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Spatiotemporal Dynamics and Wave Propagation in the Diffusive Kermack-McKendrick Model

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Dedication

Idedicate this work...

To the ones who gave me life,
who always believed in me and supported me throughout my journey since I was born.
To my parents, my everything.

To ***Hiba*** *and* ***Mouna****, my sisters,*
my first friends, my lifelong shelter.

To ***Ali*** *and* ***Mohammed****, my brothers,*
whom I love.

To ***Khadija****,* ***Abd el malik****, and* ***Anes****,*
not just friends, but family I chose.

To myself.
For every moment I wanted to quit but didn't.

Thank you

Abstract

We study the existence of traveling wave solutions for a diffusive Kermack–McKendrick SIR model with standard incidence. The three compartments—susceptible S, infected I, and recovered R—are all taken into account in the traveling waves analysis. We demonstrate that the minimum wave speed of traveling waves for this three-dimensional system can be obtained from the linearization around the initial disease-free equilibrium. The proof is based on Schauder's fixed point theorem and the Arzelà-Ascoli theorem. This work offers a valuable approach for studying high-dimensional epidemic models.

Keywords: SIR model, traveling waves, standard incidence, Schauder fixed point theorem, basic reproduction number.

Résumé

Nous étudions l'existence de solutions d'ondes progressives pour un modèle SIR diffusif de Kermack–McKendrick avec une incidence standard. Les trois compartiments—les individus susceptibles S, infectés I et rétablis R—sont tous pris en compte dans l'analyse des ondes progressives. Nous démontrons que la vitesse d'onde minimale des ondes progressives pour ce système tridimensionnel peut être obtenue à partir de la linéarisation autour de l'équilibre initial sans maladie. La preuve est basée sur le théorème du point fixe de Schauder et le théorème d'Arzelà-Ascoli. Ce travail offre une approche précieuse pour l'étude des modèles épidémiques en haute dimension.

Mots-clés : Modèle SIR, ondes progressives, incidence standard, théorème du point fixe de Schauder, nombre de reproduction de base.

Contents

Notions and Abbreviations

- $|\cdot|$: Absolute value.
- $\|\cdot\|$: The norm.
- $\boldsymbol{\frac{dy}{dt}}$: Derivative of y with respect to time t.
- $\boldsymbol{\frac{d^k y}{dt^k}}$: K-th order derivative of y with respect to time t.
- $\underset{x.}{\boldsymbol{\frac{\partial u}{\partial x}}}$: The partial derivative of the function $u(x,t)$ with respect to the spatial variable
- $\underset{t.}{\boldsymbol{\frac{\partial u}{\partial t}}}$: The partial derivative of the function $u(x,t)$ with respect to the time variable
- $\boldsymbol{C^1}$: Set of functions that are continuously differentiable once.
- $\boldsymbol{J}$: The Jacobian matrix.
- $\boldsymbol{\mathcal{R}_0}$: Basic reproduction number **(R-zero or R-nought)**.
- **det** : The determinant of a matrix.
- **Spectral radius**: The largest absolute value of the eigenvalues of a matrix .
- **ODE** : Ordinary differential equation.
- **PDE**: Partial Differential Equation.
- **Epidemic**: The rapid spread of a disease to a large number of people within a specific region over a short period of time.
- **Pandemic** : An epidemic that has spread over multiple countries or continents, affecting a large portion of the global population.

- **DFE** : Disease free equilibrium, a state where no individuals in the population are infected, which means that the disease is absent.
- **EE** : Endemic equilibrium, a state where the disease persists in the population over time.
- **Threshold**: The value $\mathcal{R}_0 = 1$ that separates disease extinction ($\mathcal{R}_0 < 1$) from disease spread ($\mathcal{R}_0 > 1$).
- **SARS**: (Severe Acute Respiratory Syndrome) is a viral respiratory illness caused by a coronavirus. It first emerged in 2002-2003 and spread globally, causing severe pneumonia and respiratory failure.
- **H1N1**: A subtype of the influenza A virus that caused the 2009 swine flu pandemic. It is a respiratory illness that spreads easily between humans.
- **Avian Influenza**: A viral infection that primarily affects birds but can sometimes spread to humans, causing severe respiratory illness (also known as bird flu).
- **Pathogen**: an infectious agent that causes disease in a host.
- **Epidemic outbreak**: the rapid increase in disease cases within a population over a short time period.

Introduction

Mathematical modeling has become an essential tool in understanding the spread and control of infectious diseases. Among the most important models in epidemiology is the Kermack-McKendrick SIR model, first introduced in 1927 [31]. This model divides a population into three compartments: susceptible (S), infected (I), and recovered (R), and describes the temporal evolution of an epidemic under the assumption that the population is well-mixed and spatially homogeneous.

