\phi}{1+\mu\phi}. \tag{3.4.29}$$

The qualitative properties of the SIR model $(3.4.23) - (3.4.26)$ are summarized in the following theorem.

Theorem 3.4.6. *1. The NSFD scheme $(3.4.23) - (3.4.26)$ defines a discrete dynamical system on the biologically feasible domain*

$$\Omega = \{(S, I, R) \in \mathbb{R}^3_+ : \ 0 \leq S + I + R = N \leq K\}.$$

2. The disease–free and the endemic fixed points are $E_0 = (K, 0, 0)$ and $E_\infty = \left(\frac{(\mu+\gamma)K}{\lambda-\alpha}, \frac{\mu K(\mathcal{R}_0-1)}{\lambda-\alpha}, \frac{\gamma K(\mathcal{R}_0-1)}{\lambda-\alpha}\right)$ where the basic reproduction number is $\mathcal{R}_0$ is given in Theorem 3.4.4.

3. The disease–free fixed point E_0 is globally asymptotically stable for $\mathcal{R}_0 < 1$ and unstable for $\mathcal{R}_0 > 1$.

4. The NSFD scheme $(3.4.23) - (3.4.26)$ *is elementary stable.*

Theorem 3.4.6 is illustrated in Figures 3.8–3.10, where we take the values $K = 1000$, $\mu = \gamma = 0.2$, $\alpha = 0.1$, $\lambda = 1.3$, $h = 0.01$ so that $\mathcal{R}_0 = 2.6$.

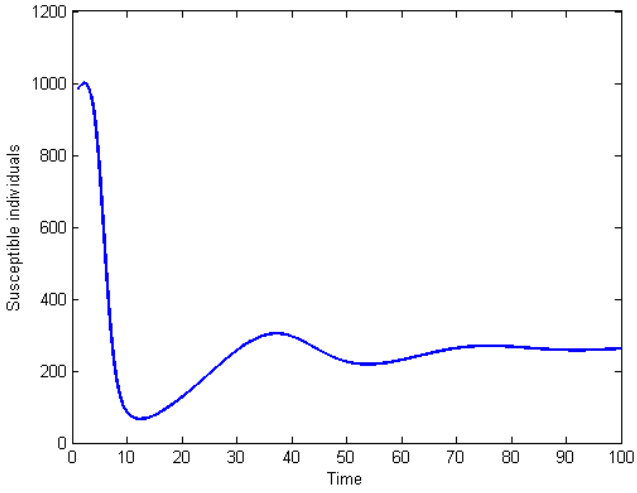


Figure 3.8: Susceptible individuals as a function of time with $S_0 = 990$.

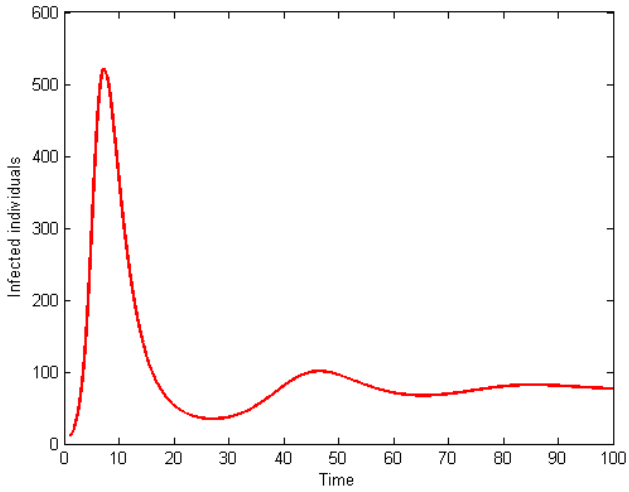


Figure 3.9: Infected individuals as a function of time with $I_0 = 10$.

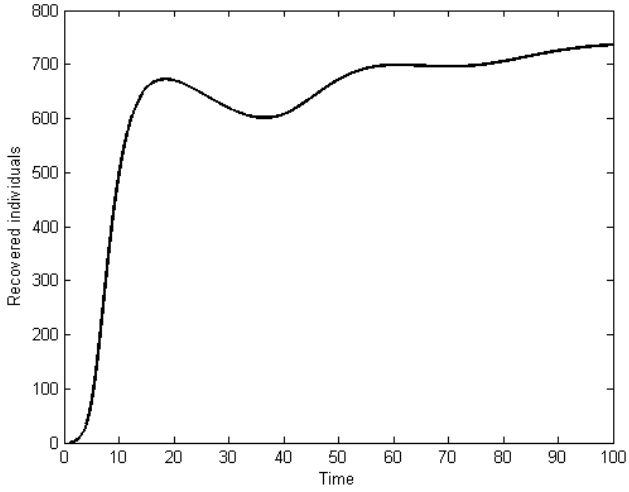


Figure 3.10: Recovered individuals as a function of time with $R_0 = 0$.

3.4.3 Illustrations for the SIS Model

The illustrations for the SIS model are based on the standard incidence formulation $(3.4.30)-(3.4.32)$ as well as the less classical model $(3.4.33)-(3.4.35)$ given below.

$$S' = \mu K - \frac{\lambda IS}{N} - \mu S + \gamma I \tag{3.4.30}$$

$$I' = \frac{\lambda IS}{N} - (\alpha + \mu + \gamma)I \tag{3.4.31}$$

$$N' = \mu(K - N) - \alpha I \tag{3.4.32}$$

$$S' = \mu K - \frac{\lambda e^N}{N(1+e^N)} SI - \mu S + \gamma I \tag{3.4.33}$$

$$I' = \frac{\lambda e^N}{N(1+e^N)} SI - (\alpha + \mu + \gamma)I \tag{3.4.34}$$

$$N' = \mu(K - N) - \alpha I. \tag{3.4.35}$$

Given the similarity of the results with what was presented for the SIR model in Subsection 3.4.2, we proceed directly with the illustrations of Theorem 3.3.1 and Theorem 3.3.5.

Observe that the NSFD scheme for $(3.4.30)-(3.4.32)$ is

$$\frac{S_{n+1} - S_n}{\phi} = \mu K - \frac{\lambda I_n S_{n+1}}{S_{n+1} + I_n} - \mu S_{n+1} + \gamma I_n \tag{3.4.36}$$

$$\frac{I_{n+1} - I_n}{\phi} = \frac{\lambda I_n S_{n+1}}{S_{n+1} + I_n} - (\alpha + \mu) I_{n+1} - \gamma I_n \tag{3.4.37}$$

$$\frac{N_{n+1} - N_n}{\phi} = \mu K - \mu N_{n+1} - \alpha I_{n+1}. \tag{3.4.38}$$

Fig 3.11 illustrates the approximation of the endemic equilibrium of the model $(3.4.33) - (3.4.35)$ by the bisection method, where $K = 1000, \quad \mu = 0.02, \quad \gamma = 0.2$. The picture gives the values $S_\infty = 5.1613, \quad I_\infty = 15.8065$ and $N_\infty = 20.9678$.

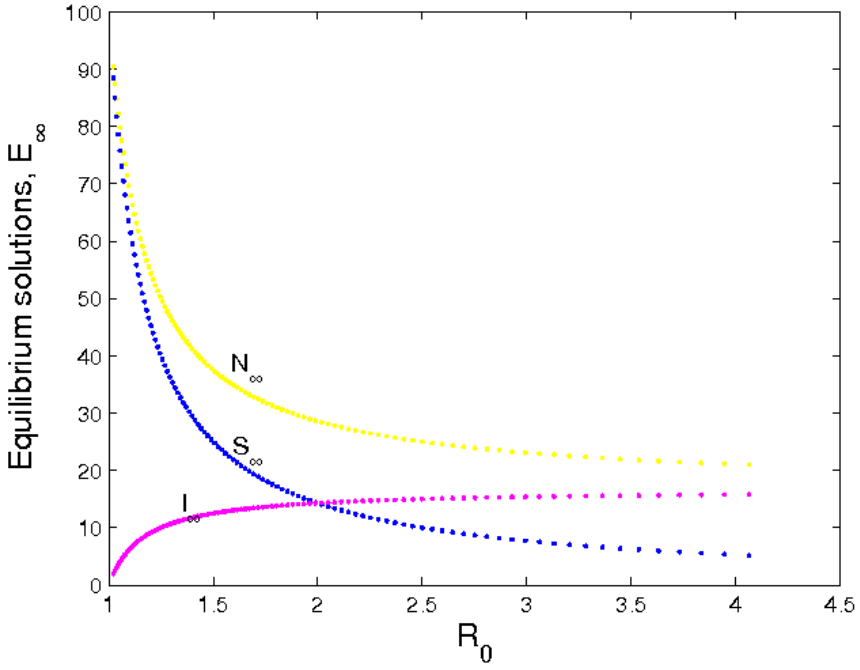


Figure 3.11: Endemic equilibrium by the bisection method for the SIS model.

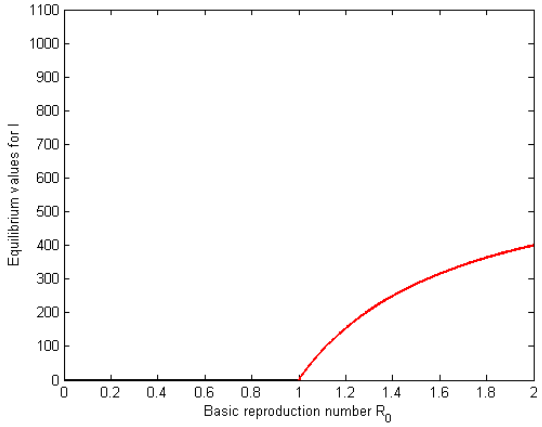
The fact that $\mathcal{R}_0 = 1$ is a forward bifurcation is depicted in Figures 3.12–3.14, where $K = 1000, \quad \mu = \gamma = 0.2$ and $\alpha = 0.1$.

The performance of the NSFD scheme $(3.4.36) - (3.4.38)$ is illustrated in Figures 3.15–3.16, where $K = 1000, \ \mu = \gamma = 0.2, \ \alpha = 0.1, \ \lambda = 1.3,$ and $h = 0.01$, which for $\mathcal{R}_0 > 1$ display the LAS of the endemic equilibrium. For $\mathcal{R}_0 < 1$, analogously the disease–free equilibrium is GAS.

3.4.4 Higher Order NSFD Schemes

In this subsection, we are interested in designing a higher order NSFD scheme for the SIS model. We assume that $N = K = constant$ and $\alpha = 0$ so that the SIS model

(a) standard incidence



(b) mass action

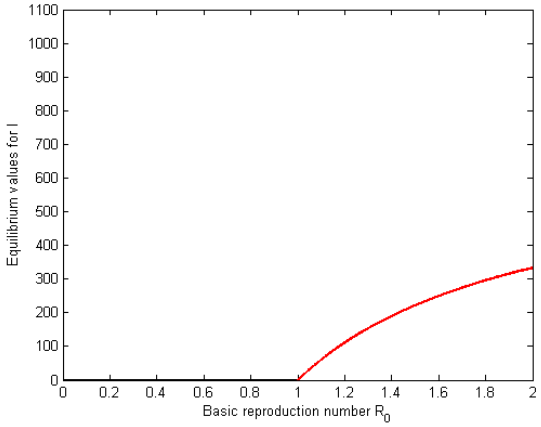


Figure 3.12: Bifurcation diagrams: I versus $\mathcal{R}_0$.

$(3.4.30) - (3.4.31)$ is reduced to the scalar equation

$$I' = (\lambda - \mu - \gamma)\left(1 - \frac{I}{N(1-\frac{1}{\mathcal{R}_0})}\right) I, \tag{3.4.39}$$

where $\mathcal{R}_0 = \frac{\lambda}{\mu+\gamma}$. From $(3.4.39)$, $I = 0$ and $I = N(1-\frac{1}{\mathcal{R}_0})$ are equilibrium points.

The higher order NSDF scheme we have in mind for $(3.4.39)$ is the 4^{th} Runge–Kutta method introduced in $(2.3.19)$. To this end and in accordance with Section 2.3.3, we define the function

$$\phi(h) = \frac{h}{1 + c[|\lambda - \mu - \gamma|h]^4}, \tag{3.4.40}$$

where $c > 0$ is any constant.

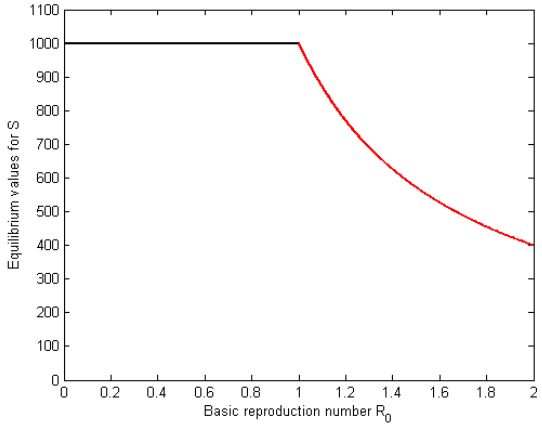
The nonstandard Runge-Kutta scheme is

$$\frac{I_{n+1} - I_n}{\phi(h)} = \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4), \tag{3.4.41}$$

where

$$\begin{aligned} f(I) &= (\lambda - \mu - \gamma)\left(1 - \frac{I}{N(1-\frac{1}{\mathcal{R}_0})}\right) I \\ k_1 &= f(I_n) \\ k_2 &= f\left(I_n + \frac{1}{2}\phi(h)k_1\right) \\ k_3 &= f\left(I_n + \frac{1}{2}\phi(h)k_2\right) \\ \text{and} \quad k_4 &= f\left(I_n + \phi(h)k_3\right). \end{aligned}$$

(a) standard incidence



(b) mass action

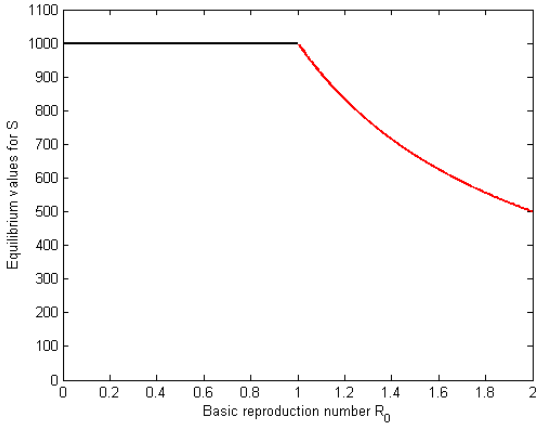
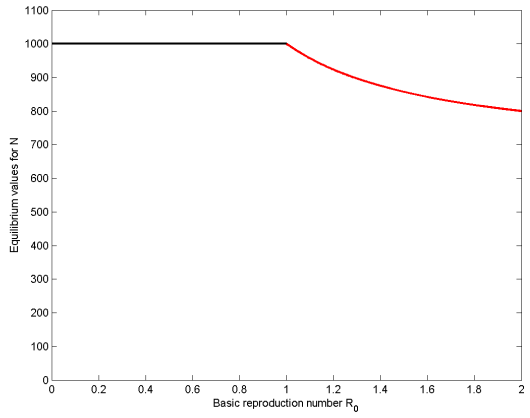


Figure 3.13: Bifurcation diagrams: S versus $\mathcal{R}_0$.

The method is illustrated in Table 3.2, which shows convergence of order 4. The excellence performance of the nonstandard Runge-Kutta method is also illustrated in Fig 3.17 and Fig 3.18, which show the GAS of the DFE ($\mathcal{R}_0 < 1$) as well as the LAS of the EE and the instability of DFE ($\mathcal{R}_0 > 1$). Note also that all discrete solutions are positive as should be, whereas the standard Runge–Kutta method could produce negative solutions.

(a) standard incidence



(b) mass action

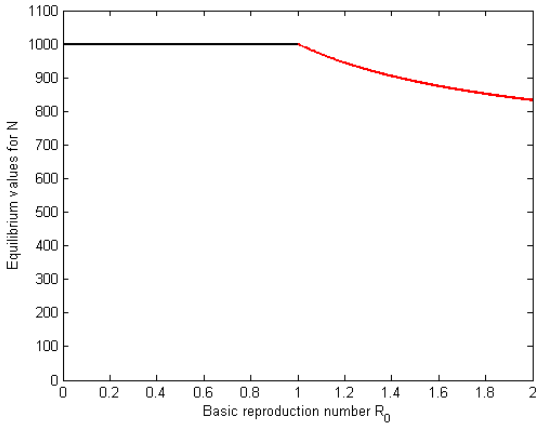


Figure 3.14: Bifurcation diagrams: N versus $\mathcal{R}_0$.

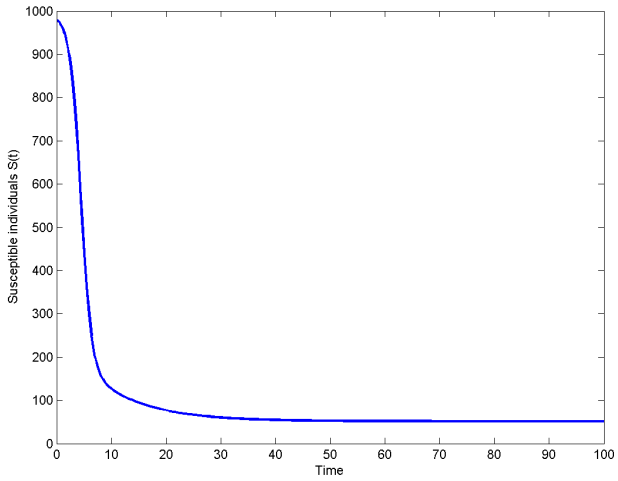


Figure 3.15: Susceptible individuals as a function of time with $S_0 = 990$ and $\mathcal{R}_0 = 2.6$.

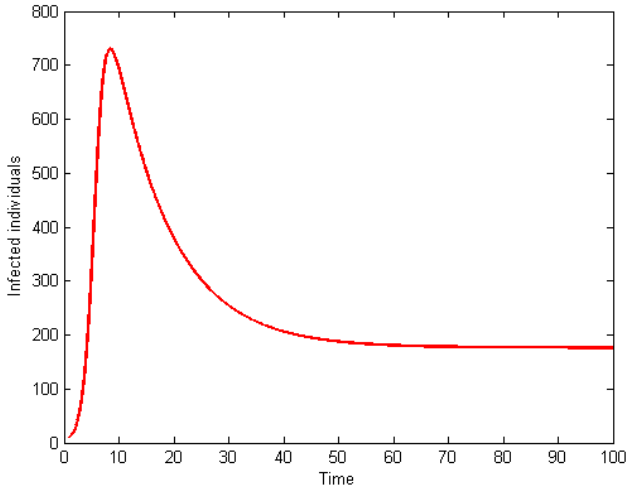


Figure 3.16: Infected individuals as a function of time with $I_0 = 10$ and $\mathcal{R}_0 = 2.6$.

t	NSFD RK4	exact solution	Error: $h = 0.5$ $\phi = 0.398$	Error: $h = 1$ $\phi = 0.1961$	Error: $h = 2$ $\phi = 0.030$
0.0	80.000000	80.000000	1.421085e-014	1.421085e-014	1.421085e-014
18.0	23.573736	23.572750	9.854203e-004	1.036865e-002	1.576336e-001
36.0	8.620017	8.619360	6.480276e-004	1.036865e-002	1.659326e-001
54.0	3.366977	3.366612	3.647248e-004	5.837070e-003	9.375971e-002
72.0	1.347421	1.347230	1.915396e-004	4.944246e-002	3.066153e-003
90.0	0.544358	0.544262	9.610898e-005	1.538893e-003	2.491507e-002
108	0.220757	0.220710	4.664874e-005	7.471302e-004	1.214611e-002
126	0.089662	0.089640	2.208081e-005	3.537403e-004	5.774793e-003
144	0.036440	0.036429	1.025124e-005	1.642706e-004	2.692999e-003
162	0.014813	0.014809	4.687258e-006	7.513052e-005	1.236873e-003
180	0.006022	0.006020	2.117170e-006	3.394436e-005	5.611959e-004
198	0.002449	0.002448	9.468135e-007	1.518416e-005	2.521040e-004

Table 3.2: NS Runge-Kutta method with $c = 100, \mathcal{R}_0 = 0.89$

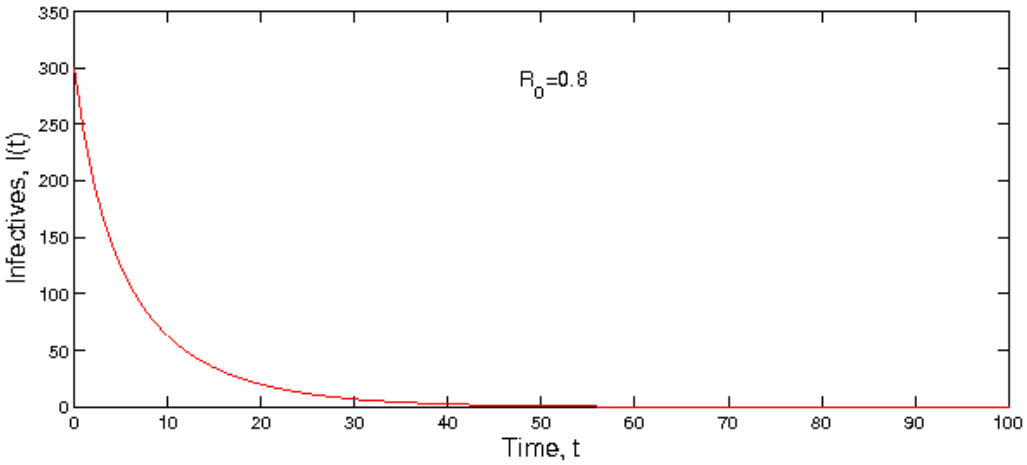


Figure 3.17: NS Runge-Kutta scheme for $I_0 = 100$ and $I_0 = 300$.

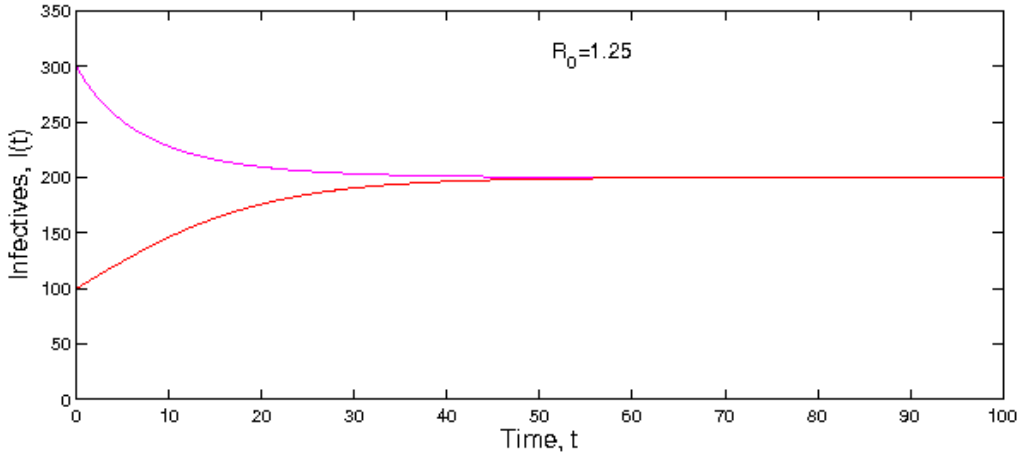


Figure 3.18: NS Runge-Kutta scheme for $I_0 = 300$.

Chapter 4

SIS Model for the Spatial Spread of an Epidemic

4.1 Introduction

In this chapter the classical SIS model studied in the previous chapter is extended to govern the spread of disease in space. This is done by including a diffusion term. This leads to a reaction–diffusion equation, the generalities and well–posedness of which are outlined in Section 4.2. This is followed by the study of the specific SIS diffusion model from the following point of view: well–posedness and continuous qualitative analysis (Section 4.3); discrete qualitative and computational analysis (Section 4.4). Our main references for the theoretical part are $[38, 52, 54]$

4.2 Generalities on Reaction–Diffusion Equations

In this section, we give some properties of one dimensional parabolic equations of the form

$$u_t - Du_{xx} = f(u). \tag{4.2.1}$$

Equation $(4.2.1)$ is referred to as a reaction–diffusion equation and the involved quantities have the following meaning:

- The number $D \geq 0$ is the diffusion–coefficient;

- The function $f : \mathbb{R} \to \mathbb{R}$ defines the reaction term;
- The unknown function $u : \mathbb{R} \times [0,\ \infty) \to \mathbb{R}$ represents the diffusion phenomenon.

Equation $(4.2.1)$ is appended with the initial condition

$$u(x, 0) \quad = \quad u_0(x), \tag{4.2.2}$$

where the function $u_0 : \mathbb{R} \to \mathbb{R}$ is given. Sometimes, Equation $(4.2.1)$ is considered on the sub–domain

$$[a,\ b] \times [0,\ \infty) \subset \mathbb{R} \times [0,\ \infty),\ -\infty < a < b < \infty,$$

in which case boundary conditions are prescribed at the end–points $x = a$ and $x = b$.

Equation $(4.2.1)$ is called linear in the case when

$$f(u) = \alpha u + \beta, \tag{4.2.3}$$

where α and/or β can be functions of the variables (x, t). Otherwise, it is nonlinear.

The particular case when $f(u) = 0$ is known as the heat or diffusion equation:

$$u_t - Du_{xx} = 0. \tag{4.2.4}$$

Theorem 4.2.1. *Assume that $u_0 : \mathbb{R} \to \mathbb{R}$ is continuous and bounded. Then the heat equation $(4.2.4)$ associated with the initial condition $(4.2.2)$ is well–posed. That is, there exists a unique solution $u : \mathbb{R} \times [0,\ \infty) \to \mathbb{R}$, which is continuous on $\mathbb{R} \times [0,\ \infty)$, C^1 in the time variable t and C^2 in the space variable x and satisfies the inequality $\sup_{x\in\mathbb{R}} |u(x, t)| \leq \sup_{x\in\mathbb{R}} |u_0(x)|$. More precisely, we have*

$$u(x, t) = \int_{-\infty}^{\infty} \frac{u_0(y)}{\sqrt{4\pi Dt}} e^{\frac{-(x-y)^2}{4Dt}} dy. \tag{4.2.5}$$

Proof: Theorem 4.2.1 is well–known. For convenience, we outline here how $(4.2.5)$ is obtained. We use the Fourier transform

$$\hat{v}(y) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} e^{-ixy} v(x) dx$$

of a function $v : \mathbb{R} \to \mathbb{R}$ as well as the inverse Fourier transform

$$v(x) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} e^{ixy} \hat{v}(y) dy, \tag{4.2.6}$$

assuming that v and $\hat{v}$ are such that these integrals make sense. Applying the Fourier transform, the initial value problem $(4.2.4)$, $(4.2.2)$ is transformed into

$$\begin{aligned} \frac{d\hat{u}}{dt} + Dy^2\hat{u} &= 0 && (4.2.7)\\ \hat{u}(y,0) &= \hat{u}_0(y) = \frac{1}{\sqrt{2\pi}}\int_{-\infty}^{\infty} e^{-ixy}u_0(x)dx. && (4.2.8) \end{aligned}$$

Here, we assume first that u_0 has a compact support so that the integral in $(4.2.8)$ is convergent. The solution of $(4.2.7) - (4.2.8)$ is

$$\hat{u}(y,t) = \hat{u}_0(y)e^{-Dy^2t}. \tag{4.2.9}$$

We have successively,

$$\begin{aligned} u(x,t) &= \frac{1}{\sqrt{2\pi}}\int_{-\infty}^{\infty} e^{ixy}\hat{u}(y,t)dy \quad \text{(by inverse Fourier transform (4.2.6))},\\ &= \frac{1}{\sqrt{2\pi}}\int_{-\infty}^{\infty} e^{ixy}\hat{u}_0(y)e^{-Dy^2t}dy \quad \text{(by (4.2.9))},\\ &= \frac{1}{\sqrt{2\pi}}\int_{-\infty}^{\infty} e^{ixy}\left(\frac{1}{\sqrt{2\pi}}\int_{-\infty}^{\infty} e^{-iyz}u_0(z)dz\right)e^{-Dy^2t}dy,\\ &= \frac{1}{2\pi}\int_{-\infty}^{\infty} u_0(z)\left(\int_{-\infty}^{\infty} e^{-iy(x-z)-Dy^2t}dy\right)dz. \end{aligned}$$

In view of Cauchy theorem, we have [22]

$$\int_{-\infty}^{\infty} e^{-iy(x-z)-Dy^2t}dy = \sqrt{\frac{\pi}{Dt}}e^{\frac{-(x-y)^2}{4Dt}}.$$

Therefore, $(4.2.5)$ gives the solution in this case.

When u_0 has no compact support, we approximate it in the sense of uniform convergence on compact sets by a sequence (u_0^j) of functions of compact support. The sequence (u_0^j) can be constructed by truncation. Thus, we take the limit as $j \to \infty$ in

$$u^j(x,t) = \int_{-\infty}^{\infty} \frac{u_0^j(y)}{\sqrt{4\pi Dt}}e^{\frac{-(x-y)^2}{4Dt}}dy,$$

and we get $(4.2.5)$.

From the representation $(4.2.5)$, we have

$$u(x,t) = \int_{-\infty}^{\infty} \frac{u_0(y)}{\sqrt{4\pi Dt}}e^{\frac{-(x-y)^2}{4Dt}}dy \leq \sup_{x\in\mathbb{R}}|u_0(x)| \qquad \forall t > 0,\ \forall\, x \in \mathbb{R}$$

because

$$\int_{-\infty}^{\infty} \frac{1}{\sqrt{4\pi Dt}}e^{\frac{-x^2}{4Dt}}dx = 1, \tag{4.2.10}$$

as a result of the following well–known fact:

$$\frac{1}{\sqrt{\pi}}\int_{-\infty}^{\infty} e^{-z^2}dz = 1.$$

This completes the proof of the theorem. □

Remark 4.2.2. *From the solution* $(4.2.5)$ *of the heat equation* $(4.2.4)$, $(4.2.2)$, *we introduce the function*

$$\mathcal{K}(x,t) = \begin{cases} \frac{1}{\sqrt{4\pi Dt}} e^{\frac{-x^2}{4Dt}}, & \text{if} \quad x \in \mathbb{R},\ t > 0, \\ 0, & \text{if}\ \ x \in \mathbb{R},\ t < 0, \end{cases}$$

which is known as the fundamental solution of heat equation $[22]$. *The kernel of convolution type defined by* $\mathcal{K}(x-y, t-s)$ *is called the Poisson kernel. It will be used shortly.*

Theorem 4.2.3. *Let* u_0 *be as in Theorem 4.2.1. Let* $g : \mathbb{R}\times[0,\ \infty) \to \mathbb{R}$ *be a continuous and bounded function in the* $x-$ *variable. Then the linear nonhomogeneous initial value problem*

$$u_t - Du_{xx} = g(x,t) \quad x \in \mathbb{R}, \quad t > 0 \tag{4.2.11}$$

$$u(x,0) = u_0(x) \tag{4.2.12}$$

admits a unique solution given by the formula

$$u(x,\ t) = \int_{-\infty}^{\infty} \mathcal{K}(x-y,t)u_0(y)dy + \int_0^t \int_{-\infty}^{\infty} \mathcal{K}(x-y,t-s)g(y,s)dyds. \tag{4.2.13}$$

Furthermore, for every time $T > 0$, *there exists* $C_T > 0$ *such that*

$$\sup_{x\in\mathbb{R}} |u(x,t)| \le \sup_{x\in\mathbb{R}} |u_0(x)| + C_T \sup_{x\in\mathbb{R}} |g(x,t)| \quad \text{for}\ \ 0 \le t \le T. \tag{4.2.14}$$

Proof: Observe that the integrals in $(4.2.13)$ are convergent in view of the properties of $u_0,\ g$ and $\mathcal{K}$. From Theorem 4.2.1, the first integral in $(4.2.13)$, i.e.

$$u_1(x,t) = \int_{-\infty}^{\infty} \mathcal{K}(x-y,t)u_0(y)dy,$$

is the unique solution of $(4.2.4)$ and $(4.2.2)$.

For a fixed time $t > 0$, denote by $\mathcal{X}_{[0,\ t]}$, the characteristic function of the interval $[0,\ t]$. By the properties of the fundamental solution $\mathcal{K}(x,t)$ of the heat equation, the function $u_2(x,t)$ defined by convolution as

$$\begin{aligned} u_2(x,t) &= \mathcal{K}(x-.,t-.) * \mathcal{X}_{[0,\ t]}g(.\ ,\ .), \\ &= \int_0^t \int_{-\infty}^{\infty} \mathcal{K}(x-y,t-s)g(y,s)dyds \end{aligned}$$

is the solution of the initial value problem:

$$u_t - Du_{xx} = g(x,\ t) \quad x \in \mathbb{R},\ \ t > 0 \tag{4.2.15}$$

$$u(x,0) = 0. \tag{4.2.16}$$

Using the principle of superposition, which applies due to the linearity of the problem, $u_1 + u_2$ is a solution of $(4.2.11) - (4.2.12)$. The representation $(4.2.13)$ proves the uniqueness of the solution as well as the relation $(4.2.14)$. $\square$.

In view of Theorem 4.2.3, it makes sense to expect the representation

$$u(x,\ t) = \int_{-\infty}^{\infty} \mathcal{K}(x-y,t)u_0(y)dy + \int_0^t \int_{-\infty}^{\infty} \mathcal{K}(x-y,t-s)f(u(y,s))dyds \tag{4.2.17}$$

for any solution of $(4.2.1) - (4.2.2)$. This is confirmed by the following result:

Lemma 4.2.4. *Assume that for each fixed $t > 0$, the function $f(v(x,t))$ is continuous and bounded whenever v is continuous and bounded. Then a function $u = u(x,t)$ is a solution of $(4.2.1) - (4.2.2)$ if and only if $u = u(x,t)$ is a solution of the integral equation $(4.2.17)$.*

Proof: If $u = u(x,t) \in C_b(\mathbb{R})$ is a solution of $(4.2.1) - (4.2.2)$, we set $g(x,t) = f(u(x,t))$. Then by Theorem 4.2.3, $u = u(x,t)$ is a solution of $(4.2.17)$. Conversely, if $u = u(x,t) \in C_b(\mathbb{R})$ is a solution of $(4.2.17)$, then by differentiation under the sum, we have

$$\begin{aligned} u_t(x,t) - Du_{xx}(x,t) &= \int_{\infty}^{\infty} \left[\mathcal{K}_t(x-y,t) - D\mathcal{K}_{xx}(x-y,t)\right] u_0(y)dy \\ &+ \int_0^t \int_{-\infty}^{\infty} \left[\mathcal{K}_t(x-y,t-s) - D\mathcal{K}_{xx}(x-y,t-s)\right] f(u(y,s))dyds \\ &+ \int_{-\infty}^{\infty} \mathcal{K}(x-y,0)f(u(y,t))dy. \end{aligned}$$

But, the property of the fundamental solution $\mathcal{K}(x-y,t)$ yields for $x \neq y$:

$$\mathcal{K}_t(x-y,t) - D\mathcal{K}_{xx}(x-y,t) = 0.$$

Furthermore, by Theorem 4.2.1 applied to the function $u_0(x) := f(u(x,t))$ which for each fixed $t > 0$ is continuous and bounded, we have

$$\int_{-\infty}^{\infty} \mathcal{K}(x-y,0)f(u(y,t))dy = f(u(x,t)).$$

Finally, from the representation $(4.2.17)$, we have the initial condition $(4.2.2)$. $\square$.

Theorem 4.2.5. *Consider the initial value problem* $(4.2.1)-(4.2.2)$. *Assume that* $f(v(x))$ *is continuous and bounded if* v *is continuous and bounded. Assume also that* u_0 *is a continuous and bounded function. Assume further that* f *is a globally Lipschitz function on* $\mathbb{R}$ *and* $f(0)=0$. *Then there exists a unique solution*

$$u : \mathbb{R} \times [0,\ \infty) \to \mathbb{R},$$

of the reaction–diffusion equation $(4.2.1)-(4.2.2)$, *which is continuous on* $\mathbb{R} \times [0,\ \infty)$, C^2 *in the space variable* x *and* C^1 *in the time variable* t.

Proof: To prove this theorem, we use the Banach contraction principle (see [60]). Let $C_b(\mathbb{R})$ be the space of all bounded continuous real–valued functions equipped with the supremum norm. We introduce the space C_k consisting of continuous functions $v : [0,\ \infty) \to C_b(\mathbb{R})$ such that

$$\|v\|_{C_k} := \sup_{0\le t<\infty} \|e^{-kt}v(.,t)\|_{C_b(\mathbb{R})} = \sup_{0\le t<\infty} e^{-kt} \sup_{x\in\mathbb{R}} |v(x,t)| < \infty.$$

The expression $\|.\|_{c_k}$, where $k > 0$ will be fixed shortly, provides a Banach structure to $C_k([0,\infty); C_b(\mathbb{R}))$. We define an operator Φ on C_k by

$$(\Phi v)(x,\ t) = \int_{-\infty}^{\infty} \mathcal{K}(x-y,t)u_0(y)dy + \int_0^t \int_{-\infty}^{\infty} \mathcal{K}(x-y,t-s)f(v(y,s))dyds. \tag{4.2.18}$$

By Lemma 4.2.4, it is clear that solving $(4.2.1)-(4.2.2)$ is equivalent to finding fixed point of the operator Φ:

$$\Phi u = u.$$

Let $v \in C_k([0,\infty); C_b(\mathbb{R}))$. Since u_0 and f are continuous and bounded functions, the function $t \rightsquigarrow (\Phi v)(.,t)$ belongs to C_k. Thus, Φ operates from C_k into C_k.

For $v,\ w \in C_k$, we have

$$\begin{aligned}
|(\Phi v)(x,t) - (\Phi w)(x,t)| &\leq \int_0^t \int_{-\infty}^{\infty} \mathcal{K}(x-y,t-s)|f(v(y,s)) - f(w(y,s))|dyds, \\
&\leq \int_0^t \int_{-\infty}^{\infty} \mathcal{K}(x-y,t-s) \sup_{x\in\mathbb{R}} |f(v(x,s)) - f(w(x,s))|ds, \\
&\leq \int_0^t \sup_{x\in\mathbb{R}} |f(v(x,s)) - f(w(x,s))|ds \quad \text{(by (4.2.10))}, \\
&\leq L\int_0^t \sup_{x\in\mathbb{R}} |v(x,s) - w(x,s)|ds \quad (\ f \text{ is globally Lipschitz}), \\
&\leq L \sup_{x\in\mathbb{R},\ s\in[0,\infty)} e^{-ks}|v(x,s) - w(x,s)| \int_0^t e^{ks}ds, \\
&\leq \frac{L}{k} \sup_{x\in\mathbb{R},\ s\in[0,\infty)} e^{-ks}|v(x,s) - w(x,s)|e^{kt}.
\end{aligned}$$

If we take supremum of both sides for $x \in \mathbb{R}$ and $t \in [0,\ \infty)$, we get

$$\|\Phi v - \Phi w\|_{C_k} \leq \frac{L}{k}\|v - w\|_{C_k}.$$

For the choice $k > L$, the operator Φ is a contraction on C_k. Therefore, the Banach contraction principle guarantees the existence of a unique solution $u \in C_k$ such that $\Phi u = u$. □

In order to relax the global Lipschitz condition, which is strong in applications, we consider the next result.

Theorem 4.2.6. *Assume that f and u_0 are functions as in Theorem 4.2.5 with f being only locally Lipschitz. That is, for every $M > 0$, there exists $L \equiv L_M > 0$ such that*

$$|f(v) - f(w)| \leq L_M|v - w|, \quad \forall\ |v| \leq M \text{ and } |w| \leq M.$$

Then, there exists a time $T > 0$ such that the problem $(4.2.1) - (4.2.2)$ admits a unique solution on the interval $[0,\ T]$ that satisfies the relation

$$\sup_{x\in\mathbb{R},\ \ t\in[0,\ T]} |u(x,t)| \leq 2\sup_{x\in\mathbb{R}} |u_0(x)|.$$

Proof: Let $k > 0$ and $T > 0$ to be fixed shortly. Define C_k to be the set of continuous functions from $[0,\ T]$ into the set of functions $C_b(\mathbb{R})$. We equip C_k with the structure of a metric space through the distance

$$d_k(v,u) = \sup_{x\in\mathbb{R},\ t\in[0,T]} e^{-kt}|v(x,t) - u(x,t)|.$$

Define a subset G of $C_k([0,T];C_b(\mathbb{R}))$ by

$$G=\{v\in C_k([0,T];\ C_b(\mathbb{R})) : \sup_{x\in\mathbb{R}}|v(x,t)-\int_{-\infty}^{\infty}\mathcal{K}(x-y,t)u_0(y)dy|\leq \sup_{x\in\mathbb{R}}|u_0(x)|,\ t\in[0,T]\}.$$

The set G is nonempty, because $v=0\in G$. The set G is also a closed subset of C_k, because any convergent sequence in G, has its limit in G.

Furthermore, for any $v\in G$, we have

$$\sup_{x\in\mathbb{R}}|v(x,t)| \ \leq\ 2\sup_{x\in\mathbb{R}}|u_0(x)|=:M. \tag{4.2.19}$$

Indeed from the the triangle inequality and the relation

$$\sup_{x\in\mathbb{R}}|\int_{-\infty}^{\infty}\mathcal{K}(x-y,t)v(y,t)dy|\leq \sup_{x\in\mathbb{R}}|v(x,t)|, \tag{4.2.20}$$

we get

$$\begin{aligned}\sup_{x\in\mathbb{R}}|v(x,t)| &\leq \sup_{x\in\mathbb{R}}|v(x,t)-\int_{-\infty}^{\infty}\mathcal{K}(x-y,t)u_0(y)dy|+\sup_{x\in\mathbb{R}}|\int_{-\infty}^{\infty}\mathcal{K}(x-y,t)u_0(y)dy|\\ &\leq \sup_{x\in\mathbb{R}}|u_0(x)|+\sup_{x\in\mathbb{R}}|u_0(x)|.\end{aligned}$$

Moreover, taking supremum of both sides on $t\in[0,\ T]$, we obtain $(4.2.19)$. We define on G the operator Φ by the formula $(4.2.18)$. By using the assumption on u_0 and f, it is clear that Φu is continuous. We claim that for a suitable time $T>0$, Φ operates from G into G. More precisely, for $v\in G$ and $t\in[0,T]$, from $(4.2.18)$ we have

$$\begin{aligned}|(\Phi v)(x,t)-\int_{-\infty}^{\infty}\mathcal{K}(x-y,t)u_0(y)dy| &\leq \int_0^t\int_{-\infty}^{\infty}\mathcal{K}(x-y,t-s)|f(v(y,s))|dyds,\\ \sup_{x\in\mathbb{R}}|(\Phi v)(x,t)-\int_{-\infty}^{\infty}\mathcal{K}(x-y,t)u_0(y)dy| &\leq \sup_{x\in\mathbb{R}}\int_0^t\int_{-\infty}^{\infty}\mathcal{K}(x-y,t-s)|f(v(y,s))|dyds,\\ &\leq \int_0^t\sup_{x\in\mathbb{R}}|f(v(x,s))|ds,\ \text{(by (4.2.10) and (4.2.20))},\\ &\leq L_M\int_0^t\sup_{x\in\mathbb{R}}|v(x,s)|ds\ \text{(by the local Lipschitz}\\ &\qquad\text{property of } f \text{ applied to } v,\ 0 \text{ and } M=2\|u_0\|),\\ &\leq 2L_M\int_0^t\sup_{x\in\mathbb{R}}|u_0(x)|ds\ \text{(by using (4.2.19))},\\ &= 2L_Mt\sup_{x\in\mathbb{R}}|u_0(x)|,\\ &\leq 2L_MT\sup_{x\in\mathbb{R}}|u_0(x)|.\end{aligned}$$

Thus, putting $T=\frac{1}{2L_M}$, we have

$$\sup_{x\in\mathbb{R}}|(\Phi v)(x,t)-\int_{-\infty}^{\infty}\mathcal{K}(x-y,t)u_0(y)dy|\leq\sup_{x\in\mathbb{R}}|u_0(x)|,$$

which shows that Φ operates from G into G for this specific time T, which we use in what follows.

For $v,\ w \in G$ and $0 \leq t \leq T$, we have

$$\begin{aligned}
|(\Phi v)(x,t) - (\Phi w)(x,t)| &\leq \int_0^t \int_{-\infty}^{\infty} \mathcal{K}(x-y, t-s)|f(v(y,s)) - f(w(y,s))|dyds \\
&\leq \int_0^t \sup_{x\in\mathbb{R}} |f(v(x,s)) - f(w(x,s))|ds \quad \text{(by (4.2.10) and (4.2.20))}, \\
&\leq L_M \int_0^t \sup_{x\in\mathbb{R}} |v(x,s) - w(x,s)|ds \qquad (\text{ f is locally Lipschitz}), \\
&\leq L_M \sup_{x\in\mathbb{R},\ s\in[0,T]} e^{-ks}|v(x,s) - w(x,s)| \int_0^t e^{ks}ds, \\
&\leq \frac{L_M}{k} \sup_{x\in\mathbb{R},\ s\in[0,T]} e^{-ks}|v(x,s) - w(x,s)|e^t.
\end{aligned}$$

The supremum of both sides for $x \in \mathbb{R}$ and $t \in [0,\ T]$ gives

$$\sup_{x\in\mathbb{R},\ t\in[0,T]} e^{-kt}|(\Phi v)(x,t) - (\Phi w)(x,t)\| \leq \frac{L_M}{k} \sup_{x\in\mathbb{R},\ t\in[0,T]} e^{-kt}|v(x,t) - w(x,t)|,$$

or

$$d_k(\Phi v, \Phi w) \leq \frac{L_M}{k} d_k(v,w).$$

For $k > L_M$, Φ is a contraction on G. Hence, by the Banach contraction principle, there exists a unique fixed point $u \in G$, which is the unique solution to the initial value problem $(4.2.1) - (4.2.2)$ and satisfies $(4.2.19)$, by definition of G. Notice that the Lipschitz condition and Gronwall inequality guarantee that there are no solutions outside G. □

Theorem 4.2.6 is even more disappointing than Theorem 4.2.5, because the solution only exists locally. Fortunately, it is possible for this theorem to lead to the existence of a global solution whenever some a priori estimate is available. This is clarified in the next result.

Theorem 4.2.7. *Assume that the conditions of Theorem 4.2.6 hold. Furthermore, we assume that there exists a constant $M > 0$ such that for any finite time interval $[T_*, T]$ on which $(4.2.1)$ admits a solution $u(x,t)$ with initial condition prescribed at $t = T_*$, we have the a priori estimate*

$$\sup_{x\in\mathbb{R},\ t\in[T_*,T]} |u(x,t)| \leq M. \tag{4.2.21}$$

Then $(4.2.1)-(4.2.2)$ *possesses a unique global solution* $u : \mathbb{R}\times[0,\ \infty) \to \mathbb{R}$ *that satisfies* $(4.2.21)$.

Proof: We provide the details of the idea outlined in [38] and [54]. Given the estimate $(4.2.21)$, it makes sense that we take the initial condition such that $\sup_{x\in\mathbb{R}} |u_0(x)| \leq M$.

By assumption, the function f is Lipschitz on the interval $[-2M,\ 2M]$ with Lipschitz constant L_M. Therefore, by Theorem 4.2.6, there exists a finite time $T = \frac{1}{2L_M}$ such that $(4.2.1)-(4.2.2)$ admits a unique solution on the interval $[0, T]$, which satisfies $(4.2.21)$ for this time T.

For $m = 0,\ 1,\ 2,\ \ldots$, we define

$$T_m = mT.$$

Denote by $u_1(x, t)$ the solution of $(4.2.1)-(4.2.2)$ on $[0, T_1]$. Let us consider the equation $(4.2.1)$ for $t \in [T_1, T_2]$ and look for a solution $u_2(x, t)$ that satisfies the initial condition $(4.2.2)$ replaced by

$$u_2(x, T_1) = u_1(x, T_1) =: u_{1,1}(x). \tag{4.2.22}$$

By Lemma 4.2.4, solving $(4.2.1)$ and $(4.2.22)$ is equivalent to solving the integral equation

$$u_2(x,t) = \int_{-\infty}^{\infty} \mathcal{K}(x-y,t)u_{1,1}(y)dy + \int_{T_1}^{t}\int_{-\infty}^{\infty} \mathcal{K}(x-y,t-s)f(u_2(y,s))dyds. \tag{4.2.23}$$

To solve $(4.2.23)$, we introduce as previously, the following objects:

- By C_k, we denote the set of continuous functions from $[T_1, T_2]$ into $C_b(\mathbb{R})$ equipped with the structure of complete metric space via the distance d_k given by

$$d_k(v, w) = \sup_{x\in\mathbb{R},\ t\in[T_1,\ T_2]} e^{-kt}|v(x, t) - w(x, t)|,$$

  where k will be fixed shortly;

- By G_1, we denote the following closed subset of C_k:

$$G_1 = \{v \in C_k([T_1, T_2]; C_b(\mathbb{R})) :\ \sup_{x\in\mathbb{R}} |v(x, t) - \int_{-\infty}^{\infty} \mathcal{K}(x-y,t)u_{1,1}(y)dy| \leq M \quad \text{for} \quad T_1 \leq t \leq T_2\};$$

  Note that for $v \in G_1$, triangle inequality and the fact that $\sup_{x\in\mathbb{R}} |u_{1,1}(x)| \leq M$ yield $\|v\|_{C_b} \leq 2M$.

- The operator Φ on G_1 is defined by

$$(\Phi v)(x,t) = \int_{-\infty}^{\infty} \mathcal{K}(x-y,t)u_{1,1}(y)dy + \int_{T_1}^{t}\int_{-\infty}^{\infty} \mathcal{K}(x-y,t-s)f(v(y,s))dyds.$$

We claim that G_1 is invariant under Φ. Indeed, it is clear that for $v \in C_k$, $\Phi v \in C_k$. Next for $v \in G_1$, we have

$$\begin{aligned}
\sup_{x\in\mathbb{R}} |(\Phi v)(x,t) - \int_{-\infty}^{\infty} \mathcal{K}(x-y,t)u_{1,1}(y)dy| &\leq \sup_{x\in\mathbb{R}} \int_{T_1}^{t}\int_{-\infty}^{\infty} \mathcal{K}(x-y,t-s)|f(v(y,s))|dyds, \\
&\leq \int_{T_1}^{t} \sup_{x\in\mathbb{R}} |f(v(x,s))|ds \quad \text{(by (4.2.10) and (4.2.20))}, \\
&\leq L_M \int_{T_1}^{t} \sup_{x\in\mathbb{R}} |v(x,s)|ds, \quad (f \text{ is Lipschitz on} \\
&\qquad \text{[-2M, 2M] and } \|v\|_{C_b} \leq 2M), \\
&\leq L_M \int_{T_1}^{T_2} 2M ds, \\
&\leq L_M 2(T_2 - T_1)M, \\
&= M \qquad \text{by definition of } T_m.
\end{aligned}$$

Thus, Φ operates from G_1 into G_1.

On the other hand, if $v \in G_1$ and $w \in G_1$ then for $x \in \mathbb{R}$ and $t \in [T_1, T_2]$, we have

$$\begin{aligned}
|(\Phi v)(x,t) - (\Phi w)(x,t)| &\leq \int_{T_1}^{t}\int_{-\infty}^{\infty} \mathcal{K}(x-y,t-s)|f(v(y,s)) - f(w(y,s))|dyds, \\
&\leq \int_{T_1}^{t}\int_{-\infty}^{\infty} \mathcal{K}(x-y,t-s) \sup_{x\in\mathbb{R}} |f(v(x,s)) - f(w(x,s))|dyds, \\
&\leq \int_{T_1}^{t} \sup_{x\in\mathbb{R}} |f(v(x,s)) - f(w(x,s))|ds \quad \text{(by (4.2.10))}, \\
&\leq L_M \int_{T_1}^{t} \sup_{x\in\mathbb{R}} |v(x,s) - w(x,s)|ds \quad (f \text{ is Lipschitz on } [-2M,\ 2M]), \\
&\leq L_M \sup_{x\in\mathbb{R},\ s\in[T_1,\ T_2]} e^{-ks}|v(x,s) - w(x,s)| \int_{T_1}^{t} e^{ks}ds, \\
&\leq \frac{L_M}{k} \sup_{x\in\mathbb{R},\ s\in[T_1,\ T_2]} e^{-ks}|v(x,s) - w(x,s)|e^{kt}.
\end{aligned}$$

Thus,

$$e^{-kt}|(\Phi v)(x,t) - (\Phi w)(x,t)| \leq \frac{L_M}{k} \sup_{x\in\mathbb{R},\ s\in[T_1,\ T_2]} e^{-ks}|v(x,s) - w(x,s)|.$$

Taking the supremum in $x \in \mathbb{R}$ and $t \in [T_1, T_2]$ on both sides, we get

$$d_k(\Phi v, \Phi w) \leq \frac{L_M}{k} d_k(v,w).$$

For the choice $k > L_M$, Φ is a contraction and has therefore a unique fixed point u_2 in G_1.

Here again, there are no fixed–points of Φ outside G_1. Since by Lemma 4.2.4, $u_2 \in G_1$ is the unique solution of $(4.2.1)$ and $(4.2.22)$ on $[T_1, T_2]$, we infer from the assumption $(4.2.21)$ that

$$\sup_{x\in\mathbb{R},\, t\in[T_1,T_2]} |u_2(x,t)| \leq M.$$

Proceeding by induction, we obtain a sequence of functions $u_m \in C_k\left([T_{m-1}, T_m]; C_b(\mathbb{R})\right)$ such that each u_m is the unique solution of $(4.2.1)$ that satisfies the initial condition, defined recursively by

$$u_1(x,0) = u_0(x) \quad \text{and} \quad u_{m+1}(x,T_m) = u_m(x,T_m) =: u_{m,m}(x) \quad \text{for} \quad m = 1,\ 2,\ 3,\ \ldots,$$

as well as the inequalities

$$\sup_{x\in\mathbb{R},\, t\in[T_m,T_{m+1}]} |u_{m+1}(x,t) - \int_{-\infty}^{\infty} \mathcal{K}(x-y,y)u_{m,m}(y)|dy \leq M$$

and

$$\sup_{x\in\mathbb{R},\, t\in[T_m,\, T_{m+1}]} |u_{m+1}(x,t)| \leq M.$$

Since

$$\bigcup_{m\geq 0} [T_m,\ T_{m+1}] = [0,\ \infty),$$

the function

$$u := \bigcup_{m\geq 0} u_m : \mathbb{R}\times[0,\ \infty) \to [-M,\ M]$$

is the unique solution of $(4.2.1) - (4.2.2)$. □

Finding solutions of Equation $(4.2.1)$ is in general not possible. For this reason, we will consider its simplest solutions and compare them with any other solutions when the time evolves. The concept of these simple solution is clarified in the next definition.

Definition 4.2.8. $[54]$ *A function* $\bar{u} : \mathbb{R} \to \mathbb{R}$ *such that*

$$f(\bar{u}) + D\bar{u}_{xx} \quad = \quad 0, \quad x \in \mathbb{R} \tag{4.2.24}$$

is called an equilibrium solution of the reaction–diffusion equation $(4.2.1)$.

Remark 4.2.9. *For any* $\bar{u} : \mathbb{R} \to \mathbb{R}$ *satisfying* $(4.2.24)$*, the time independent function* $u : \mathbb{R} \times [0, \infty)$ *defined by* $u(x,t) = \bar{u}(x)$ *is necessarily a solution of the reaction–diffusion equation* $(4.2.1)$*. This motivates the terminology in Definition 4.2.8.*

The specific manner in which equilibrium solutions of $(4.2.1)$ are compared to its other solutions reads as follows:

Definition 4.2.10. $[54]$ *An equilibrium solution* $\bar{u}$ *of* $(4.2.1)$ *is said to be stable if for every* $\epsilon > 0$*, there exists* $\delta > 0$ *such that for any initial condition* $u_0 : \mathbb{R} \to \mathbb{R}$ *satisfying* $\sup_{x\in\mathbb{R}} |u_0(x) - \bar{u}(x)| < \delta$*, we have* $\sup_{x\in\mathbb{R}} |u(x,t) - \bar{u}(x)| < \epsilon$ *for all* $t > 0$*. In addition, if* $\lim_{t\to\infty} \sup_{x\in\mathbb{R}} |u(x,t) - \bar{u}(x)| = 0$ *for* $\sup_{x\in\mathbb{R}} |u_0(x) - \bar{u}(x)|$ *sufficiently small, then* $\bar{u}$ *is called locally asymptotically stable. If* $\bar{u}$ *is not stable, it is said to be unstable.*

In practice, the stability is established by the linearization process described below.

Let $\bar{u}$ be an equilibrium solution of $(4.2.1)$. By Taylor expansion about $\bar{u}$ and by $(4.2.24)$, we have

$$\begin{aligned} f(u) &\approx f(\bar{u}) + f'(\bar{u})(u - \bar{u}), \\ &= -D\bar{u}_{xx} + f'(\bar{u})(u - \bar{u}). \end{aligned}$$

Therefore, the nonlinear reaction–diffusion Equation $(4.2.1)$ can be replaced by the linear equation

$$\Psi_t = D\Psi_{xx} + f'(\bar{u})\Psi, \tag{4.2.25}$$

where $\Psi = u - \bar{u}$. By separation of variables, i.e $\Psi(x,t) = \omega(t)\phi(x)$, Equation $(4.2.25)$ leads to the equation

$$\frac{\omega'(t)}{\omega(t)} = \frac{D\phi''(x)}{\phi(x)} + f'(\bar{u}) = K,$$

which is equivalent to the system

$$\omega'(t) = K\omega(t) \tag{4.2.26}$$

$$D\phi''(x) = (K - f'(\bar{u}))\phi(x), \tag{4.2.27}$$

where K is independent of x and t. We append $(4.2.27)$ with the Dirichlet boundary conditions

$$\phi(0) = \phi(b) = 0 \tag{4.2.28}$$

to make it a Sturm–Liouville problem. The stability of equilibrium solutions is determined by the next theorem.

Theorem 4.2.11. *Suppose that* $\bar{u}$ *is an equilibrium solution of* $(4.2.1)$. *If* $f'(\bar{u}) < \frac{\pi^2 D}{b^2}$, *then* $\bar{u}$ *is locally asymptotically stable; if there exists an* $n \in \mathbb{N}$ *such that* $f'(\bar{u}) > \frac{n^2\pi^2 D}{b^2}$, *then* $\bar{u}$ *is an unstable equilibrium solution.*

Proof: It is well–known that

$$\Phi_n(x) = \frac{2}{b}\sin\left(\frac{n\pi}{b}x\right), \quad n = 1,\ 2,\ \ldots$$

constitute the eigenfunctions of the Sturm–Liouville problem $(4.2.27) - (4.2.28)$ with associated eigenvalues

$$K_n = f'(\bar{u}) - \frac{n^2\pi^2 D}{b^2}.$$

Equally, it is known that the sequence $(\phi_n)_{n\geq 1}$ is a Hilbert basis of the space $L_2(0, b)$. Therefore, any solution $u(x) = u(x, t) \in \mathbb{R} \times (0, b)$ admits the Fourier expansion

$$u(x,t) = \sum_{n=1}^{\infty} c_n e^{K_n t}\sin\left(\frac{n\pi}{b}x\right), \quad x \in (0,b), \quad t > 0, \tag{4.2.29}$$

where $c_n = \frac{2}{b}\int_0^b u_0(x)\sin\left(\frac{n\pi x}{b}\right)$. From Equation $(4.2.29)$, it follows that $\bar{u}(x)$ is locally asymptotically stable if $K_n < 0$ or $f'(\bar{u}) < \frac{\pi^2 D}{b^2} \leq \frac{n^2\pi^2 D}{b^2}$ for all $n \in \mathbb{N}$ and unstable if there exists $n \in \mathbb{N}$ such that $K_n > 0$ or $f'(\bar{u}) > \frac{n^2\pi^2 D}{b^2}$. □.

Remark 4.2.12. *The linearization process is not applicable when the involved Sturm–Liouville problem has at least one eigenvalue with zero real part.*

4.3 SIS Epidemic Model with Diffusion

In this section, we assume that a population of size $N = N(x, t)$ consists of only two disjoint compartments, susceptible $S = S(x, t)$ and infective $I = I(x, t)$, which interact:

$$S(x,t) + I(x,t) = N(x,t). \tag{4.3.1}$$

We model the dynamics of I and S by simple diffusion. Our additional assumption is that the dispersion is completely random and has the same structural properties. Then the

model is given by

$$S_t = \mu K - \frac{\lambda IS}{N} - \mu S + \gamma I + S_{xx} \tag{4.3.2}$$

$$I_t = \frac{\lambda IS}{N} - (\mu + \gamma)I + I_{xx}. \tag{4.3.3}$$

In general, a diffusion coefficient D, which could be species-dependent [20], is needed in front of the terms S_{xx} and I_{xx} of the model $(4.3.2) - (4.3.3)$. Here, we take $D = 1$, which is possible by the dimensionless process.

By adding equations $(4.3.2) - (4.3.3)$, we have the conservation law:

$$N_t = \mu(K - N) + N_{xx}. \tag{4.3.4}$$

In this model, there is no death induced by the disease. The assumptions in Chapter 3 regarding the parameters apply in this section and are recalled here for convenience:

- The constant $\mu > 0$ is the birth or natural death rate.
- The constant $\gamma > 0$ is the rate infective individuals return to the susceptible class.
- The constant K is the carrying capacity of the environment.

We have used the standard incidence formulation where $\beta(N) = \frac{\lambda}{N}$, though it is possible to consider a general contact rate as in the previous chapters.

Theorem 4.3.1. *Assume that Equation* $(4.3.4)$ *is coupled with a continuous initial data* $N_0 : \mathbb{R} \to \mathbb{R}$,

$$N(x, 0) = N_0(x), \tag{4.3.5}$$

such that $0 \leq N_0(x) \leq K$. *Then, Equation* $(4.3.4) - (4.3.5)$ *admits a unique solution* $N : \mathbb{R} \times [0, \infty) \to \mathbb{R}$ *that satisfies the condition* $0 \leq N(x, t) \leq K$.

Proof: For a given initial data $N_0(x)$, the existence of a unique solution $N(x, t)$ for $(4.3.4) - (4.3.5)$ is guaranteed by Theorem 4.2.3. By the transformation

$$N(x, t) = K - u(x, t)e^{-\mu t}$$

$(4.3.4) - (4.3.5)$, becomes the standard heat equation,

$$u_t = u_{xx}, \tag{4.3.6}$$

$$u(x,0) = K - N_0(x), \tag{4.3.7}$$

which, in view of Theorem 4.2.1 , has its unique solution $u(x,t)$ represented by

$$u(x,t) = \int_{-\infty}^{\infty} \frac{(K - N_0(y))}{\sqrt{4\pi t}} e^{\frac{-(x-y)^2}{4t}} dy.$$

Hence, the corresponding solution $N(x,t)$ of $(4.3.4) - (4.3.5)$ is

$$N(x,t) = K - e^{-\mu t} \int_{-\infty}^{\infty} \frac{(K - N_0(y))}{\sqrt{4\pi t}} e^{\frac{-(x-y)^2}{4t}} dy. \tag{4.3.8}$$

By using Equation $(4.3.8)$, we have $0 \leq N(x,t) \leq K$, since $0 \leq N_0(x) \leq K$. □

In what follows, the reaction–diffusion system $(4.3.2) - (4.3.3)$ will be considered as a scalar reaction–diffusion equation in the dependent variable I. This is possible, due to the explicit expression $(4.3.8)$ of the solution of $(4.3.4) - (4.3.5)$ and to the equation $(4.3.1)$, which lead to the parabolic equation

$$I_t = \frac{\lambda I(N - I)}{N} - (\mu + \gamma)I + I_{xx}. \tag{4.3.9}$$

The fact that we are dealing with the spread of the disease in space implies biologically the following for the basic reproduction number $\mathcal{R}_0$:

$$\mathcal{R}_0 = \frac{\lambda}{\mu + \gamma} > 1. \tag{4.3.10}$$

In terms of this epidemiological threshold parameter, Equation $(4.3.9)$ has the equivalent formulation

$$I_t = (\lambda - \mu - \gamma)\left(1 - \frac{I}{N(1 - \frac{1}{\mathcal{R}_0})}\right) I + I_{xx}. \tag{4.3.11}$$

Theorem 4.3.2. *Under the condition of Theorem 4.3.1, let us assume that Equation* $(4.3.11)$ *is coupled with the initial condition*

$$I(x,0) = I_0(x), \tag{4.3.12}$$

where $I_0 : \mathbb{R} \to \mathbb{R}$ *is a given continuous function such that* $0 \leq I_0(x) < N_0(x) \leq K$. *Then the reaction–diffusion equation* $(4.3.11) - (4.3.12)$ *admits a unique solution* $I(x,t)$ *that satisfies the condition* $0 \leq I(x,t) \leq N(x,t) \leq K$.

Proof: We introduce the differential operator L defined by

$$L(I) = I_t - I_{xx} - (\lambda - \mu - \gamma)\left(1 - \frac{I}{N(1-\frac{1}{\mathcal{R}_0})}\right) I.$$

Let I be a solution of the problem $(4.3.11)$ with initial condition $0 \leq I_0(x) \leq N_0(x)$.

It is clear that

$$L(0) = L(I) = 0.$$

On the other hand, we have

$$\begin{aligned} L(N) &= N_t - N_{xx} - (\lambda - \mu - \gamma)\left(1 - \frac{1}{(1-\frac{1}{\mathcal{R}_0})}\right) N \\ &= \mu(K - N) - (\lambda - \mu - \gamma)\left(1 - \frac{1}{(1-\frac{1}{\mathcal{R}_0})}\right) N \qquad \text{by} \quad (4.3.4) \\ &> 0, \qquad \text{since} \quad \mathcal{R}_0 > 1 \ (\text{see} \ (4.3.10)) \ \text{and} \ \ 0 < N \leq K. \end{aligned}$$

Thus, we have

$$L(0) \leq L(I) \leq L(N) \quad \text{on} \quad \mathbb{R} \times (0, \infty)$$

and

$$0 \leq I_0(x) \leq N_0(x) \quad \text{on} \quad \mathbb{R},$$

which show that the null function 0 is a sub–solution of $(4.3.11)$ whereas the function N is a super–solution of the same equation [25].

By the comparison theorem (see [38], [54]), we have

$$0 \leq I(x,t) \leq N(x,t) \quad \text{on} \quad \mathbb{R} \times (0, \infty). \tag{4.3.13}$$

In view of the fact that $N \leq K$, the condition $(4.3.13)$ means that any solution of $(4.3.11) - (4.3.12)$ satisfies a priori boundedness estimate. Since the function

$$f(I) = (\lambda - \mu - \gamma)\left(1 - \frac{I}{N(1-\frac{1}{\mathcal{R}_0})}\right) I \tag{4.3.14}$$

is locally Lipschitz (being of class C^∞), we apply Theorem 4.2.7 to conclude that the problem $(4.3.11) - (4.3.12)$ admits a unique solution I such that $0 \leq I \leq N$. □

The well–posedness of the problems $(4.3.4) - (4.3.5)$ and $(4.3.11) - (4.3.12)$ being established, we are now interested in its stability analysis. A constant equilibrium solution

$(\bar{I}, \bar{N})$ must satisfy the following system:

$$(\lambda - \mu - \gamma)\left(1 - \frac{I}{N(1-\frac{1}{\mathcal{R}_0})}\right) I + I_{xx} = 0 \tag{4.3.15}$$

$$\mu(K - N) + N_{xx} = 0. \tag{4.3.16}$$

Simple computation show that the constant equilibrium solutions are:

$$(\bar{I}_1, \bar{N}) = (0,\ K) \quad \text{and} \quad (\bar{I}_2, \bar{N}) = \left(K(1 - \frac{1}{\mathcal{R}_0}), K\right).$$

Theorem 4.3.3. *The equilibrium solution $\bar{N} = K$ of the conservation law $(4.3.4)$ is globally asymptotically stable. The equilibrium solution $\bar{I}_1 = 0$ of $(4.3.11)$ is unstable whereas the equilibrium solution $\bar{I}_2 = K(1 - \frac{1}{\mathcal{R}_0})$ is locally asymptotically stable.*

Proof: The GAS of $\bar{N} = K$ for $(4.3.4)$ follows from the explicit expression $(4.3.8)$. Regarding $\bar{I}_1$ and $\bar{I}_2$, we apply Theorem 4.2.11 where with $f(I)$ given in $(4.3.14)$. We have

$$f'(0) = \lambda - \mu - \gamma > 0 \quad \text{and} \quad f'\left(K(1 - \frac{1}{\mathcal{R}_0})\right) = -(\lambda - \mu - \gamma) < 0. \qquad \square$$

Remark 4.3.4. *To get a nonconstant equilibrium solution $(\bar{I}, \bar{N})$ of $(4.3.15) - (4.3.16)$, we need to solve first Equation $(4.3.16)$. Its general solution is*

$$\bar{N}(x) = c_1 e^{\sqrt{\mu}x} + c_2 e^{-\sqrt{\mu}x} + K,$$

where c_1 and c_2 are constants. We plug this function into Equation $(4.3.15)$ to determine the corresponding component $\bar{I}$ of $(\bar{I}, \bar{N})$. Note that the resulting equation in $\bar{I}$ is a Bernoulli equation when N is constant $(N = K)$ and can therefore be easily solved. When N is not a constant, the solution of the equation can be difficult.

Often, the disease is spread in space as a wave with speed c. It is therefore legitimate to seek for traveling wave solutions in the following sense:

Definition 4.3.5. *A traveling wave solution (TWS) with speed $c > 0$ for the equation $(4.3.11) - (4.3.12)$ is a solution $I(x,t)$ of the form*

$$I(x,t) = W(z), \quad z = x - ct \in \mathbb{R} \tag{4.3.17}$$

such that

$$\lim_{z \to \pm\infty} W(z) \in \mathbb{R}. \tag{4.3.18}$$

Theorem 4.3.6. *A Traveling Wave Solution to* $(4.3.11) - (4.3.12)$ *exists if and only if* $N = K = constant.$

Proof: Assume that $(4.3.11)-(4.3.12)$ has a TWS. This implies that Equation $(4.3.4)-(4.3.5)$ also admits a TWS of the form

$$N(x,t) = M(z), \quad z = x - ct \in \mathbb{R}.$$

If we substitute this in Equation $(4.3.4)$, we get

$$M'' + cM' + \mu(K - M) = 0$$

which has the general solution

$$M(z) = c_1 e^{r_1 z} + c_2 e^{r_2 z} + K,$$

where

$$r_1 = \frac{-c - \sqrt{c^2 + 4\mu}}{2} < 0,$$
$$r_2 = \frac{-c + \sqrt{c^2 + 4\mu}}{2} > 0,$$

$c_1 \in \mathbb{R}$ and $c_2 \in \mathbb{R}$. The analogue condition $(4.3.18)$ applied to $M(z)$ implies that

$$c_1 = c_2 = 0.$$

Hence, $M(z) = K$ and $N(x,t) = K = constant$, as announced. Conversely, assume that $N = K = constant$. We want to show that Equation $(4.3.11) - (4.3.12)$ admits a TWS. Let a traveling wave solution

$$I(x,t) = W(z) \tag{4.3.19}$$

of the form $(4.3.17)$ be such that $W(z)$ is non-negative and bounded. Since $I_1 = 0$ and $I_2 = K(1 - \frac{1}{\mathcal{R}_0}) > 0$ are unstable and stable equilibrium solutions of $(4.3.11)$ respectively, we look for a TWS that satisfies

$$0 \leq W(z) \leq K\left(1 - \frac{1}{\mathcal{R}_0}\right),$$

with the relation $(4.3.18)$ being specifically

$$\lim_{z \to -\infty} W(z) = K\left(1 - \frac{1}{\mathcal{R}_0}\right) \quad \text{and} \quad \lim_{z \to \infty} W(z) = 0. \tag{4.3.20}$$

We have to determine the wave form W as well as the speed c. Using the chain rule, we have from $(4.3.17)$

$$\frac{\partial I}{\partial t} = -c\frac{dW}{dz} = -cW' \quad \text{and} \quad \frac{\partial^2 I}{\partial x^2} = \frac{d^2W}{dz^2} = W''.$$

Then Equation $(4.3.11)$ becomes:

$$W'' + cW' + (\lambda - \mu - \gamma)\left(1 - \frac{\mathcal{R}_0 W}{K(\mathcal{R}_0 - 1)}\right) W = 0. \tag{4.3.21}$$

For the qualitative analysis of the equation $(4.3.21)$, we make the substitution

$$W' = V$$

so that $(4.3.21)$ is equivalent to first order system of autonomous differential equations

$$W' = V =: f(W, V) \tag{4.3.22}$$

$$V' = -cV - (\lambda - \mu - \gamma)\left(1 - \frac{\mathcal{R}_0 W}{K(\mathcal{R}_0 - 1)}\right) W =: g(W, V). \tag{4.3.23}$$

Firstly, let $D \subset \mathbb{R}^2$ be a simply connected region. For the functions f and g in $(4.3.22) - (4.3.23)$ which are of class C^1 (in fact C^∞) on D, we have

$$\frac{\partial f}{\partial W} + \frac{\partial g}{\partial V} = -c < 0$$

for any $c > 0$.

By Bendixson's criterion (see Theorem 2.2.34), we infer that the system $(4.3.22) - (4.3.23)$ has no closed orbit lying entirely in D. Note that this statement holds true for any simply connected region D.

Next, we observe that the equilibria of the system $(4.3.22) - (4.3.23)$ are

$$P = (0, 0) \quad \text{and} \quad Q = \left(K(1 - \frac{1}{\mathcal{R}_0}), 0\right).$$

The Jacobian of the system being

$$J(W, V) = \begin{pmatrix} 0 & 1 \\ -(\lambda - \mu - \gamma)\left(1 - \frac{2W\mathcal{R}_0}{K(\mathcal{R}_0 - 1)}\right) & -c \end{pmatrix},$$

we have

$$J(0, 0) = \begin{pmatrix} 0 & 1 \\ -(\lambda - \mu - \gamma) & -c \end{pmatrix}$$

with eigenvalues

$$r_{1,2} = \frac{-c \pm \sqrt{c^2 - 4(\lambda - \mu - \gamma)}}{2} \tag{4.3.24}$$

and

$$J(K(1 - \tfrac{1}{\mathcal{R}_0}), 0) = \begin{pmatrix} 0 & 1 \\ \lambda - \mu - \gamma & -c \end{pmatrix}$$

with eigenvalues

$$r_{3,4} = \frac{-c \pm \sqrt{c^2 + 4(\lambda - \mu - \gamma)}}{2}. \tag{4.3.25}$$

Note that $\lambda > \mu + \gamma$ by $(4.3.10)$.

For $c \neq 0$, it follows from $(4.3.24)$ and $(4.3.25)$ that the eigenvalues have nonzero real parts. Thus the equilibria are hyperbolic, which makes Hartman-Grobman theorem applicable (see Definition 2.2.13 and Theorem 2.2.14). Applying this theorem, we find that the equilibrium $P = (0, 0)$ is locally asymptotically stable if $c \geq 2\sqrt{\lambda - \mu - \gamma}$, because the eigenvalues are negative; whereas this equilibrium is a stable spiral if $c < 2\sqrt{\lambda - \mu - \gamma}$, because the eigenvalues are complex numbers with negative real parts.

Moreover the equilibrium $Q = (K(1 - \frac{1}{\mathcal{R}_0}), 0)$ is a saddle point, because the eigenvalues are real numbers of opposite signs. Therefore, $c \geq 2\sqrt{\lambda - \mu - \gamma}$ is the right wave speed for the required TWS. Hence, for $N = K = constant$, Equation $(4.3.11) - (4.3.12)$ admits a TWS. □

Remark 4.3.7. *When $N = K$, Equation $(4.3.11)$ is the famous Fisher equation, which has been extensively studied (see $[51]$).*

In addition to Theorem 4.3.6 which guarantees the existence of a TWS, we have the next result which specifies its monotonic property.

Theorem 4.3.8. *Assume that $N(x, t) = K = constant$. Then the TWS $W(z) = I(x, t)$ obtained in Theorem 4.3.6 is a monotonic decreasing function with horizontal asymptotes $W = 0$ and $W = K(1 - \frac{1}{\mathcal{R}_0})$ (see Fig 4.2).*

Proof: Let $c \geq 2\sqrt{\lambda - \mu - \gamma}$ be the speed of the TWS $W(z)$, which exists and is unique by Theorem 4.3.6. For convenience, we work in the phase plane $W - V$.

Let E_3 and E_4 be the eigenspaces (associated with the eigenvalues $r_3 > 0$ and $r_4 < 0$, respectively which are straight lines in this case)(see Fig 4.1). Then the trajectories on E_3 leave Q whereas those on E_4 are attracted by Q.

Let D be a simply connected subset of the positive sector $W \geq 0,\ V \geq 0$ such that D is compact, invariant and contains the stable equilibrium point $P = (0, 0)$ and the saddle point $Q = (K(1 - \frac{1}{\mathcal{R}_0}), 0)$. By $Poincaré - Bendixon$ Theorem (Theorem 2.2.36) there exists a unique trajectory S called separatrix which coincides with E_3 near Q and such that the omega limit, $\omega(S) = P$ and the alpha limit, $\alpha(S) = Q$.

Furthermore any point $R \in D\backslash S$ is the initial point of a unique trajectory that does not intersect with S and is attracted by P. Transposed to the $z - W$ axes, the above–constructed unique trajectory S constitutes the TWS $W(z)$ which is a decreasing function (see Fig 4.2). □

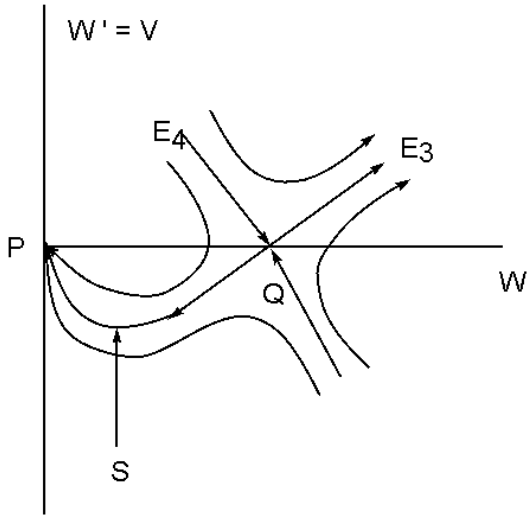


Figure 4.1: Phase portrait for $(4.3.20) - (4.3.21)$ when $c \geq 2\sqrt{\lambda - \mu - \gamma}$.

Remark 4.3.9. *The explicit expression of the TWS is available in* $[10]$ *and reads as*

$$I(x,t) = \frac{K(\mathcal{R}_0 - 1)}{\mathcal{R}_0[1 + b\ exp(z)]^2}, \tag{4.3.26}$$

where

$$z = \frac{\sqrt{\lambda - \mu - \gamma}}{\sqrt{6}}x - \frac{5}{6}(\lambda - \mu - \gamma)t$$

and $b = constant.$

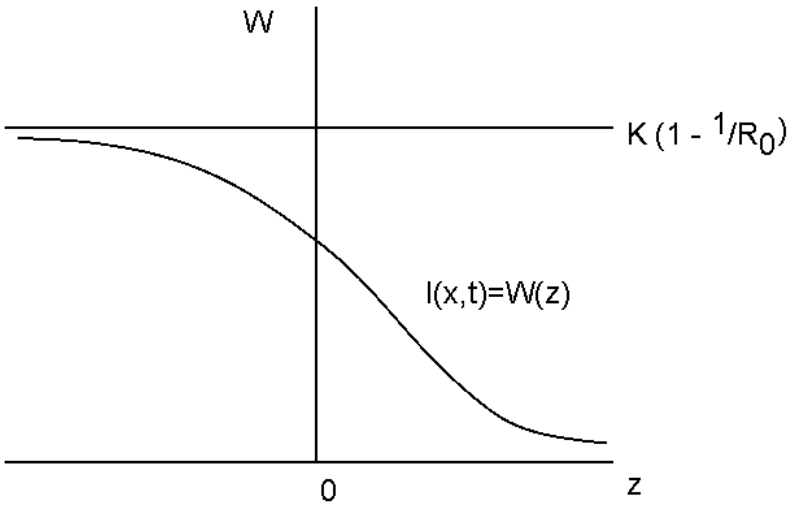


Figure 4.2: Traveling wave solution for $c \geq 2\sqrt{\lambda - \mu - \gamma}$.

4.4 Dynamically Consistent NSFD Schemes

In this section, we construct numerical schemes that are dynamically consistent with the properties of the SIS-diffusion model stated in Theorems 4.3.1, 4.3.2 . We recall that the time variable $t \in [0, \infty)$ and the space variable $x \in \mathbb{R}$ are replaced by the discrete variable $t_k = k\Delta t, \quad k \in \mathbb{N}$ and $x_n = n\Delta x, \quad n \in \mathbb{Z}$ with Δt and Δx being the time and the space step sizes, respectively. The notation u_n^k means an approximation of $u(x,t)$ at $x = x_n$ and $t = t_k$.

We start with the conservation law $(4.3.4)$ and we use the methodology based on sub–equations as developed in $[2]$ and $[48]$.

The space independent equation of the conservation law $(4.3.4)$ is the linear equation

$$N_t = \mu(K - N), \qquad N(0) = N_0 \tag{4.4.1}$$

which has the exact solution

$$N(t) = (N_0 - K)e^{-\mu t} + K.$$

At the time $t = t_{k+1}$, the exact solution

$$\begin{aligned} N(t_{k+1}) &= (N_0 - K)e^{-\mu t_{k+1}} + K \\ &= (N(t_k) - K)e^{-\mu \Delta t} + K, \end{aligned} \tag{4.4.2}$$

has the equivalent formulation

$$\frac{N^{k+1}-N^k}{\phi_1(\Delta t)} = \mu(K - N^{k+1}), \tag{4.4.3}$$

or

$$\frac{N^{k+1}-N^k}{\phi_2(\Delta t)} = \mu(K - N^{k}), \tag{4.4.4}$$

where $N^k = N(t_k)$,

$$\phi_1(\Delta t) = \frac{e^{\mu\Delta t}-1}{\mu} \quad \text{and} \quad \phi_2(\Delta t) = \frac{1-e^{-\mu\Delta t}}{\mu}. \tag{4.4.5}$$

The equivalent equation $(4.4.2)$, $(4.4.3)$ or $(4.4.4)$ is, following $[48]$, the exact scheme of $(4.4.1)$. More generally, any scheme of the form

$$\frac{N^{k+1}-N^k}{\phi(\Delta t)} = \mu(K - N^{k+1}) \tag{4.4.6}$$

or

$$\frac{N^{k+1}-N^k}{\phi(\Delta t)} = \mu(K - N^{k}) \tag{4.4.7}$$

where the denominator function $\phi(\Delta t)$ satisfies the relation

$$\phi(\Delta t) = \Delta t + \mathcal{O}(\Delta t^2) \tag{4.4.8}$$

is called a NSFD scheme for $(4.4.1)$ (see Section 2.3.3).

The stationary equation of the conservation law $(4.3.4)$ is the linear equation

$$N_{xx} + \mu(K - N) = 0 \tag{4.4.9}$$

or equivalently

$$u_{xx} - \mu u = 0, \quad \text{where} \quad u := N - K. \tag{4.4.10}$$

Equation $(4.4.10)$ has general solutions $u_1(x) = e^{\sqrt{\mu}x}$ and $u_2(x) = e^{-\sqrt{\mu}x}$. Thus setting $u_n = u(x_n)$, the theory of linear difference equations shows that the second order linear difference equation

$$\begin{vmatrix} u_{n-1} & e^{\sqrt{\mu}x_{n-1}} & e^{-\sqrt{\mu}x_{n-1}} \\ u_n & e^{\sqrt{\mu}x_n} & e^{-\sqrt{\mu}x_n} \\ u_{n+1} & e^{\sqrt{\mu}x_{n+1}} & e^{-\sqrt{\mu}x_{n+1}} \end{vmatrix} = 0$$

or equivalently

$$\frac{u_{n+1} - 2u_n + u_{n-1}}{\frac{4}{\mu}sinh^2(\frac{\sqrt{\mu}\Delta x}{2})} - \mu u_n = 0$$

is the exact scheme of $(4.4.10)$ (see [42]). Consequently, the exact scheme of the Equation $(4.4.9)$ is

$$\frac{N_{n+1} - 2N_n + N_{n-1}}{\frac{4}{\mu}sinh^2(\frac{\sqrt{\mu}\Delta x}{2})} + \mu(K - N_n) = 0. \tag{4.4.11}$$

Again any scheme of the form

$$\frac{N_{n+1} - 2N_n + N_{n-1}}{\psi^2(\Delta x)} + \mu(K - N_n) = 0, \tag{4.4.12}$$

where

$$\psi(\Delta x) = \Delta x + \mathcal{O}(\Delta x^2) \tag{4.4.13}$$

is a NSFD scheme for $(4.4.9)$.

We will also make use of the following NSFD scheme:

$$\frac{N_{n+1} - 2N_n + N_{n-1}}{\psi^2(\Delta x)} + \mu\left(K - \frac{N_{n+1} + N_n + N_{n-1}}{3}\right) = 0. \tag{4.4.14}$$

Three possible combinations of $(4.4.6),\ (4.4.7),\ (4.4.12)$ and $(4.4.14)$ yield below three NSFD schemes for the conservation law $(4.3.4)$:

$$\frac{N_n^{k+1} - N_n^k}{\phi(\Delta t)} = \mu(K - N_n^{k+1}) + \frac{N_{n+1}^k - 2N_n^k + N_{n-1}^k}{\psi^2(\Delta x)}, \tag{4.4.15}$$

$$\frac{N_n^{k+1} - N_n^k}{\phi(\Delta t)} = \mu(K - N_n^k) + \frac{N_{n+1}^k - 2N_n^k + N_{n-1}^k}{\psi^2(\Delta x)} \tag{4.4.16}$$

and

$$\frac{N_n^{k+1} - N_n^k}{\phi(\Delta t)} = \mu\left(K - \frac{N_{n+1}^k + N_n^k + N_{n-1}^k}{3}\right) + \frac{N_{n+1}^k - 2N_n^k + N_{n-1}^k}{\psi^2(\Delta x)}. \tag{4.4.17}$$

For their implementation, the schemes $(4.4.15)$, $(4.4.16)$ and $(4.4.17)$ are rearranged into the following explicit forms:

$$N_n^{k+1} = \frac{\mu\phi K + \frac{\phi}{\psi^2}(N_{n+1}^k + N_{n-1}^k) + (1 - \frac{2\phi}{\psi^2})N_n^k}{1 + \mu\phi}, \tag{4.4.18}$$

$$N_n^{k+1} = \mu\phi K + \frac{\phi}{\psi^2}(N_{n+1}^k + N_{n-1}^k) + (1 - \frac{2\phi}{\psi^2})N_n^k, \tag{4.4.19}$$

and

$$N_n^{k+1} = \mu\phi K + \left(\frac{\phi}{\psi^2} - \frac{\mu\phi}{3}\right)\left(N_{n+1}^k + N_{n-1}^k\right) + \left(1 - \frac{\mu\phi}{3} - \frac{2\phi}{\psi^2}\right)N_n^k. \tag{4.4.20}$$

The methodology of sub–equations is also used for Equation $(4.3.11)$. The space independent equation of $(4.3.11)$ reads as

$$I_t = (\lambda - \mu - \gamma)\left(1 - \frac{I}{N(1 - \frac{1}{\mathcal{R}_0})}\right)I, \quad I(0) = I_0. \tag{4.4.21}$$

To proceed, we assume for the moment that N is constant. Then $(4.4.21)$ is the logistic equation. Its exact solution is

$$I(t) = \frac{N(1 - \frac{1}{\mathcal{R}_0})I_0}{I_0 + \left(N(1 - \frac{1}{\mathcal{R}_0}) - I_0\right)e^{-(\lambda-\mu-\gamma)t}}. \tag{4.4.22}$$

Thus, when N is constant the exact scheme of $(4.4.22)$ is

$$I(t_{k+1}) = \frac{N(1 - \frac{1}{\mathcal{R}_0})I(t_k)}{I(t_k) + \left(N(1 - \frac{1}{\mathcal{R}_0}) - I(t_k)\right)e^{-(\lambda-\mu-\gamma)\Delta t}} \tag{4.4.23}$$

which is equivalent to

$$\frac{I^{k+1} - I^k}{\frac{(1-exp(-(\lambda-\mu-\gamma)\Delta t))}{\lambda-\mu-\gamma}} = (\lambda - \mu - \gamma)\left(1 - \frac{I^{k+1}}{N(1 - \frac{1}{\mathcal{R}_0})}\right)I^k. \tag{4.4.24}$$

The stationary equation of $(4.3.11)$ is

$$I_{xx} + (\lambda - \mu - \gamma)\left(1 - \frac{I}{N(1 - \frac{1}{\mathcal{R}_0})}\right)I = 0. \tag{4.4.25}$$

To proceed, we assume once again that N is constant. Then Equation $(4.4.25)$ is the type of conservative oscillators investigated in [2] and [48]. Ignoring from $(4.4.25)$ the nonlinear part, we obtain the harmonic oscillator

$$I_{xx} + (\lambda - \mu - \gamma)I = 0 \tag{4.4.26}$$

whose exact scheme, obtained using the procedure applied to $(4.4.10)$, is (see $[42]$ and $[48]$):

$$\frac{I_{n+1}-2I_n+I_{n-1}}{\frac{4}{\lambda-\mu-\gamma}sin^2\left(\frac{\sqrt{\lambda-\mu-\gamma}}{2}\Delta x\right)}+(\lambda-\mu-\gamma)I_n=0. \tag{4.4.27}$$

At this point in time, there are several possibilities of extending $(4.4.27)$ in order to have a NFSD scheme that approximates the nonlinear equation $(4.4.25)$ when N is constant. We will use the NSFD scheme

$$\frac{I_{n+1}-2I_n+I_{n-1}}{\frac{4}{\lambda-\mu-\gamma}sin^2\left(\frac{\sqrt{\lambda-\mu-\gamma}}{2}\Delta x\right)}+(\lambda-\mu-\gamma)\left(1-\frac{I_n}{N(1-\frac{1}{\mathcal{R}_0})}\right)\left(\frac{I_{n+1}+I_n+I_{n-1}}{3}\right)=0 \tag{4.4.28}$$

investigated in $[2]$, which has the advantage of replicating the property of conservation of energy that characterizes Equation $(4.4.25)$ when N is constant.

In view of $(4.4.24)$ and $(4.4.28)$, we can now consider the following NSFD schemes for $(4.4.21)$ and $(4.4.25)$, respectively when N is not constant:

$$\frac{I^{k+1}-I^k}{\frac{1-exp[-(\lambda-\mu-\gamma)\Delta t]}{\lambda-\mu-\gamma}}=(\lambda-\mu-\gamma)\left(1-\frac{I^{k+1}}{N^{k+1}(1-\frac{1}{\mathcal{R}_0})}\right), \tag{4.4.29}$$

and

$$\frac{I_{n+1}-2I_n+I_{n-1}}{\frac{4}{\lambda-\mu-\gamma}sin^2\left(\frac{\sqrt{\lambda-\mu-\gamma}}{2}\Delta x\right)}+(\lambda-\mu-\gamma)\left(1-\frac{I_n}{N_n(1-\frac{1}{\mathcal{R}_0})}\right)\left(\frac{I_{n+1}+I_n+I_{n+1}}{3}\right)=0. \tag{4.4.30}$$

Combining $(4.4.29)$ and $(4.4.30)$, our NSFD scheme for $(4.3.11)$ reads as

$$\begin{aligned}\frac{I_n^{k+1}-I_n^k}{\phi(\Delta t)} &= (\lambda-\mu-\gamma)\left(1-\frac{I_n^{k+1}}{N_n^{k+1}(1-\frac{1}{\mathcal{R}_0})}\right)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)\\ &+ \frac{I_{n+1}^k-2I_n^k+I_{n-1}^k}{(\psi(\Delta x))^2},\end{aligned} \tag{4.4.31}$$

where

$$\phi(\Delta t)=\frac{1-exp\left[-(\lambda-\mu-\gamma)\Delta t\right]}{\lambda-\mu-\gamma} \quad \text{and} \quad \psi(\Delta x)=\frac{2}{\sqrt{\lambda-\mu-\gamma}}sin\left(\frac{\sqrt{\lambda-\mu-\gamma}}{2}\Delta x\right). \tag{4.4.32}$$

Note that the implementation of the NSFD scheme (3.7) is carried out by using its equivalent formulation

$$I_n^{k+1}=N_n^{k+1}(1-\frac{1}{\mathcal{R}_0})\frac{\frac{\phi}{\psi^2}(I_{n+1}^k+I_{n-1}^k)+\left(1-\frac{2\phi}{\psi^2}\right)I_n^k+\phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)}{N_n^{k+1}(1-\frac{1}{\mathcal{R}_0})+\phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)}. \tag{4.4.33}$$

Remark 4.4.1. *Simple manipulation shows that the NSFD scheme* $(4.4.31)$ *also admits the equivalent formulation*

$$\begin{aligned}\frac{I_n^{k+1}-I_n^k}{\phi(\Delta t)} &= \lambda\frac{S_n^{k+1}}{N_n^{k+1}}\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)-(\mu+\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)\\ &+ \frac{I_{n+1}^k-2I_n^k+I_{n-1}^k}{\psi^2(\Delta x)},\end{aligned} \tag{4.4.34}$$

which compares nicely with the original Equation $(4.3.3)$. *Furthermore, subtracting* $(4.4.34)$ *from* $(4.4.17)$, *we obtain the following NSFD scheme for* $(4.3.2)$:

$$\begin{aligned}\frac{S_n^{k+1}-S_n^k}{\phi(\Delta t)} &= \mu K - \frac{\lambda S_n^{k+1}}{N_n^{k+1}}\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right) - \mu\left(\frac{S_{n+1}^k+S_n^k+S_{n-1}^k}{3}\right)\\ &+ \gamma\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right) + \left(\frac{S_{n+1}^k-2S_n^k+S_{n-1}^k}{\psi^2(\Delta x)}\right). \end{aligned} \tag{4.4.35}$$

By rearranging $(4.4.35)$, *we get*

$$S_n^{k+1} = \frac{\mu\phi\left(K-\frac{S_{n+1}^k+S_n^k+S_{n-1}^k}{3}\right)+\gamma\phi\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)+\frac{\phi}{\psi^2}\left(S_{n+1}^k-2S_n^k+S_{n-1}^k\right)+S_n^k}{1+\frac{\lambda\phi}{N_n^{k+1}}\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)}. \tag{4.4.36}$$

Remark 4.4.2. *Since the conservation law* $(4.3.4)$ *is studied in conjunction with the epidemic model* $(4.3.11)$, *it makes sense to consider in the NSFD scheme* $(4.4.15)-(4.4.17)$ *the denominator functions in* $(4.4.32)$ *where all the epidemiological parameters are involved instead of the denominator functions* ϕ_1 *in* $(4.4.3)$ *and* ψ *in* $(4.4.11)$.

Theorem 4.4.3. *Under the functional relation*

$$\frac{\phi}{\psi^2} = \frac{1}{3} \tag{4.4.37}$$

between the step sizes and the condition

$$1-\mu\phi \geq 0, \tag{4.4.38}$$

the NSFD scheme $(4.4.17)$ *replicates the positivity and boundedness properties of the exact solution. This means, if* $0 \leq N_n^k \leq K$ *then* $0 \leq N_n^{k+1} \leq K$.

Proof: Assume that $0 \leq N_n^k \leq K$ for all $k \in \mathbb{N}$ and $n \in \mathbb{Z}$. By using Equations $(4.4.37)$ and $(4.4.38)$, Equation $(4.4.20)$ is reduced into

$$N_n^{k+1} = \mu\phi K + \frac{1}{3}\left(N_{n+1}^k+N_n^k+N_{n-1}^k\right)(1-\mu\phi) \geq 0. \tag{4.4.39}$$

Thus, $N_n^{k+1} \leq \mu\phi K + K(1-\mu\phi)$, since $N_{n+1}^k+N_n^k+N_{n-1}^k \leq 3K$.

$$= K.$$

□

Theorem 4.4.4. *Under the functional relation*

$$\frac{\phi}{\psi^2} = \frac{1}{2} \tag{4.4.40}$$

between the step sizes, the NSFD scheme $(4.4.15)$ *replicates the positivity and boundedness properties of the exact solution. This means, if* $0 \leq N_n^k \leq K$ *then* $0 \leq N_n^{k+1} \leq K$.

Proof: We assume that $0 \leq N_n^k \leq K$. By using the functional relation $(4.4.40)$, from Equation $(4.4.18)$, we have

$$\begin{aligned} 0 \leq N_n^{k+1} &= \frac{\mu\phi K + \frac{N_{n+1}^k + N_{n-1}^k}{2}}{1+\mu\phi} \\ &\leq K. \end{aligned}$$

□

Theorem 4.4.5. *Under the conditions of Theorem 4.4.3, the NSFD scheme* $(4.4.31)$ *replicates the positivity and boundedness properties of the exact solution. This means if* $0 \leq I_n^k \leq N_n^k \leq K$ *then* $0 \leq I_n^{k+1} \leq N_n^{k+1} \leq K$.

Proof: By using $(4.4.37)$, Equations $(4.4.33)$ and $(4.4.36)$ are reduced into

$$I_n^{k+1} = N_n^{k+1}(1-\frac{1}{\mathcal{R}_0})\frac{\frac{1}{3}(I_{n+1}^k + I_n^k + I_{n-1}^k) + \phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)}{N_n^{k+1}(1-\frac{1}{\mathcal{R}_0}) + \phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)} \tag{4.4.41}$$

and

$$S_n^{k+1} = \frac{\mu\phi\left(K - \frac{S_{n+1}^k+S_n^k+S_{n-1}^k}{3}\right) + \gamma\phi\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right) + \frac{1}{3}\left(S_{n+1}^k S_n^k + S_{n-1}^k\right)}{1+\frac{\lambda\phi}{N_n^{k+1}}\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)}, \tag{4.4.42}$$

respectively. For $0 \leq I_n^k \leq N_n^k \leq K$, from Theorem 4.4.3 and $(4.4.41)$, we have $N_n^{k+1} \geq 0$ and $I_n^{k+1} \geq 0$. Similarly, Equation $(4.4.42)$ gives $0 \leq S_n^{k+1}$ whenever $0 \leq S_n^k \leq N_n^k \leq K$. Thus, from

$$S_n^{k+1} + I_n^{k+1} = N_n^{k+1},$$

we have

$$0 \leq I_n^{k+1},\ S_n^{k+1} \leq N_n^{k+1} \leq K.$$

This completes the proof. □

Theorem 4.4.5 is of course valid for traveling wave solution when $N = K$ is constant. More importantly, in this case, we have the next result where the condition between step sizes is more relaxed.

Theorem 4.4.6. *Under the functional relation* $(4.4.40)$, *the NSFD scheme* $(4.4.33)$ *replicates the positivity and boundedness properties of the exact solution. More precisely,*

$$0 \leq I_n^k \leq K(1-\frac{1}{\mathcal{R}_0}) \quad \Rightarrow \quad 0 \leq I_n^{k+1} \leq K(1-\frac{1}{\mathcal{R}_0}), \tag{4.4.43}$$

and $$K(1-\frac{1}{\mathcal{R}_0}) \leq I_n^k \leq K \Rightarrow K(1-\frac{1}{\mathcal{R}_0}) \leq I_n^{k+1} \leq K. \tag{4.4.44}$$

Proof: By using $(4.4.40)$, Equation $(4.4.33)$ reduced into

$$I_n^{k+1} = K(1-\frac{1}{\mathcal{R}_0})\frac{\frac{1}{2}(I_{n+1}^k+I_{n-1}^k)+\phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)}{K(1-\frac{1}{\mathcal{R}_0})+\phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)}. \quad (4.4.45)$$

By using the assumption $0 \leq I_n^k \leq K(1-\frac{1}{\mathcal{R}_0})$, we get the inequality:

$$\frac{I_{n+1}^k+I_{n-1}^k}{2} \leq K(1-\frac{1}{\mathcal{R}_0}). \quad (4.4.46)$$

Adding

$$\phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)$$

in both sides of Equation $(4.4.46)$, after some manipulations, gives

$$\frac{\frac{1}{2}\left(I_{n+1}^k+I_{n-1}^k\right)+\phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)}{K(1-\frac{1}{\mathcal{R}_0})+\phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)} \leq 1.$$

This combined with $(4.4.45)$ yields

$$I_n^{k+1} \leq K(1-\frac{1}{\mathcal{R}_0}).$$

On the other hand, assume that $K(1-\frac{1}{\mathcal{R}_0}) \leq I_n^k \leq K$. By using the relations

$$K(1-\frac{1}{\mathcal{R}_0}) = K(1-\frac{1}{\mathcal{R}_0})\frac{K(1-\frac{1}{\mathcal{R}_0})+\phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)}{K(1-\frac{1}{\mathcal{R}_0})+\phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)},$$

and $K(1-\frac{1}{\mathcal{R}_0}) \leq \frac{1}{2}(I_{n+1}^k+I_{n-1}^k)$ with Equation $(4.4.45)$, we obtain

$$K(1-\frac{1}{\mathcal{R}_0}) \leq I_n^{k+1}.$$

Further simplification of $(4.4.45)$ gives

$$I_n^{k+1} = K\frac{(1-\frac{1}{\mathcal{R}_0})\frac{1}{2}(I_{n+1}^k+I_{n-1}^k)+(1-\frac{1}{\mathcal{R}_0})\phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)}{K(1-\frac{1}{\mathcal{R}_0})+\phi(\lambda-\mu-\gamma)\left(\frac{I_{n+1}^k+I_n^k+I_{n-1}^k}{3}\right)} \leq K,$$

since $\frac{I_{n+1}^k+I_{n-1}^k}{2} \leq K$. □

To conclude this chapter, we illustrate for the NSFD scheme $(4.4.15)$ its dynamical consistency with respect to positivity and boundedness, as stated in Theorem 4.4.4 (Fig 4.3).

In Fig 4.4, the same thing is done for the NSFD scheme $(4.4.31)$ whose properties are given in Theorems 4.4.5 and 4.4.6. In both examples, we took $\lambda = 1.3,\ \mu = \gamma = 0.2,\ K = 100$ so that $\mathcal{R}_0 = 3.1$. The initial conditions are taken to be $N_0(x) = 10 + 10\sin(2\pi x/5)$ and $I_0(x) = 10 + 10\sin(2\pi x/5)$. The figures show that the positivity and boundedness properties are indeed preserved.

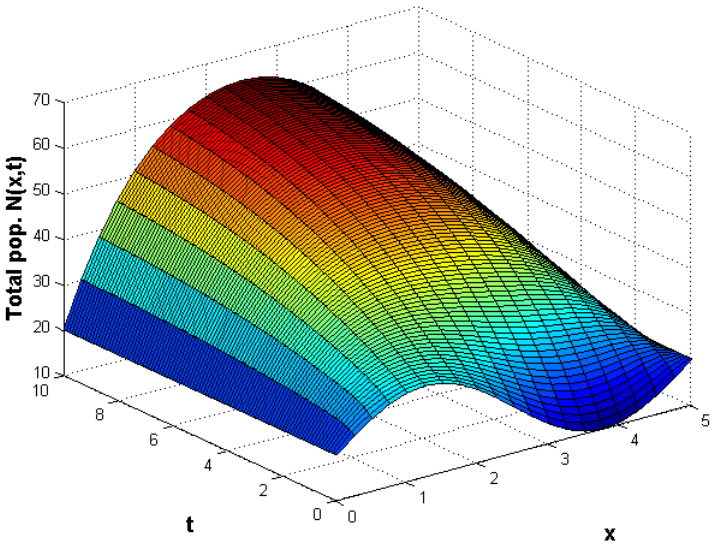


Figure 4.3: NSFD scheme $(4.4.15)$ and Theorem 4.4.4.

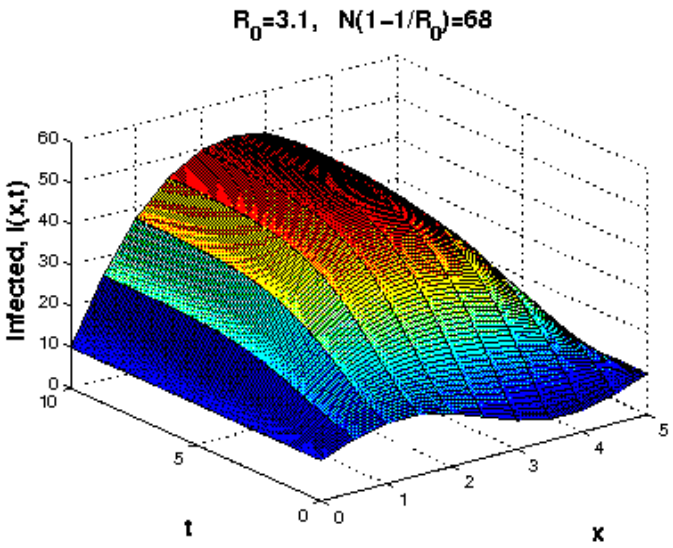


Figure 4.4: NSFD scheme $(4.4.31)$ and Theorem 4.4.6.

Chapter 5

SIS–Volterra Integral Equation Model

5.1 Introduction

In the previous chapter, the classical SIS model which is equivalent to a specific class of Volterra integral equations, was extended to a diffusion-reaction partial differential equation to govern the spread of disease in space. In this chapter, we go a bit further in the formulation of the SIS model by using some more general Volterra integral equations of the second kind where the contact rate is assumed to be a function of the infective individuals.

One of the main advantages of this approach is that the period of infectivity is incorporated in the model. Furthermore, the formulation by Volterra integral equations permits us to exhibit important biological phenomena, which do not arise in the simple setting of the classical SIS model. These include the existence of one or multiple endemic equilibria, which could be locally asymptotically stable even though the basic reproduction number is less than the threshold value 1. This refers to the so-called backward bifurcation phenomenon. Usually, for epidemiological models defined by a system of ordinary differential equations, the backward bifurcation phenomenon arises when there are multiple strains of the disease and there are multiple compartments of infective individuals [3, 24].

This chapter is meant to be a "simple" introduction to the role of Volterra integral equations in epidemiology. We restrict the study to the SIS model following the work of [57]. Our main focus is firstly on the existence and uniqueness of solutions of Volterra integral equations (Section 5.2). Secondly, we formulate the SIS-Volterra integral equation model in Section 5.3. This is followed by Section 5.4 where we demonstrate theoretically

and computationally the existence of multiple endemic equilibria. The stability analysis of equilibria of Volterra integral equations is omitted from this introductory study. We will undertake this study elsewhere.

5.2 Generalities on Volterra Integral Equations

In this section, we essentially gather the material that is needed to prove well-posedness results. This will then be applied to the epidemiological model considered in the next section. Our standard reference in this section is [12].

Let $f : [0,\ a] \to \mathbb{R}$ and $g : \Delta_a \times \mathbb{R} \to \mathbb{R}$ be given functions where Δ_a is the triangle

$$\Delta_a := \{(t, s) \in \mathbb{R}^2 : 0 \leq s \leq t < a\}.$$

We are interested in finding a function $x : [0,\ a] \to \mathbb{R}$ such that

$$x(t) = f(t) + \int_0^t g(t, s, x(s))ds. \tag{5.2.1}$$

Notice that the number a can be finite or infinite. In the later case, we consider the interval $[0,\ \infty)$ instead of $[0,\ \infty]$ and we write Δ instead of Δ_∞. Furthermore, we assume that the integral in $(5.2.1)$ is convergent.

Definition 5.2.1. *Equation $(5.2.1)$ is called a Volterra integral equation of the second kind. When the unknown function is not involved outside the integral symbol, i.e*

$$0 = f(t) + \int_0^t g(t, s, x(s))ds,$$

the equation is referred to as the Volterra integral equation of the first kind.

Remark 5.2.2. *The fundamental difference between Volterra integral equations and ordinary differential equations is seen on differentiating formally Equation $(5.2.1)$ with respect to the variable t. Indeed, in doing so, we obtain the following relation which is the so-called integro-differential equation:*

$$x'(t) = f'(t) + g(t, t, x(t)) + \int_0^t \frac{\partial g}{\partial t}(t, s, x(s))ds. \tag{5.2.2}$$

Without any assumption on the data f and g, there is no hope for the Volterra integral equation $(5.2.1)$ to have a solution. In order to deal with the important aspect of existence and uniqueness of solutions, we start with the following concept.

Definition 5.2.3. *A real-valued function $g = g(t, s, x)$ defined on $\Delta_a \times \mathbb{R}$ is said to be globally Lipschitz in the third argument provided that there exists a constant $L \geq 0$, called Lipschitz constant, such that*

$$|g(t, s, x_1) - g(t, s, x_2)| \leq L|x_1 - x_2| \tag{5.2.3}$$

for any (t, s, x_1) and (t, s, x_2) in the set $\Delta_a \times \mathbb{R}$.

Theorem 5.2.4. *Assume that $f : [0, \infty) \to \mathbb{R}$ and $g : \Delta \times \mathbb{R} \to \mathbb{R}$ are bounded continuous functions such that g is globally Lipschitz in the sense of Definition 5.2.3. Then there exists a continuous function $x : [0, \infty) \to \mathbb{R}$, which is the unique solution of the Volterra integral equation $(5.2.1)$.*

Proof: We employ the Banach contraction principle (see [60]). To this end, we introduce the space $C_k([0,\ \infty);\ \mathbb{R})$ consisting of continuous real-valued functions $x : [0,\ \infty) \to \mathbb{R}$ such that $\sup_{t\in[0,\ \infty)} e^{-kt}|x(t)| < \infty$. The number k will be determined shortly.

It is clear that $C_k([0,\ \infty);\ \mathbb{R})$ is a Banach space under the norm

$$\|x\|_{C_k} := \sup_{0\leq t<\infty} e^{-kt}|x(t)|.$$

We consider the operator Φ on $C_k([0,\ \infty);\ \mathbb{R})$ defined by

$$(\Phi x)(t) = f(t) + \int_0^t g(t, s, x(s))ds. \tag{5.2.4}$$

It is also clear that solving $(5.2.1)$ is equivalent to finding fixed-points of the operator Φ:

$$\Phi x = x.$$

Since f and g are bounded functions, the obviously continuous function $t \rightsquigarrow (\Phi w)(t)$ belongs to the space $C_k([0,\ \infty);\ \mathbb{R})$ if $w \in C_k([0,\ \infty);\ \mathbb{R})$. Thus, Φ operates from $C_k([0,\ \infty);\ \mathbb{R})$ into $C_k([0,\ \infty);\ \mathbb{R})$.

Using the Lipschitz condition in Definition 5.2.3, with Lipschitz constant L, we have

for $v,\ w \in C_k([0,\ \infty);\ \mathbb{R})$:

$$\begin{aligned}
|(\Phi v)(t) - (\Phi w)(t)| &\leq \int_0^t |g(t,\ s,\ v(s)) - g(t,s,w(s))|ds \\
&\leq L\int_0^t |v(s) - w(s)|ds \\
&= L\int_0^t e^{ks}e^{-ks}|v(s) - w(s)|ds \\
&\leq L\|v - w\|_{C_k}\int_0^t e^{ks}ds. \\
&\leq \frac{L}{k}\|v - w\|_{C_k}e^{kt}.
\end{aligned}$$

Thus

$$e^{-kt}|(\Phi v)(t) - (\Phi w)(t)| \leq \frac{L}{k}\|v - w\|_{C_k}$$

and

$$\|\Phi v - \Phi w\|_{C_k} \leq \frac{L}{k}\|v - w\|_{C_k}.$$

For the choice $k > L,\ \Phi$ is a contraction and has therefore a unique fixed point, solution of Equation $(5.2.1)$. □

In the next result, we get rid of the boundedness assumption that was used in Theorem 5.2.4.

Theorem 5.2.5. *Assume that $f : [0,\infty) \to \mathbb{R}$ and $g : \Delta \times \mathbb{R} \to \mathbb{R}$ are continuous functions such that g is globally Lipschitz in the sense of Definition 5.2.3. Then there exists a continuous function $x : [0,\infty) \to \mathbb{R}$, which is the unique solution of the Volterra integral equation $(5.2.1)$.*

Proof: The difficulty to use the proof of Theorem 5.2.4 is in showing that the space $C_k([0,\ \infty);\ \mathbb{R})$ is invariant under the operator Φ defined in Equation $(5.2.4)$.

To overcome this difficulty, we fix a time $T > 0$ and consider rather the space $C_k([0,\ T];\ \mathbb{R})$ of continuous real–valued functions on $[0,\ T]$ equipped with the structure of Banach space through the norm

$$\|x\|_{C_k} := \sup_{0\leq t\leq T} e^{-kt}|x(t)|.$$

Then proceeding as in the proof of Theorem 5.2.4, $\Phi :\ C_k([0,\ T];\mathbb{R}) \to C_k([0,\ T];\mathbb{R})$ is, for an appropriate choice of $k > 0$, a contraction that admits a unique fixed point

$x \in C_k([0,\ T];\mathbb{R})$, which is the unique solution of the Volterra integral equation $(5.2.1)$ for $0 \leq t \leq T$.

Define

$$T_m = mT, \quad m = 0,\ \ 1,\ \ 2,\ \ \ldots\ \ .$$

What we did earlier can be rephrased as follows: There exists a continuous function $x_1 : [0,\ T_1] \to \mathbb{R}$, which is the unique solution of the Volterra integral equation $(5.2.1)$ for $0 \leq t \leq T_1$:

$$x_1(t) = f(t) + \int_0^t g(t, s, x_1(s))ds, \qquad h_0(t) = f(t), \quad 0 \leq t \leq T_1. \tag{5.2.5}$$

We want to obtain a solution x_2 of the Volterra integral equation $(5.2.1)$ for $0 \leq t \leq T_2$ such that

$$x_2(t) = x_1(t) \quad \text{for} \quad 0 \leq t \leq T_1.$$

We look first at the restriction of $x_2(t)$ to $T_1 \leq t \leq T_2$, which we denote by $x_2^*(t)$:

$$x_2^* := x_2|_{[T_1,\ T_2]}.$$

By translation, we have for $0 \leq t \leq T_1$:

$$\begin{aligned} x_2^*(t+T_1) &= f(t+T_1) + \int_0^{t+T_1} g(t+T_1, s, x_2(s))ds \\ x_2^*(t+T_1) &= h_0(t+T_1) + \int_0^{T_1} g((t+T_1, s, x_1(s)))ds \\ &+ \int_{T_1}^{t+T_1} g(t+T_1, s, x_2^*(s))ds. \end{aligned} \tag{5.2.6}$$

Thus, for $T_1 \leq t \leq T_2$, we have

$$x_2^*(t) = h_1(t) + \int_{T_1}^t g(t, s, x_2^*(s))ds, \tag{5.2.7}$$

where

$$h_1(t) = h_0(t) + \int_0^{T_1} g(t, s, x_1(s))ds. \tag{5.2.8}$$

As we did before, we can define a contraction operator $\Phi : C_k([T_1,\ T_2];\ \mathbb{R}) \to C_k([T_1,\ T_2];\ \mathbb{R})$ whose fixed point $x_2^* \in C_k([T_1,\ T_2];\ \mathbb{R})$ is the unique solution of the integral equation $(5.2.7)$. The required solution of the Volterra integral equation $(5.2.1)$ for $0 \leq t \leq T_2$ is then defined by

$$x_2 = x_1 \cup x_2^* \quad \text{i.e} \quad x_2(t) = \begin{cases} x_1(t), & \text{if} \quad 0 \leq t \leq T_1 \\ x_2^*(t), & \text{if} \quad T_1 \leq t \leq T_2. \end{cases}$$

Assume by induction that two sequences $(h_0,\ h_1,\ \ldots,\ h_{m-1})$ and $(x_1,\ x_2,\ \ldots,\ x_m)$ of continuous functions have been constructed such that for $T_{i-1} \leq t \leq T_i$, $i = 2,\ 3,\ \ldots, m$, the following holds:

$$h_{i-1}(t) = h_{i-2}(t) + \int_0^{T_{i-1}} g(t, s, x_{i-1}(s)ds,$$

and

$$x_i(t) = \begin{cases} x_{i-1}(t), & \text{if} \quad 0 \leq t \leq T_{i-1} \\ x_i^*(t), & \text{if} \quad T_{i-1} \leq t \leq T_i, \end{cases}$$

where, x_i^* is the unique solution of the integral equation

$$x_i^*(t) = h_{i-1}(t) + \int_{T_{i-1}}^t g(t, s, x_i^*(s))ds,$$

and x_i is the unique solution of the Volterra integral equation $(5.2.1)$ for $0 \leq t \leq T_i$.

To construct the functions h_m, x_{m+1}^* and x_{m+1}, we proceed as we did for the construction of x_2 from x_1. More precisely, we want to obtain the solution x_{m+1} of the Volterra integral equation $(5.2.1)$ for $0 \leq t \leq T_{m+1}$, such that

$$x_{m+1}(t) = x_m(t), \quad \text{for} \quad 0 \leq t \leq T_m.$$

The restriction of x_{m+1} to $[T_m, T_{m+1}]$ is denoted by

$$x_{m+1}^* := x_{m+1}|_{[T_m,\ T_{m+1}]}.$$

By translation, we have for $0 \leq t \leq T$,

$$\begin{aligned} x_{m+1}^*(t + T_m) &= f(t + T_m) + \int_0^{t+T_m} g(t + T_m, s, x_{m+1}(s))ds \\ x_{m+1}^*(t + T_m) &= h_0(t + T_m) + \int_0^{T_m} g((t + T_m, s, x_m(s))ds \\ &+ \int_{T_m}^{t+T_m} g(t + T_1, s, x_{m+1}^*(s))ds. \end{aligned} \tag{5.2.9}$$

Thus, for $T_m \leq t \leq T_{m+1}$, we have

$$x_{m+1}^*(t) = h_m(t) + \int_{T_m}^t g(t, s, x_{m+1}^*(s))ds, \tag{5.2.10}$$

where

$$h_m(t) = h_{m-1}(t) + \int_0^{T_m} g(t, s, x_m(s))ds. \tag{5.2.11}$$

As we did previously, we can define a contraction operator

$$\Phi : C_k([T_m,\ T_{m+1}];\ \mathbb{R}) \to C_k([T_m,\ T_{m+1}];\ \mathbb{R})$$

whose fixed point $x^*_{m+1} \in C_k([T_m,\ T_{m+1}];\ \mathbb{R})$ is the unique solution of the integral equation $(5.2.10)$. The required solution x_{m+1} of the Volterra integral equation $(5.2.1)$ for $0 \le t \le T_{m+1}$ is then given by

$$x_{m+1} = x_m \cup x^*_{m+1} \quad \text{i.e} \quad x_{m+1}(t) = \begin{cases} x_m(t), & \text{if} \quad 0 \le t \le T_m \\ x^*_{m+1}(t), & \text{if} \quad T_m \le t \le T_{m+1}, \end{cases}$$

Hence, we have by induction constructed a sequence $(x_m)_{m\ge1}$ of continuous functions $x_m : [0,\ T_m] \to \mathbb{R}$ that are the unique solutions of the Volterra integral equation $(5.2.1)$ and that satisfy the compatibility condition

$$x_{m+1}|_{[0,\ T_m]} = x_m.$$

Since

$$\bigcup_{m\ge0} [T_m,\ T_{m+1}] = [0,\ \infty),$$

the function

$$x(t) := \bigcup_{m\ge1} x_m(t) : [0,\ \infty) \to \mathbb{R}$$

is the unique solution of $(5.2.1)$. □

In practice, the global Lipschitz requirement is weakened as follows.

Definition 5.2.6. *With the notation in Definition 5.2.3, a function g is said to be locally Lipschitz in the third argument provided that g restricted to any $\Delta_a \times [-b,\ b]$, where $b > 0$, is Lipschitz in the third argument. That is, the inequality $(5.2.3)$ is valid for (t, s, x_1) and (t, s, x_2) in $\Delta_a \times [-b,\ b]$, with the constant L depending on b : $L \equiv L_b$.*

Theorem 5.2.7. *Let $a > 0$ and $b > 0$. Consider the compact set*

$$U_{a,\ b,\ f} := \{(t, s, x) \in \Delta_a \times \mathbb{R} : \quad |x - f(t)| \le b\}.$$

Assume that

1. *the function f is continuous on [0,a].*

2. *the function g is continuous on $U_{a,\,b,\,f}$.*

3. *the function $g : U_{a,\,b,\,f} \to \mathbb{R}$ is Lipschitz in the third argument x with Lipschitz constant $L \equiv L_{b,\,f} > 0$ not depending on the first two arguments.*

Then the Volterra integral equation $(5.2.1)$ has a unique solution on $[0, T]$, where

$$T = \min\{a,\ \frac{b}{1 + \max_{(t,s,x)\in U_{a,\,b,\,f}} |g(t, s, x)|}\}.$$

Proof: We will, as in the previous situations, employ the fixed point theorem. But, this time C_k is the set (not space) of continuous functions from $[0, T]$ into

$$V = \{x \in \mathbb{R} : |x - f(t)| \leq b \ \ \forall t \in [0, a]\ \},$$

where k will be fixed shortly. We equip C_k with the structure of a metric space through the distance defined by

$$d_k(v, w) = \sup_{0\leq t\leq T} e^{-kt}|v(t) - w(t)|.$$

Since the set $V \subset \mathbb{R}$ is compact, the metric space C_k is complete. Similarly to $(5.2.4)$, we define on C_k the operator Φ:

$$(\Phi v)(t) = f(t) + \int_0^t g(t, s, v(s))ds, \qquad 0 \leq t \leq a. \tag{5.2.12}$$

We claim that Φ operates from C_k into C_k. Indeed, for $v \in C_k$, the continuity of Φv is obvious. Furthermore, we have

$$\begin{aligned} |(\Phi v)(t) - f(t)| &\leq \int_0^t |g(t, s, v(s))|ds, \\ &\leq \max_{(t,s,x)\in U_{a,b,f}} |g(t, s, x)|T, \\ &\leq b. \qquad \text{(by definition of T)} \end{aligned}$$

On the other hand, we have for $v,\ w \in C_k$,

$$\begin{aligned}
|(\Phi v)(t) - (\Phi w)(t)| &\leq \int_0^t |g(t,s,v(s)) - g(t,s,w(s))|ds, \\
&\leq L\int_0^t |v(s) - w(s)|ds, \\
&= L\int_0^t e^{ks}e^{-ks}|v(s) - w(s)|ds, \\
&\leq L \sup_{0\leq s\leq T} e^{-ks}|v(s) - w(s)| \int_0^t e^{ks}ds, \\
&= L \sup_{0\leq s\leq T} e^{-ks}|v(s) - w(s)|\frac{e^{kt}-1}{k}, \\
&\leq \frac{L}{k} \sup_{0\leq s\leq T} e^{-ks}|v(s) - w(s)|e^{kt}.
\end{aligned}$$

Thus,

$$\sup_{0\leq t\leq T} e^{-kt}|(\Phi v)(t) - (\Phi w)(t)| \leq \frac{L}{k} \sup_{0\leq t\leq T} e^{-kt}|v(t) - w(t)|$$

and

$$d_k(\Phi v, \Phi w) \leq \frac{L}{k} d_k(v,w).$$

By choosing k such that $k > L,\ \Phi$ is a contraction on C_k. Hence, the contraction mapping theorem guarantees the existence of a unique solution for the Volterra integral equation $(5.2.1)$. $\square$.

While the global Lipschitz requirement in Theorem 5.2.4 and Theorem 5.2.5 are too strong, the local existence and uniqueness Theorem 5.2.7 is equally not interesting, because the end time is finite. In what follows, we establish the existence and uniqueness of a global solution under realistic assumptions.

Theorem 5.2.8. *Let $f : [0,\infty) \to \mathbb{R}$ be continuous. Let $g : \Delta \times \mathbb{R} \to \mathbb{R}$ be a continuous function which is locally Lipschitz in the third argument and bounded in $(s,t) \in \triangle$. Assume that there exists a constant $M > 0$ such that*

$$\sup_{0\leq s\leq t} |x(s) - f(s)| \leq M \tag{5.2.13}$$

for any time $t \geq 0$ where a solution $x(t)$ of Equation $(5.2.1)$ exists. Then the Volterra integral equation $(5.2.1)$ admits one and only one solution defined on the interval $[0,\infty)$.

Proof: Fix $a > 0$ and define $b := \sup_{0\leq t\leq a} |f(t)|$. With $\epsilon > 0$ sufficiently small, we associate U_ϵ, the ϵ-neighborhood of $U_{a,b,f}$ given by

$$U_\epsilon := \{(t, s, x + x_\varepsilon) : \ 0 \leq s \leq t \leq a; \ |x - f(t)| \leq b; \ |x_\epsilon| \leq \epsilon\}.$$

By the assumption made in the theorem, the function $g : U_\epsilon \to \mathbb{R}$ is locally Lipschitz in the third argument with Lipschitz constant independent on $(s,\ t)$ and denoted by L_ϵ. By Theorem 5.2.7, there exists a unique solution $x(t)$ of the Volterra integral equation $(5.2.1)$ on $[0, T_\epsilon]$ for some finite time $T_\epsilon > 0$. Note that this solution must satisfy the relation $(5.2.13)$ for $t = T_\epsilon$.

For $m = 0,\ 1,\ 2,\ ...,$ we define

$$T_m = m \times \min\{a,\ \frac{\epsilon}{\sup\{|g(t, s, x)| : (t, s) \in \triangle,\ \ |x - f(t)| \leq b\}}\}.$$

As in the proof of Theorem 5.2.5, we let C_k be the set of continuous function from $[T_m,\ T_{m+1}]$ into $V_\epsilon = \{x + x_\epsilon \in \mathbb{R} : \ |x - f(t)| \leq b,\ |x_\epsilon| \leq \epsilon\}$. We equip C_k with the structure of a complete metric space via the distance d_k given by

$$d_k(v, w) = \sup_{t\in[T_m,T_{m+1}]} e^{-kt}|v(t) - w(t)|,$$

where k is determined by proceeding as in the proof of Theorem 4.2.4 to get a contraction operator $\Phi : C_k([0,\ T_\epsilon];\ V_\epsilon) \to C_k([0,\ T_\epsilon];\ V_\epsilon)$ such that its fixed point is the unique solution of $(5.2.1)$.

As we did in the proof of Theorem 5.2.5, define the operator Φ on $C_k([T_m,\ T_{m+1}];\ V_\epsilon)$ whose fixed–point x^*_{m+1} is the unique solution of the integral equation $(5.2.10)$. Thus, the solution x_{m+1} of the Volterra integral equation $(5.2.1)$ for $t \in [0,\ T_{m+1}]$ is given by

$$x_{m+1}(t) = \begin{cases} x_m(t), & \text{if} \quad 0 \leq t \leq T_m \\ x^*_{m+1}(t), & \text{if} \quad T_m \leq t \leq T_{m+1}, \end{cases}$$

Hence, by mathematical induction principle, we constructed a sequence $(x_m)_{m\geq 1}$ of continuous function

$$x_m : [0,\ T_m] \to V_\epsilon$$

which is the unique solution of the Volterra integral equation $(5.2.1)$.

Since

$$\bigcup_{m\geq 0} [T_m,\ T_{m+1}] = [0, \infty),$$

the function

$$x := \bigcup_{m\geq 0} x_m : [0,\ \infty) \to V_\epsilon$$

is the unique solution of the Volterra integral equation $(5.2.1)$. In view of $(5.2.13)$, $x(t)$ satisfies $|x(t) - f(t)| \leq M$ for all $t \in [0, \infty)$. □

Remark 5.2.9. *If the boundedness assumption on the function $g(t, s, x)$ is not satisfied, the argument similar to that in the proof of Theorem 5.2.8 shows that we can obtain a sequence of times $(T_m)_{m\geq 0}$ of which two consecutive times are not equally distanced and such that $\bigcup_{m\geq 0}[T_m,\ T_{m+1}] \neq [0,\ \infty)$. Thus, the integral equation $(5.2.1)$ has a unique non-global solution x on $\bigcup_{m\geq 0}[T_m,\ T_{m+1}]$.*

As for ordinary differential equations, the qualitative analysis of Volterra integral equations amounts to comparing solutions with simple solutions. The simplest of such solutions are equilibrium points as defined as follows.

Definition 5.2.10. *For a Volterra integral equation $(5.2.1)$, a point $\bar{x} \in \mathbb{R}$ is called an equilibrium solution if the constant function $x(t) = \bar{x},\quad t \geq 0$, is solution of the integral equation:*

$$\bar{x} = f(t; \bar{x}) + \int_0^t g(t, s, \bar{x})ds.$$

Despite the fact that we intend to consider the qualitative analysis of Volterra integral equations in our further work, it is worthwhile to specify here the stability of equilibrium points. This is done in the next definition.

Definition 5.2.11. $[12]$ *Let $\bar{x}$ be an equilibrium solution of Equation $(5.2.1)$ where $f : [0,\ \infty) \to \mathbb{R}$ represents any possible initial function.*

1. *The equilibrium $\bar{x}$ is (Lyapunov) stable if, for each $\epsilon > 0$ and $t_0 \geq 0$, there exists $\delta \equiv \delta(\epsilon,\ t_0) > 0$ such that for any f satisfying*

$$|f(t) - \bar{x}| < \delta \quad \text{for} \quad t \in [0, t_0], \quad \text{we have} \quad |x(t, f) - \bar{x}| < \epsilon$$

for all $t \geq t_0$, where the function $x(t) \equiv x(t, f)$ is solution of the Volterra integral equation $(5.2.1)$.

2. *The equilibrium $\bar{x}$ is uniformly stable if, for each $\epsilon > 0$, there exists $\delta \equiv \delta(\epsilon) > 0$ such that for $t_0 \geq 0$ and f satisfying*

$$|f(t) - \bar{x}| < \delta \quad \text{for} \quad t \in [0, t_0], \quad \text{we have} \quad |x(t, f) - \bar{x}| < \epsilon$$

for all $t \geq t_0$.

3. *The equilibrium $\bar{x}$ is locally asymptotically stable if it is stable and if for each $t_0 \geq 0$, there exists $\eta \equiv \eta(t_0) > 0$ such that for f satisfying*

$$|f(t) - \bar{x}| < \eta \quad \text{for} \quad t \in [0, t_0], \quad \text{we have} \quad \lim_{t \to \infty} x(t, f) = \bar{x}.$$

If the limit holds for any initial function f, $\bar{x}$ is said to be globally asymptotically stable.

4. *The equilibrium $\bar{x}$ is uniformly asymptotically stable, if it is uniformly stable and if there exists a number $\eta > 0$(independent of t_0) such that, for $t_0 \geq 0$, f satisfying*

$$|f(t) - \bar{x}| < \eta \quad \text{for} \quad t \in [0, t_0], \quad \text{we have} \quad \lim_{t \to \infty} x(t, f) = \bar{x}.$$

5.3 Model Formulation

In this section, we consider an extension of the classical SIS model in terms of the Volterra integral equation. The study is based on the paper [57] and is aimed at a better understanding of this work. We will therefore elaborate whenever it is necessary and clarify some of the concepts that are used .

As a motivation to this section, we consider the classical SIS model investigated in Chapter 3. To simplify the presentation, we make once and for all the following assumptions:

- There is no death induced by the disease: $\alpha = 0$;
- The recruitment term by birth is μN with the birth and the natural death rate constants being both equal to $\mu > 0$;
- The rate of leaving infective class for susceptible class is $\gamma > 0$.

Under these assumptions, the total population

$$N = S + I \tag{5.3.1}$$

is constant. As we did in Section 3.4, the SIS system can be written in terms of fractions $i = \frac{I}{N}$ and $s = \frac{S}{N}$ as dependent variables (see $(3.4.30) - (3.4.31)$):

$$s' = \mu - Csi - \mu s + \gamma i \tag{5.3.2}$$

$$i' = Csi - (\mu + \gamma)i. \tag{5.3.3}$$

Clearly, the system $(5.3.2) - (5.3.3)$ is equivalent to the scalar equation

$$i' = Ci(1 - i) - (\mu + \gamma)i, \tag{5.3.4}$$

which takes the following equivalent form in terms of the basic reproduction number

$$\mathcal{R}_0 = \frac{C}{\mu + \gamma} : \tag{5.3.5}$$

$$i' = C(1 - i)i\left(1 - \frac{1}{\mathcal{R}_0(1 - i)}\right). \tag{5.3.6}$$

By the fundamental theorem of calculus, Equation $(5.3.6)$ is equivalent to the following Volterra integral equation of the second kind:

$$i(t) = i_0 + \int_0^t C\left[1 - i(u)\right] i(u)\left(1 - \frac{1}{\mathcal{R}_0(1 - i(u))}\right) du. \tag{5.3.7}$$

In Equation $(5.3.7)$, the integrand is the balance of infected individuals that are entering or leaving the infective class at time $0 \leq u \leq t$. More precisely, if $\mathcal{R}_0 < 1$, then we will have infected individuals continuously leaving the infective class until the disease dies out. On the contrary, if $\mathcal{R}_0 > 1$, then we will have infected individuals entering into the infective class. This interpretation of Equation $(5.3.7)$ is the basis of its extension that we will present now. But, before we get there, it is worth mentioning that $C \equiv C(N)$ in $(5.3.7)$ is a constant because N is constant. Therefore, it is impossible to subject C to the conditions $(3.2.1) - (3.2.4)$. What makes sense is to assume that the contact rate is a function of infective individuals, namely

$$\lambda \equiv \lambda(i) \geq 0 \quad \text{for} \quad i \in [0, 1]. \tag{5.3.8}$$

Other conditions on the contact rate $\lambda(i)$ will be stated later.

Let us now come back to the issue of extending $(5.3.7)$. In view of the fact that the variable u runs from the time 0 to the time t, it is realistic to incorporate the infectivity period or duration in the model. To this end, with $i(u)$, representing the fraction of infective individuals at time $u \geq 0$, we associate the following notation and definitions:

- For $0 \leq u \leq t$, $P_u(t)$ denotes the fraction of individuals that one infective individual has infected at time u and they remain infective through to time t;
- For $0 \leq u \leq t$, $p_u(t)$ denotes the probability for an individual to be infected at time u by one infective and to remain infective at least t time units before either dying or returning to the susceptible class;
- We adopt the following convention: $P(t) = P_0(t)$.

Let an initial value function $i_0 \equiv i_0(t), \quad 0 \leq t < \infty$ be given. That is for a fixed $t \geq 0$, $i_0(t)$ is the fraction of individuals that were infective at time 0 and have remained infective through to time t. Then the fraction of infective individuals at time $t \geq 0$ is given by the Volterra integral equation (of the second kind)

$$i(t) = i_0(t) + \int_0^t \lambda\left(i(u)\right)\left[1 - i(u)\right] i(u) P_u(t) p_u(t) du. \tag{5.3.9}$$

Note that the integral in $(5.3.9)$ sums the individuals that entered the infective class at time $u \geq 0$ and have remained infective through to time t. Indeed, $\lambda(i(u))\left[1 - i(u)\right] i(u)$ represents the individuals that enter the infective class at time $u \geq 0$, while $P_u(t)p_u(t)$ is the fraction of all individuals infected at time u by one infective individual and remained infective at least t time units before either dying or returning to the susceptible class.

Our next task is to make the Volterra integral equation $(5.3.9)$ explicit and meaningful. We start with the following assumptions:

$(D1)$ The contact rate $\lambda(i)$ is such that $\lambda(i) > 0$ on $(0, \infty)$, $\lambda(0) \geq 0$, $\lambda(i)$ is continuous and the rate of infection $\lambda(i)i(1-i)$ has a continuous derivative on its domain; (5.3.10)

$(D2)$ The function $P(t) \geq 0$ is non-increasing, differentiable for $t \geq 0$ and satisfies $P(0^+) = 1$; (5.3.11)

$(D3)$ The initial function $i_0(t) \geq 0$ is non-increasing, differentiable for $t \geq 0$ and satisfies $\lim_{t\to\infty} i_0(t) = 0.$ (5.3.12)

Lemma 5.3.1. *With $\mu > 0$ being the death rate and $\gamma > 0$ the recovery rate, we have the following results for $0 \leq u \leq t$:*

- *The kernel $P_u(t)p_u(t)$ in $(5.3.9)$ is of convolution type; more precisely:*

$$p_u(t) = p_0(t-u) = e^{-(\mu+\gamma)(t-u)} \tag{5.3.13}$$

$$P_u(t) = P(t-u). \tag{5.3.14}$$

Proof: To show the first part of $(5.3.13)$ and $(5.3.14)$, let $i_0 = i(0)$ represent individuals that are infective at time 0. As time progresses continuously from $s = 0$ to $s = t$, we know by definition that $P_0(t)$ is the fraction of individuals i_0 that were infected by one infective at time $s = 0$ and have remained infective through to time $s = t$. Now, if the process starts at time $r = u$ and ends at time $r = t$, we make the change of dependent variable $\tilde{i}(s) = i(s+u)$, where $0 \leq s := r - u \leq t - u$. Then the fraction $P_u(t)$ generated by one infective from $i(u)$ at time $r = u$ through to time $r = t$ is equal to the fraction $P_0(t-u) = P(t-u) = P_u(t)$ due to the same one infective from $i(u)$ at $s = 0$ through to time $s = t - u$. The second part of $(5.3.13)$ holds because the function $t \rightsquigarrow p_u(t)$ satisfies the following differential equation, (in accordance with Malthus law for the dynamics of population $[56]$):

$$\frac{dp_u(t)}{dt} = -(\mu+\gamma)p_u(t), \text{ with initial condition } p_u(0) = 1. \tag{5.3.15}$$

Indeed, following $[9]$, we have for small $h > 0$,

$$\begin{aligned} \frac{p_u(t+h) - p_u(t)}{h} &= \frac{p_u(t)p_t(t+h) - p_u(t)}{h} \\ &= -\frac{1 - p_t(t+h)}{h} p_u(t), \end{aligned}$$

where we make use of the semi-group property

$$p_r(t) = p_r(s)p_s(t) \quad \text{for} \quad r \leq s \leq t.$$

If we consider the limit of both sides as $h \to 0$, we get the differential equation $(5.3.15)$, because $1 - p_t(t+h)$ is by definition the probability of an individual to be removed from the infective class by natural death or recovery from time t to time $t+h$. □

Remark 5.3.2. *As a consequence of Lemma 5.3.1 and in accordance with standard definition in statistics* $[1]$*, the mean time an individual remains infective or the life expectancy of an individual or the expected value of the function* $P(u)$ *is given by the convergent integral*

$$\tau = \int_0^\infty P(u)e^{-(\mu+\gamma)u}du. \tag{5.3.16}$$

Note that the improper integral in $(5.3.16)$ is indeed convergent due to the assumptions made on the bounded function $P(t)$. Furthermore, in the language of ecologists $[1]$, the function $t \rightsquigarrow e^{-(\mu+\gamma)t}$ or more generally, the function $t \rightsquigarrow exp\left(-\int_0^t[\mu(s)+\gamma(s)]ds\right)$, when the death rate μ and the recovery rate γ are not constant is called the "survival function probability".

In view of the notation in Lemma 5.3.1, the Volterra integral equation $(5.3.9)$ becomes

$$i(t) = i_0(t) + \int_0^t \lambda\left[i(u)\right] i(u)\left[1-i(u)\right] P(t-u)e^{-(\mu+\gamma)(t-u)}du. \tag{5.3.17}$$

It should be noted that the presence of the variable t in the integrand makes the Volterra integral equation $(5.3.17)$ fundamentally different from the classical SIS model $(5.3.7)$. Indeed, if we formally differentiate Equation $(5.3.17)$, with respect to the time variable t, we obtain:

$$\begin{aligned}\frac{di}{dt}(t) &= \frac{di_0}{dt}(t) + \lambda\left[i(t)\right] i(t)\left[1-i(t)\right] \\ &+ \int_0^t \lambda\left[i(u)\right] i(u)\left[1-i(u)\right]\left(\frac{dP(t-u)}{dt} - (\mu+\gamma)\right) e^{-(\mu+\gamma)(t-u)}du.\end{aligned} \tag{5.3.18}$$

Thus, the Volterra integral equation $(5.3.17)$ is rather equivalent to the integro-differential equation $(5.3.18)$, which is more complicated than the ODE $(5.3.4)$ (for the study of integro-differential equation, see $[12]$ and $[58]$).

The well-posedness of the Volterra integral equation $(5.3.17)$ is considered in the next theorem.

Theorem 5.3.3. *Assume that the function* $i_0(t)$ *satisfying the assumption* $(D3)$ *or* $(5.3.12)$ *is such that* $0 \leq i_0(t) \leq 1$*. Then the Volterra integral equation* $(5.3.17)$ *admits a unique solution* $i : [0,\ \infty) \to \mathbb{R}$*, which is a continuous function satisfying the condition* $0 \leq i(t) \leq 1$ *on* $[0,\ \infty)$*. If in addition the datum* i_0 *is differentiable on* $[0,\ \infty)$*, then the solution* i *is differentiable on the same interval.*

Proof: To show the existence of a unique solution, we proceed as in the previous sections by introducing the space C_k of real–valued continuous functions from $[0,\ T]$

equipped with the Banach structure defined by the norm

$$\|v\|_{C_k} = \sup_{t\in[0,\,T]} e^{-kt}|v(t)|,$$

where $k > 0$ and T will be determined shortly.

Define G a subset of C_k by

$$\begin{aligned} G &= \{i \in C_k :\ |i(t) - i_0(t)| \le i_0(t) \qquad \forall\, t \in [0,\ T]\} \\ &= \{i \in C_k :\ 0 \le i(t) \le 2i_0(t) \quad \forall\, t \in [0,\ T]\}. \end{aligned}$$

Then the set G is nonempty, because $i = 0 \in G$. The set G is also a closed subset of C_k, because any convergent sequence in G has its limit in G.

On G, we define the operator Φ by

$$(\Phi i)(t) = i_0(t) + \int_0^t \lambda\,[i(u)]\,i(u)\,[1 - i(u)]\,P(t-u)e^{-(\mu+\gamma)(t-u)}du.$$

Then, we have for $i \in G$ and $0 \le t \le T$

$$\begin{aligned} |(\Phi i)(t) - i_0(t)| &= |\int_0^t \lambda\,[i(u)]\,i(u)\,[1 - i(u)]\,P(t-u)e^{-(\mu+\gamma)(t-u)}du|, \\ &\le t \sup_{s\in[0,\,2]} [1 + |\lambda(s)(1-s)|]\, 2 \sup_{u\in[0,\,t]} i_0(u), \\ &\le T \sup_{s\in[0,\,2]} [1 + |\lambda(s)(1-s)|]\, 2 \sup_{u\in[0,\,T]} i_0(u). \end{aligned}$$

We therefore take

$$T = \frac{1}{2\sup_{s\in[0,\,2]}[1 + |\lambda(s)(1-s)|]},$$

which implies that

$$|(\Phi i)(t) - i_0(t)| \le \sup_{u\in[0,\,T]} i_0(u)$$

and so Φ operates from G into G.

On the other hand, putting

$$g(t, u, i) = \lambda(i)i(1-i),$$

we have for $i_1,\ i_2 \in G$

$$\begin{aligned} |(\Phi i_1)(t) - (\Phi i_2)(t)| &= |\int_0^t [g(t,u,i_1) - g(t,u,i_2)]\,P(t-u)e^{-(\mu+\gamma)(t-u)}du| \\ &\le \int_0^t |g(t,u,i_1) - g(t,u,i_2)|\,P(t-u)e^{-(\mu+\gamma)(t-u)}du. \end{aligned}$$

Since g is Lipschitz on $[0,2]$ in the third argument in view of the assumption $(D1)$ or $(5.3.10)$ with Lipschitz constant denoted by L_G, we have

$$\begin{aligned}|(\Phi i_1)(t) - (\Phi i_2)(t)| &\leq L_G \int_0^t |i_1(u) - i_2(u)|du, \\ &= L_G \int_0^t e^{kt}e^{-kt}|i_1(u) - i_2(u)|du \\ &\leq L_G \|i_1 - i_2\|_{C_k} \int_0^t e^{kt}du \\ &\leq \frac{L_G}{k}\|i_1 - i_2\|_{C_k} e^{kt}.\end{aligned}$$

This gives $\|\Phi i_1 - \Phi i_2\|_{C_k} \leq \frac{L_G}{k}\|i_1 - i_2\|_{C_k}$. For the choice $k > L_G$, the operator Φ is a contraction. By Banach contraction principle, there exists a unique solution $i \in G$ such that

$$i(t) = i_0(t) + \int_0^t \lambda\left[i(u)\right] i(u)\left[1 - i(u)\right] P(t-u)e^{-(\mu+\gamma)(t-u)}du, \qquad 0 \leq t \leq T.$$

Using the translation method as in the proof of Theorem 5.2.8, it can be shown that the integral equation $(5.3.17)$ admits a global solution i which is continuous and satisfies the inclusion

$$0 \leq i(t) \leq 2 \quad \forall\, t \in [0,\ \infty).$$

From the condition $(5.3.1)$ or

$$s(t) + i(t) = 1, \quad t \geq 0 \tag{5.3.19}$$

of the model, the integral equation $(5.3.17)$ in i leads to the following integral equation in s:

$$s(t) = s_0(t) - \int_0^t \lambda[1 - s(u)]s(u)[1 - s(u)]P(t-u)e^{-(\mu+\gamma)(t-u)}du, \tag{5.3.20}$$

where $s_0(t) = 1 - i_0(t)$.

By duality, it follows using the previous reasoning, that there exists a unique continuous solution $s:\ [0,\ \infty) \to [0,\ 2]$ of the integral equation $(5.3.20)$. In view of $(5.3.19)$, we necessarily have $0 \leq i(t),\ s(t) \leq 1$.

When i_0 is differentiable, then the solution i is differentiable with its derivative being given by $(5.3.18)$, because the integral equation is a continuous function in u and the $t \rightsquigarrow P(t-u)e^{-(\mu+\gamma)(t-u)}$ is differentiable. $\square$.

Remark 5.3.4. *By the assumption* $(D3)$ *or* $(5.3.12)$*, we have* $i_0(t) = 0$ *for all* $t \geq 0$ *if* $i_0(0) = 0$*. In this case, the unique solution of the integral equation* $(5.3.17)$ *is the null function* $i \equiv 0$*. This solution is referred to here and after as the disease-free equilibrium. A nontrivial solution will then be obtained whenever* $i_0(0) > 0$*.*

Remark 5.3.5. *The proof of the positivity and boundedness of the solution* i *in* $[57]$ *and* $[29]$ *is not clear, since it is based on the assumption* $s \geq 0$*, which precisely need to be proved.*

5.4 Equilibrium Solutions

In order to do the qualitative study of the integro–differential equation $(5.3.18)$, it is essential by analogy with the classical SIS model $(5.3.2)-(5.3.3)$ or $(5.3.7)$ to rewrite $(5.3.17)$ in such a way that the parameter that characterizes the dynamics of this system is incorporated. The said characteristic parameter is the basic reproduction number $\mathcal{R}_0^*$ of the model. Using Equation $(3.2.17)$ of the basic reproduction number, we have

$$\mathcal{R}_0^* = \lambda(0)\tau, \tag{5.4.1}$$

where τ given in $(5.3.16)$ is the period of infectivity for a single infective individual, while $\lambda(0)$ assumed to be greater than 0, is the adequate contact per unit time made by a single infective near the disease-free equilibrium $i = 0$. However, since by assumption we can have $\lambda(0) = 0$, Equation $(5.4.1)$ for the definition $\mathcal{R}_0^*$ need to be adjusted. To this end, we introduce the parameter

$$\lambda_0 = \begin{cases} \lambda(0), & \text{if} \quad \lambda(0) > 0\ ; \\ 1, & \text{if} \quad \lambda(0) = 0. \end{cases}$$

The adjusted reproduction number to be used in what follows is then defined by

$$\mathcal{R}_0 = \lambda_0\tau. \tag{5.4.2}$$

For convenience, we also introduce the following notation in order to simplify the integrand in $(5.3.17)$ through an adjusted force of infection $f(i)$ and Kernel $\tilde{P}(t-u)$:

$$f(i) = \frac{1}{\lambda_0}\lambda(i)(1-i), \qquad 0 \leq i \leq 1; \tag{5.4.3}$$

$$\tilde{P}(t) = \frac{1}{\tau}P(t)e^{-(\mu+\gamma)t}, \qquad t \geq 0. \tag{5.4.4}$$

The Volterra integral equation $(5.3.17)$ can then be written in the form

$$i(t) \quad = \quad i_0(t) + \mathcal{R}_0 \int_0^t i(u) f(i(u)) \tilde{P}(t-u) du. \tag{5.4.5}$$

Proposition 5.4.1. *A real number $\underline{i} \in [0,1]$ is an equilibrium solution of the Volterra integral equation $(5.3.17)$ or $(5.4.5)$ if and only if*

$$\underline{i} = \mathcal{R}_0 \underline{i} f(\underline{i}). \tag{5.4.6}$$

Proof: Assume first that $i(t) = \underline{i}$ is a constant solution to Equation $(5.4.5)$ with the corresponding initial function denoted by $i_0(t) = i_0(t; \underline{i})$. Then we have

$$\underline{i} = i_0(t; \underline{i}) + \mathcal{R}_0 \underline{i} f(\underline{i}) \int_0^t \tilde{P}(t-u) du. \tag{5.4.7}$$

If we consider the limit of both sides of $(5.4.7)$ as t goes to infinity, we obtain the expression

$$\underline{i} = \mathcal{R}_0 \underline{i} f(\underline{i}), \qquad 0 \leq \underline{i} \leq 1,$$

in view of the assumption $(5.3.12)$ and of the formula

$$\int_0^\infty \tilde{P}(u) du = 1 \tag{5.4.8}$$

due to $(5.3.16)$ and $(5.4.4)$. Conversely, assume that $\underline{i}$ is a constant solution of $(5.4.6)$. Consider the function $i_0(t; \underline{i})$ defined by

$$i_0(t; \underline{i}) = \underline{i} - \mathcal{R}_0 \underline{i} f(\underline{i}) \int_0^t \tilde{P}(t-u) du.$$

Then this function meets the requirement $(D3)$ or $(5.3.12)$ due to $(5.4.6)$ and $(5.4.8)$. Furthermore, we have

$$\underline{i} = i_0(t; \underline{i}) + \mathcal{R}_0 \underline{i} f(\underline{i}) \int_0^t \tilde{P}(t-u) du,$$

which shows that $\underline{i}$ is a solution of $(5.4.5)$. □

Remark 5.4.2. *Note that $\underline{i} = 0$ always solves $(5.4.6)$ and is, as mentioned earlier in Remark 5.3.4, referred to as the disease-free equilibrium. Any $\underline{i} \in (0,1)$ that solves $(5.4.6)$ is called an endemic equilibrium; we denote an endemic equilibrium by i_e. In this case, $(5.4.6)$ leads to*

$$\mathcal{R}_0 f(i_e) = 1, \tag{5.4.9}$$

which is equivalent to saying that in the $i - y$ axes, the graph of the function $y = f(i)$ intersects with the horizontal line $y = \frac{1}{\mathcal{R}_0}$.

The last comment in Remark 5.4.2 regarding the role of the horizontal line $y = \frac{1}{\mathcal{R}_0}$ in the existence of endemic equilibria leads us to doing some analysis on the extremum values of the function $y = f(i)$. Being continuous on the compact interval $[0, 1]$, the function $i \rightsquigarrow f(i)$ admits a (global) maximum M and a minimum m values. Notice that from the explicit expression of f in $(5.4.3)$, we have

$$0 = m = f(c),$$

where $c = 1$ or $c = 0$ for $\lambda(0) = 0$. However, M is in general not explicitly known. In order to get further insight on the extremum values of f, we consider the next definition.

Definition 5.4.3. *Let $h : [a,\ b] \to \mathbb{R}$ be given for $a,\ b \in \mathbb{R}$. For a number $c \in (a,\ b)$, $h(c)$ is called a local maximum value of h on $[a,\ b]$ provided that there exists $\delta > 0$ such that $(c-\delta, c+\delta) \subset (a,\ b)$ and $h(x) \leq h(c)$ for all $x \in (c-\delta, c+\delta)$. In the case when we have the opposite inequality, $h(x) \geq h(c),\ \ \forall x \in (c-\delta,\ c+\delta)$, then the number $h(c)$ is called a local minimum value. The terminology global minimum / maximum is used whenever the above inequalities hold for $x \in [a,\ b]$.*

Since the function f in $(5.4.3)$ is differentiable on $(0,\ 1)$, the set $[0,\ 1]$ on which we are looking for its minimum and/or maximums can be reduced to a much smaller set in view of the following well-known result:

Theorem 5.4.4. *If a function $h : [a,\ b] \to \mathbb{R}$ has local maximum or minimum value at $c \in (a,\ b)$ and if $h'(c)$ exists, then c is a critical point of h. That is $h'(c) = 0$. Consequently, for $h : [a,\ b] \to \mathbb{R}$ continuous and differentiable on $(a,\ b)$, we have*

$$\max_{x \in [a,\ b]} h(x) = \max_{x \in B} h(x); \quad \min_{x \in [a,\ b]} h(x) = \min_{x \in B} h(x),$$

where

$$B = \{a\} \cup \{b\} \cup \{\ c \in (a,\ b)\ :\ h'(c) = 0\}.$$

Applying Theorem 5.4.4 to our function $f\ : [0,\ 1] \to \mathbb{R}$ given in $(5.4.3)$ and taking into account the fact that $f(1) = 0$, the global minimum, we exclude the right end-point 1 from the set B to obtain the set

$$A = \{0\} \cup \{\ c \in (0,\ 1)\ :\ f'(c) = 0\}, \tag{5.4.10}$$

for which we have

$$\max_{i\in[0,\,1]} f(i) = \max_{i\in A} f(i) =: \frac{1}{\mathcal{R}_0^c}. \tag{5.4.11}$$

In addition to $(5.4.11)$, we consider the local minimum $\min_{i\in A} f(i)$, which is not the global minimum $\min_{i\in B} f(i) = 0$, since $1 \notin A$. We put

$$\min_{i\in A} f(i) =: \frac{1}{\mathcal{R}_0^m} \quad \text{if} \quad f(0) \neq 0, \quad i.e \quad f(0) = 1. \tag{5.4.12}$$

Notice that the exclusion of the number 1 from the set A and the definition of $\mathcal{R}_0^m$ imply that

$$\mathcal{R}_0^m \geq 1. \tag{5.4.13}$$

Furthermore, we have the relation

$$0 \leq \mathcal{R}_0^c \leq \mathcal{R}_0^m < \infty. \tag{5.4.14}$$

The material accumulated so far regarding the extremum values of the function f enables us to specify the possible intersections between $y = f(i)$ and $y = \frac{1}{\mathcal{R}_0}$ in terms of the following result:

Theorem 5.4.5. *For the disease transmission model* $(5.4.5)$*, with assumptions* $(5.3.10)$, $(5.3.11)$ *and* $(5.3.12)$*, we have the following facts:*

1. *The constant* $\underline{i} = 0$ *is always an equilibrium (disease-free equilibrium);*
2. *There is no endemic equilibrium* i_e *if* $\mathcal{R}_0 < \mathcal{R}_0^c$*;*
3. *There exists at least one endemic equilibrium* i_e *if* $\mathcal{R}_0 > \mathcal{R}_0^c$*;*
4. *There exists exactly one endemic equilibrium* i_e *if* $\mathcal{R}_0 > \mathcal{R}_0^m$.

Proof:

1. On setting $i_0(t) = 0$, it is clear that the constant function $i(t) = \underline{i} = 0$ is the unique solution of the Volterra integral equation $(5.4.5)$.
2. Assume that $\mathcal{R}_0 < \mathcal{R}_0^c$. Then by Equation $(5.4.11)$, we have $f(i) \leq \max_{c\in A} f(c) < \frac{1}{\mathcal{R}_0}$ for all $i \in [0, 1]$. Thus, there is no intersection between the graphs of $y = f(i)$ and $y = \frac{1}{\mathcal{R}_0}$ (see Fig 5.1a).

3. If $\mathcal{R}_0 > \mathcal{R}_0^c$, then $\max_{i\in A} f(i) > \frac{1}{\mathcal{R}_0}$ by Equation $(5.4.11)$. Since $f(1) = 0 < \frac{1}{\mathcal{R}_0} < \max_{i\in A} f(i)$ and $f(i)$ is continuous on $[0, 1]$, the intermediate value theorem guarantees the existence of at least one $i_e \in (0,\ 1)$ such that $f(i_e) = \frac{1}{\mathcal{R}_0}$ (see Fig 5.1b).

4. Assume that $\mathcal{R}_0 > \mathcal{R}_0^m$, which implies that $f(0) = 1$. Since $\mathcal{R}_0^m \geq \mathcal{R}_0^c$, we infer from part (3) above that there exists at least one endemic equilibrium $i_e \in (0,\ 1)$.

   We claim that the endemic equilibrium is unique. To this end, we assume by contradiction that there exist two endemic equilibria $i_{e_1},\ i_{e_2} \in (0,\ 1)$ such that $i_{e_1} < i_{e_2}$. Since $f(i_{e_1}) = f(i_{e_2}) = \frac{1}{\mathcal{R}_0}$ and the continuous function $f : [i_{e_1},\ i_{e_2}] \to \mathbb{R}$ is differentiable on $(i_{e_1},\ i_{e_2})$, it follows from Rolle's theorem that there exists $c \in (i_{e_1},\ i_{e_2})$ such that $f'(c) = 0$, which means that $c \in A$. Then we have two cases. The first case is when $f(c) < \frac{1}{\mathcal{R}_0}$. i.e $f(c)$ is a local minimum. This is impossible in view of the fact that the smallest local minimum satisfies $\min_{i\in A} f(i) > \frac{1}{\mathcal{R}_0}$(see Fig 5.2a). We are then left with the second case, which read as $f(c) > \frac{1}{\mathcal{R}_0}$. i.e $f(c)$ is a local maximum (see Fig 5.2b). Thus $f(c) \geq \min_{i\in A} f(i) > \frac{1}{\mathcal{R}_0} > 0$. Under these circumstances, there exists a point $i_{e_3} \in (0,\ 1) \cap A$ with $i_{e_3} \neq c$ and $i_{e_3} \neq r$, where $f(r) = \min_{i\in A} f(i),\quad r \in (0,\ 1)$, such that $f(i_{e_3}) < \frac{1}{\mathcal{R}_0}$ is a local minimum. This contradicts the fact that $f(r)$ is the smallest local minimum. Therefore, there exists a unique endemic equilibrium in this case. □

Some comments are in order regarding Theorem 5.4.5 as compared to the classical SIS model for which we have $\mathcal{R}_0^m = \mathcal{R}_0^c$. When $\mathcal{R}_0^m \geq 1$ and $\mathcal{R}_0 > \mathcal{R}_0^m$, the fact that Theorem 5.4.5 guarantees the existence of a unique endemic equilibrium i_e agrees with the situation of the classical SIS model and other classical epidemiological models. By analogy with this classical case, we expect the disease–free equilibrium to be unstable, while the unique endemic equilibrium i_e is locally asymptotically stable. Similarly for $\mathcal{R}_0 < \mathcal{R}_0^c \leq 1$, the fact that the disease-free equilibrium is the only equilibrium is in line with the classical case and so we expect this equilibrium to be globally asymptotically stable in this case. The situation $\mathcal{R}_0^c < \mathcal{R}_0 < \mathcal{R}_0^m$ which, according to Theorem 5.4.5 could lead to multiple endemic equilibrium, is a major difference between the classical SIS model and the one considered here. This coupled with $\mathcal{R}_0^m \leq 1$ is the case when the backward bifurcation

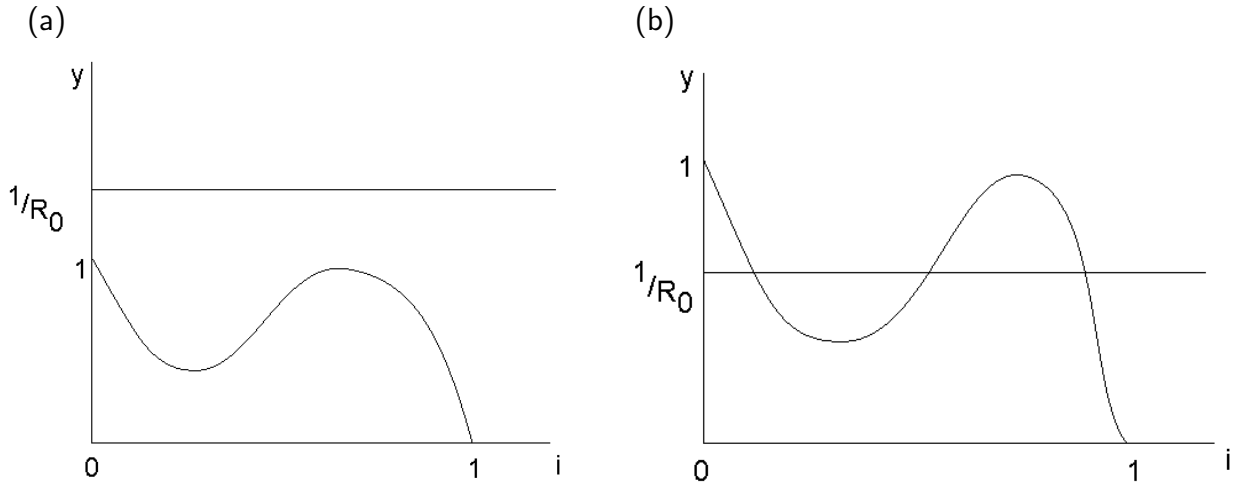


Figure 5.1: Non–existence (a) and existence (b) of endemic equilibrium

phenomena can surprisingly occur for such a simple model.

These expectations on the stability and bifurcation of the equilibria turn out to confirm the results established in [57]. We will more carefully consider the stability and bifurcation analysis of general Volterra integral equations in our future work. Our interest here is restricted in demonstrating computationally the results of [57] regarding (5.3.17) or (5.4.5) on numerical examples.

In all examples given below, we use the initial condition function

$$i_0(t) = e^{-t},$$

which clearly satisfies the assumption $(D3)$ or $(5.3.12)$.

Furthermore, in accordance with assumption $(D2)$ or $(5.3.11)$, the fraction $P(t)$ of individuals that an infective individual has infected at time 0 and remain infective through to time t is taken to be

$$P(t) = e^{-t}.$$

Given the fact that the existence of the solution of the integral equation $(5.3.17)$ was obtained by Banach fixed theorem, the successive approximation method is applicable. It reads as follows:

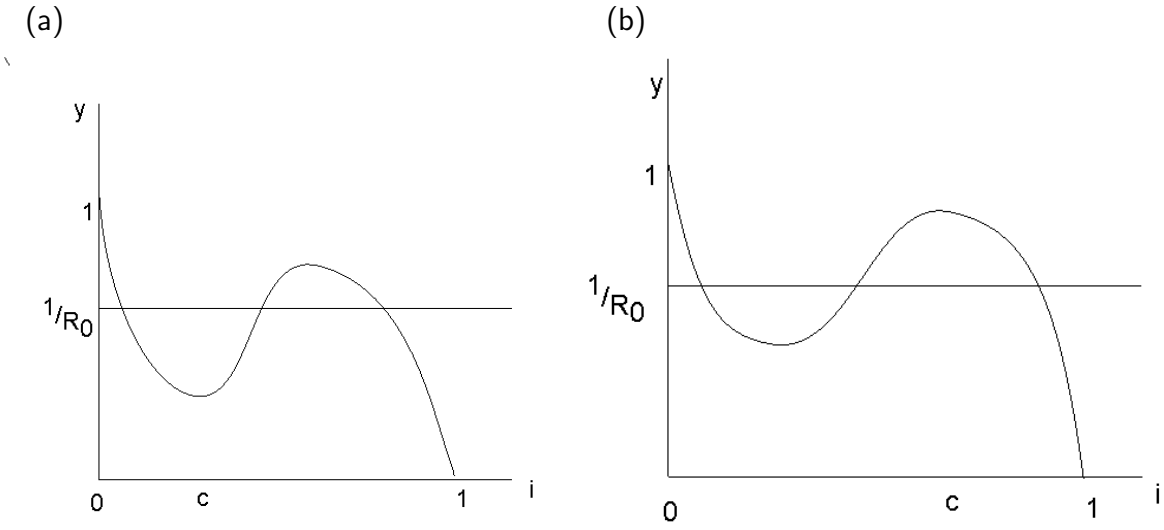


Figure 5.2: Existence of unique endemic equilibrium

From the initial guess $i^0(t) = i_0(t)$, we generate a sequence of approximations $i^k(t), \quad k = 0, 1, \ldots$, given recursively by

$$i^{k+1}(t) = e^{-t} + \int_0^t \lambda\left(i^k(u)\right) i^k(u) \left[1 - i^k(u)\right] e^{-(1+\mu+\gamma)(t-u)} du. \tag{5.4.15}$$

To approximate the integral in $(5.4.15)$, we use the composite trapezoidal rule $[11]$ based on the nodes defined as follows for a fixed t and integer $n \geq 2$:

$$u_k = k\Delta t, \quad k = 0,\ 1,\ \ldots,\ n := \frac{t}{\Delta t}. \tag{5.4.16}$$

Introducing the notation

$$g(i; t, u) = \lambda(i(u))i(u)[1 - i(u)]e^{-(1+\mu+\gamma)(t-u)},$$

we eventually obtain the scheme

$$i^{k+1}(t) = e^{-t} + \frac{\Delta t}{2}\left(g(i^k; t, 0) + 2\sum_{j=1}^{n-1} g(i^k; t, u_j) + g(i^k; t, t)\right). \tag{5.4.17}$$

Example 5.4.6. *In this numerical example, we are interested in the case when* $\mathcal{R}_0 < \mathcal{R}_0^c \leq 1$. *To this end, in* $(5.3.8)$ *and* $(5.4.3)$, *we take* $f(i) = 1 - i$ *and* $\lambda(i) = 1$. *Then, from* $(5.3.16)$ *we have* $\mathcal{R}_0 = \frac{1}{1+\mu+\gamma} < 1 = \mathcal{R}_0^c$ *so that there is no intersection between* $y = f(i) = 1 - i$ *and* $y = \frac{1}{\mathcal{R}_0}$. *Figure 5.3 for the scheme* $(5.4.17)$ *confirms this and displays further the fact that the disease-free equilibrium is globally asymptotically stable for appropriate choice of* $\mu > 0$ *and* $\gamma > 0$.

Example 5.4.7. *We focus on the case when* $\mathcal{R}_0^c < \mathcal{R}_0 < \mathcal{R}_0^m \leq 1$. *We take* $f(i) = (1+5i)(1-i)$ *and* $\lambda(i) = 1+5i$ *so that* $\mathcal{R}_0 = \frac{1}{1+\mu+\gamma}$, $\mathcal{R}_0^c = \frac{5}{9}$ *and* $\mathcal{R}_0^m = 1$. *Figure 5.4 for the scheme* (5.4.17) *illustrates the existence of one or multiple endemic equilibria when* $\mathcal{R}_0 < 1$ *as well as the backward bifurcation phenomenon.*

Remark 5.4.8. *In order to make use of the powerful NSFD schemes developed in the previous chapters, we outline below what can be done for the integro-differential equation* (5.3.18). *If there was no integral term in* (5.3.18), *the results of the previous chapters would have led to the following NSFD scheme:*

$$\frac{i^{k+1}-i^k}{\phi(\Delta t)} = \frac{i_0(t)}{dt} + \lambda(i^k)i^k(1-i^{k+1}), \tag{5.4.18}$$

where $\phi(\Delta t) = \frac{e^{\mu\Delta t}-1}{\mu}$.

In order to approximate the integral in (5.3.18), *we can use the first mean value theorem for integrals* [45]: *there exists a number* $c \equiv c_t \in (0,\ t)$ *such that*

$$\int_0^t \lambda[i(u)]i(u)\left[1-i(u)\right]\left(\frac{d}{dt}P(t-u)-(\mu+\gamma)\right)e^{-(\mu+\gamma)(t-u)}du = \lambda[i(c)]i(c)[1-i(c)]\int_0^t \left(\frac{d}{dt}P(t-u)-(\mu+\gamma)\right)e^{-(\mu+\gamma)(t-u)}du. \tag{5.4.19}$$

Fix a discrete time $t_k = k\Delta t$, *where we recall that we want to obtain the approximation* i^{k+1} *of* $i(t_{k+1})$ *assuming that* i^k *is known. Given an integer* $n \geq 2$, *we partition the interval* $[0,\ t_k]$ *through the nodes* $u_{k,\,j}$ *defined similarly to* (5.4.16) *as follows:*

$$u_{k,\,j} = jd_k, \quad j = 0,\ 1,\ 2,\ \ldots,\ n := \frac{t_k}{d_k}. \tag{5.4.20}$$

Now in view of (5.4.18) *and* (5.4.20), *we can start the process of obtaining a numerical scheme for* (5.3.18):

$$\begin{aligned}\frac{i^{k+1}-i^k}{\phi(\Delta t)} &= \frac{di_0}{dt}(t_k) + \lambda(i^k)i^k[1-i^{k+1}] \\ &+ \sum_{j=1}^{n}\int_{u_{k,\,j-1}}^{u_{k,\,j}} \lambda[i(u)]i(u)[1-i(u)]\left(\frac{d}{dt}P(t-u)-(\mu+\gamma)\right)e^{-(\mu+\gamma)(t_k-u)}du.\end{aligned} \tag{5.4.21}$$

Taking into account the explicit values $i_0(t) = e^{-t}$ *and* $P(t) = e^{-t}$, *Equation* (5.4.21) *becomes*

$$\begin{aligned}\frac{i^{k+1}-i^k}{\phi(\Delta t)} &= -e^{-t} + \lambda(i^k)i^k[1-i^{k+1}] \\ &+ \sum_{j=1}^{n}\int_{u_{k,\,j-1}}^{u_{k,\,j}} \lambda[i(u)]i(u)[1-i(u)]\left(-(1+\mu+\gamma)\right)e^{-(1+\mu+\gamma)(t_k-u)}du.\end{aligned} \tag{5.4.22}$$

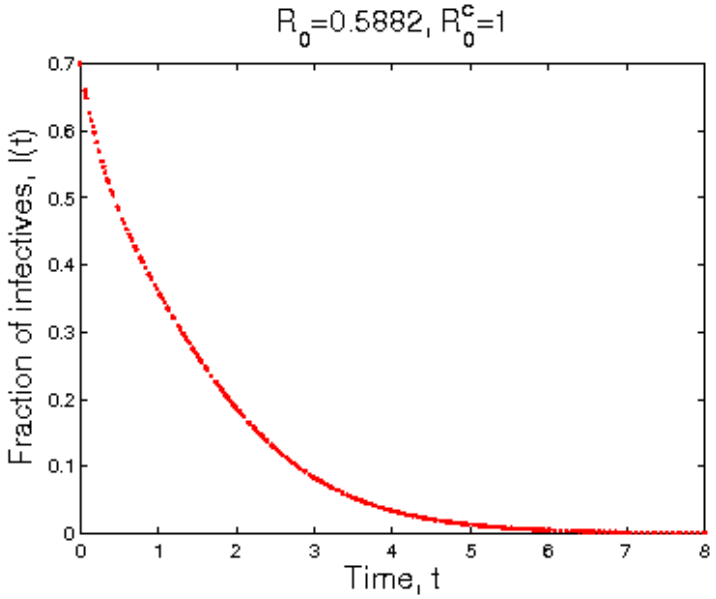


Figure 5.3: Example 5.4.6: GAS of the disease–free equilibrium.

To finalize the process, we approximate each integral on the subinterval $[u_{k,\,j-1},\ u_{k,\,j}]$ *using the product integration method of Atkinson* [5]. *That is, we use the formula* (5.4.19), *where we take* $c = u_{k,\,j}$. *This gives the following NSFD scheme:*

$$\begin{aligned} \frac{i^{k+1}-i^k}{\phi(\Delta t)} &= -e^{-t_k} + \lambda(i^k)i^k[1-i^{k+1}] \\ &+ \sum_{j=1}^{n} \lambda(i^j)i^j[1-i^j] \int_{u_{k,\,j-1}}^{u_{k,\,j}} \left(-(1+\mu+\gamma)\right) e^{-(1+\mu+\gamma)(t_k-u)} du, \end{aligned} \tag{5.4.23}$$

or equivalently

$$\begin{aligned} i^{k+1} &= \frac{\left(-e^{-t_k} + \lambda(i^k)i^k\right)\phi(\Delta t)}{1+\lambda(i^k)i^k} \\ &+ \frac{\phi(\Delta t)}{1+\lambda(i^k)i^k} \sum_{j=1}^{n} \lambda(i^j)i^j[1-i^j] e^{-(1+\mu+\gamma)t_k} \left[e^{(1+\mu+\gamma)u_{k,\,j-1}} - e^{(1+\mu+\gamma)u_{k,\,j}}\right]. \end{aligned} \tag{5.4.24}$$

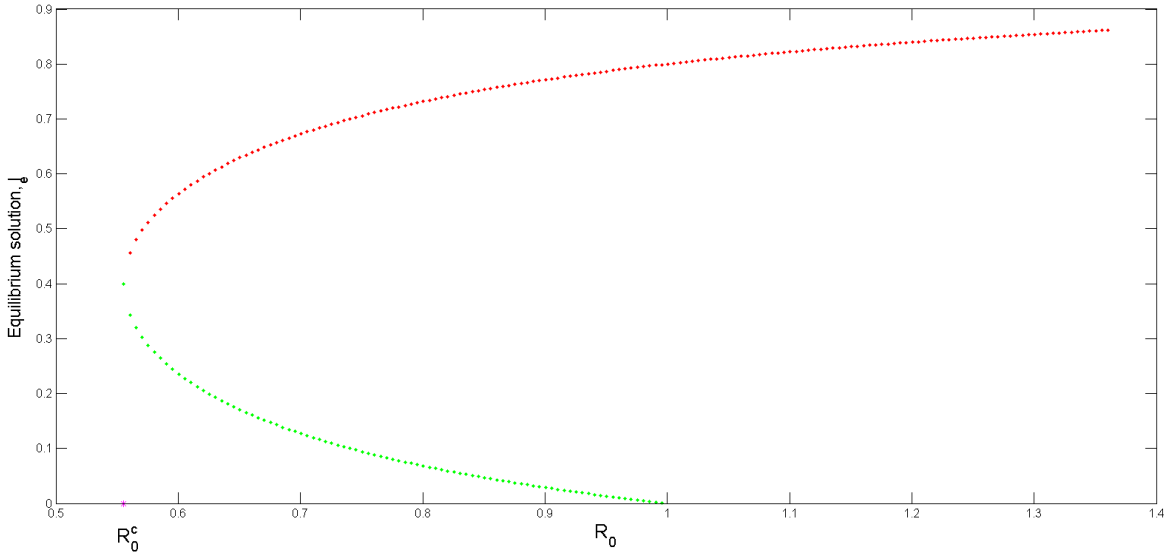


Figure 5.4: Example 5.4.7: Existence of endemic equilibria when $\mathcal{R}_0 < 1$.

Chapter 6

Conclusion

This dissertation was initially motivated by the work [24], where it is shown theoretically and computationally that some models for the transmission dynamics of multiple strains of a disease in a given population can undergo the backward bifurcation phenomenon. That is a stable endemic equilibrium co–exists with a stable disease–free equilibrium despite the fact that the classical epidemiological threshold condition $\mathcal{R}_0 < 1$ holds, where $\mathcal{R}_0$ is the associated basic reproduction number.

Given the complexity of models with multiple strains of diseases and the interesting results obtained in [57], our goal changed into the investigation of the backward bifurcation in the simple setting of the SIS model. One of the key ingredients in [57] is a general formulation of the contact rate. This led us to focus this dissertation on the study of the SIR and SIS models with the contact rate expressed more generally as a function of the total population such a way that this extended contact rate satisfies properties that are biologically relevant [8].

In this general setting of the contact rate, we showed and better understood the following results:

- the SIR and SIS models are dynamical systems on biologically feasible regions;
- the value $\mathcal{R}_0 = 1$ of the basic reproduction number is a forward bifurcation. That is the disease–free equilibrium is globally asymptotically stable when $\mathcal{R}_0 < 1$ whereas it is unstable and an additional locally asymptotically stable endemic equilibrium is born when $\mathcal{R}_0 > 1$. In this regard, we used the bisection method to find the endemic

equilibrium in the case when the contact rate is an implicit function of the total population.

On the other hand, we placed strong emphasis on the design and analysis of nonstandard finite difference schemes, which are dynamically consistent with respect to all the essential properties (e.g. positivity, boundedness of solutions, etc.) of the continuous models. In particular, we designed for the first time a nonstandard Runge–Kutta scheme, which is a method of order 4.

The analysis for the SIS model with $\mathcal{R}_0 > 1$ was taken one step further in considering the SIS diffusion model for the spread of the disease in space. We proved that the disease–free equilibrium is unstable and the endemic equilibrium is locally asymptotically stable. Here again, these dynamics of the model were preserved by innovative nonstandard finite difference schemes that we designed.

Coming back to our initial goal, the SIS–Volterra integral equation model, we did not manage to go into details due to time constraints. Nevertheless, we established the existence of one or multiple endemic equilibria when the basic reproduction number is less than 1. This property was confirmed on a numerical test.

The natural continuation of this dissertation is therefore a full qualitative analysis of the SIS–Volterra integral equation model. Once this is done, another challenge is the design of nonstandard finite difference schemes that are dynamically consistent with the properties (including the backward bifurcation phenomenon) of the SIS–Volterra integral equation model.

It is also of great interest to investigate other situations when the SIR model undergoes the backward bifurcation phenomenon. In this regard, the work [31] can be mentioned.

As far as partial differential equations are concerned, the extension of the SIR and SIS models into advection–reaction diffusion equations and the corresponding numerical treatment are desirable.

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