However, real-world disease spread is strongly influenced by spatial factors such as population movement, immigration, vaccination campaigns, border control, and quarantine measures. The importance of these spatial structures has been clearly demonstrated during recent global outbreaks of SARS, H1N1, and avian influenza [3, 4]. Traveling waves of spatial epidemic models represent the transition of an outbreak from an initial disease-free state to another disease-free state, propagating as a wave with fixed shape and speed [20, 34]. Understanding these traveling waves provide crucial insight into the invasion speed of infectious diseases [32].

In this dissertation, we extend the classical Kermack-McKendrick SIR model by incorporating diffusion terms to describe the random movement of individuals, transforming the system into reaction-diffusion equations [9]. We study traveling waves for three distinct incidence forms: mass-action incidence, standard incidence without recovered individuals (SI), and standard incidence with recovered individuals (SIR). For each model, we derive the basic reproduction number $\mathcal{R}_0$, which determines whether an outbreak can occur, and the minimum wave speed c^* at which the disease spreads.

The main results of this dissertation are the following:

- For the diffusive SIR model with standard incidence, we prove that a traveling wave solution exists if and only if $\mathcal{R}_0 = \dfrac{\beta}{\gamma + \delta} > 1$ and the wave speed satisfies $c \geq c^* = 2\sqrt{d_2(\beta - \gamma - \delta)}$. The existence proof is based on Schauder's fixed point theorem [27] and the Arzelà-Ascoli theorem [26], using the construction of super-solutions and sub-solutions.

- The asymptotic behavior of the traveling wave solution is described in proposition

(3.3.1), showing that the susceptible population decreases from $S_{-\infty}$ ahead of the wave to S_{∞} behind the wave, while the recovered population increases.

This dissertation is organized as follows:

- **Chapter 1**: collects the necessary mathematical preliminaries, including definitions of ordinary and partial differential equations [28, 10], the Cauchy-Lipschitz theorem [16], positive invariance [11], equilibrium points [30], Jacobian matrix [35], the basic reproduction number and the next-generation method [24, 23], stability notions [19], linearized stability [35], traveling wave theory [20, 34, 32], Leibniz rule [18], Schauder fixed point theorem [27], and the Arzelà-Ascoli theorem [26].

- **Chapter 2**: presents the classical Kermack-McKendrick SIR model [31, 25], first without demography and then with demographic processes [21, 22]. The equilibrium points, basic reproduction number, and stability analysis [14] are established for each case.

- **Chapter 3**: devotes the traveling wave solutions of diffusive SIR models [9] into three incidence forms: mass-action incidence [12, 13, 1, 2, 17], standard incidence without recovered population (SI) [33], and standard incidence with recovered population (SIR) [9], and proved the existence of travling waves.

Chapter 1

Preliminaries

In this chapter, we introduce the important preliminary concepts, definitions, notations, theorems, and mathematical tools essential to our mathematical framework.

1.1 Ordinary differential equation

Definition 1.1.1: [10, 28]

An equation involving dependent variables, independent variables (usually time t), and the derivatives of the dependent variables with respect to the independent variables is called an ordinary differential equation. The most general form of an ***ODE*** *of order* $\boldsymbol{n}$ *is:*

$$F\left(t, y, \frac{dy}{dt}, \frac{d^2y}{dt^2}, ..., \frac{d^ny}{dt^n}\right) = 0,$$

where:

- $\boldsymbol{t}$ *is the independent variable,*
- $\boldsymbol{y = y(t)}$ *is the dependent variable,*
- $\boldsymbol{n}$ *is the order of the differential equation,*
- $\boldsymbol{\frac{d^ky}{dt^k}}$ *is the k-th derivative* $(k = 1, \ldots, n)$.

1.2 Partial differential equation

Definition 1.2.1: [15]

A partial differential equation is an equation for a function which depends on more than one independent variable which involves the independent variables, the function, and partial derivatives of the function.

*Here is the general form that defines a **(PDE)**:*

$$F\left(x_1, x_2, \ldots, x_n, u, \frac{\partial u}{\partial x_1}, \ldots, \frac{\partial u}{\partial x_n}, \frac{\partial^2 u}{\partial x_1 \partial x_1}, \ldots, \frac{\partial^2 u}{\partial x_1 \partial x_n}, \ldots, \frac{\partial^k u}{\partial x_1^{k_1} \cdots \partial x_n^{k_n}}, \ldots\right) = 0$$

where:

- $\boldsymbol{u = u(x_1, x_2, \ldots, x_n)}$ *is the unknown function,*
- $\boldsymbol{x_1, x_2, \ldots, x_n}$ *are the independent variables ($n \geq 2$),*
- $\boldsymbol{\frac{\partial u}{\partial x_i}}$ *are first-order partial derivatives,*
- $\boldsymbol{\frac{\partial^2 u}{\partial x_i \partial x_j}}$ *are second-order partial derivatives,*
- $\boldsymbol{\frac{\partial^k u}{\partial x_1^{k_1} \cdots \partial x_n^{k_n}}}$ *are k-th order partial derivatives (where $k_1 + k_2 + \cdots + k_n = k$).*

1.3 Existence and unicity of solutions

Let us consider the following system:

$$\begin{cases} \dfrac{dx}{dt} = f(x(t)), & t \in (0, b), \\ x(0) = x_0. \end{cases} \tag{1.1}$$

Where $f : \Omega \longrightarrow \mathbb{R}^n$ is a function, Ω is an open subset of $\mathbb{R}^n$, $x_0 \in \Omega$, and $b \in \mathbb{R}_+^*$.

Theorem 1.3.1: Cauchy-Lipschitz [16]

If $\boldsymbol{f}$ is of class $\boldsymbol{C^1}$ on $\boldsymbol{\Omega}$ and if there exists a constant $\boldsymbol{T > 0}$ such that:

$$\boldsymbol{\|f(x_1) - f(x_2)\|_{\mathbb{R}^n} \leq T\|x_1 - x_2\|_{\mathbb{R}^n}, \quad \forall x_1, x_2 \in \Omega,}$$

then problem (1.1) has a unique local solution.

1.4 Positive invariance

Theorem 1.4.1: Positive Invariance[11]

*Consider the system (1.1),let $\Psi \subset \Omega$ be a closed set. If for every $x \in \partial\Psi$ (the boundary of Ψ), the vector $f(x)$ points inside Ψ (or is tangent), then Ψ is **positively invariant**. That is, if $x_0 \in \Psi$, then $x(t) \in \Psi$.*

1.5 Equilibrium points

Suppose the following **ODE**:

$$\frac{dx}{dt} = f(x), \tag{1.2}$$

where $f : \Omega \subset \mathbb{R}^n \longrightarrow \mathbb{R}^n$ is a function of class C^1.

Definition 1.5.1: [30]

An equilibrium point $\boldsymbol{x^*}$ of (1.2) is a point for which $\boldsymbol{f(x^*) = 0}$.

1.6 Jacobian matrix

Definition 1.6.1: [35]

Let $\boldsymbol{f} : \mathbb{R}^{\boldsymbol{n}} \longrightarrow \mathbb{R}^{\boldsymbol{m}}$ be a vector-valued function whose component functions $\boldsymbol{f_1, f_2, ..., f_m}$ have first-order partial derivatives at a point $\boldsymbol{X = x_1, x_2, ..., x_n}$. The Jacobian matrix of $\boldsymbol{f}$ at $\boldsymbol{X}$ denoted $\boldsymbol{J_f(X)}$ or simply $\boldsymbol{J(X)}$, is the $m \times n$ matrix of all first-order partial derivatives.
The Jacobian matrix is defined as follows:

$$J(x) = \begin{pmatrix} \frac{\partial f_1}{\partial x_1} & \frac{\partial f_1}{\partial x_2} & \cdots & \frac{\partial f_1}{\partial x_n} \\ \frac{\partial f_2}{\partial x_1} & \frac{\partial f_2}{\partial x_2} & \cdots & \frac{\partial f_2}{\partial x_n} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\partial f_m}{\partial x_1} & \frac{\partial f_m}{\partial x_2} & \cdots & \frac{\partial f_m}{\partial x_n} \end{pmatrix}.$$

Remark 1.6.1

When $\boldsymbol{m = n}$, the determinant of this Jacobian matrix is called the Jacobian determinant, denoted $\boldsymbol{|J_f(X)|}$ or $\boldsymbol{\det\left(J_f(X)\right)}$.

1.7 The basic reproduction Number

Definition 1.7.1: [24]

The basic reproduction number, denoted $\mathcal{R}_0$*, is the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual when the population is on the disease-free equilibrium* ***(DFE)****.*

1.7.1 The next generation method

The next generation method [24] is a technique proposed by **Paul van den Driessche** and **James Watmough** to compute the basic reproduction rate $\mathcal{R}_0$.
It proceeds as follows:

- **Step 1:** Identifying the variables that describe the infection.
- **Step 2:** Writing the equations corresponding to the infected compartments in the form:
$$\frac{dx_i}{dt} = \mathcal{F}_i(x) - \mathcal{V}_i(x), \ \mathrm{i} = 1...n,$$
where x_i represents the infected compartments, $\mathcal{F}_i(x)$ represents the rate of new infection entering each infected compartment, and $\mathcal{V}_i(x) = \mathcal{V}_i^- - \mathcal{V}_i^+$ represents the rate of transfer of individuals (recovery, death, or movement) into and out of each compartment.
- **Step 3:** Linearizing around the disease free equilibrium **(DFE)**.
If x_0 is a disease free equilibrium of the model, then the $m \times m$ Jacobian matrices of F and V are evaluated at x_0 as follows:
$$F = \left[\frac{\partial \mathcal{F}_i}{\partial x_j}(x_0)\right], \text{ and } V = \left[\frac{\partial \mathcal{V}_i}{\partial x_j}(x_0)\right],$$
with $1 \leq i, j \leq m$.
- **Step 4:** The next generation matrix is defined as follows:
$$K = FV^{-1}.$$
Following **Diekmann** [23], the basic reproduction number $\mathcal{R}_0$ is defined as the spectral radius **(largest eigenvalue)** of **K** and set:
$$\mathcal{R}_0 = \rho(K). \tag{1.3}$$

Remark 1.7.1

- *If* $\mathcal{R}_0 < 1$*, each infected individual produces less than one new infection during their infectious period, and the disease cannot spread through the population.*
- *If* $\mathcal{R}_0 > 1$*, each infected individual produces more than one new infection during their infectious period, allowing the disease to spread.*
- *If* $\mathcal{R}_0 = 1$*, each infected individual causes exactly one new infection on average. This is* ***the epidemic threshold****, the disease neither grows nor declines, but persists at a constant level in the population.*

1.8 Stability notions [19]

Definition 1.8.1

The equilibrium point $\boldsymbol{x^*}$ *of* (1.2) *is said to be* ***locally stable*** *if for every* $\boldsymbol{\epsilon > 0}$*, there exists* $\boldsymbol{\eta > 0}$ *such that for any solution* $\boldsymbol{x(t)}$ *of* (1.2)*, we have:*

$$\|\boldsymbol{x}(0) - \boldsymbol{x}^*\| < \boldsymbol{\eta} \;\Rightarrow\; \forall \boldsymbol{t} \geq 0,\ \|\boldsymbol{x}(\boldsymbol{t}) - \boldsymbol{x}^*\| < \boldsymbol{\epsilon}.$$

Definition 1.8.2

The equilibrium point $\boldsymbol{x^*}$ *of* (1.2) *is said to be* ***asymptotically stable*** *if it is stable, and if there exists* $\boldsymbol{\epsilon > 0}$ *such that for any solution* $\boldsymbol{x(t)}$ *of* (1.2)*, we have:*

$$\|\boldsymbol{x}(0) - \boldsymbol{x}^*\| < \boldsymbol{\epsilon} \;\Rightarrow\; \lim_{\boldsymbol{t}\to\infty} \|\boldsymbol{x}(\boldsymbol{t}) - \boldsymbol{x}^*\| = 0.$$

Definition 1.8.3

The equilibrium $\boldsymbol{x^*}$ *of* (1.2) *is said to be* ***globally attractive*** *if:*

$$\lim_{\boldsymbol{t}\to+\infty} \|\boldsymbol{x}(\boldsymbol{t}) - \boldsymbol{x}^*\| = 0.$$

Definition 1.8.4

The equilibrium $\boldsymbol{x^*}$ *of* (1.2) *is said to be* ***globally asymptotically stable*** *if it is stable and globally attractive.*

1.9 Linearized stability [35]

Consider the non-linear system (1.1), let $\boldsymbol{A} = \boldsymbol{J_f(x^*)}$ be the Jacobian matrix of $\boldsymbol{f}$ evaluated at the equilibrium point $\boldsymbol{x^*}$.

The stability of the equilibrium is governed entirely by the eigenvalues $\boldsymbol{\lambda_1, \lambda_2, ..., \lambda_n}$ of the matrix $\boldsymbol{A}$.

Theorem 1.9.1

Let $\boldsymbol{f} \in \boldsymbol{C^1(\Omega)}$ and let $\boldsymbol{x^*} \in \boldsymbol{\Omega}$ be an equilibrium point of (1.1). Denote by $\boldsymbol{A = J_f(x^*)}$ the Jacobian matrix at $\boldsymbol{x^*}$, and let $\boldsymbol{\lambda_1, \ldots, \lambda_n}$ be its eigenvalues.

- ***Asymptotic stability:*** *If $\mathrm{Re}(\lambda_i) < 0$ for every $i = 1, \ldots, n$, then $\boldsymbol{x^*}$ is an asymptotically stable equilibrium of the nonlinear system (1.1).*
- ***Instability:*** *If $\mathrm{Re}(\lambda_i) > 0$ for at least one $i \in \{1, \ldots, n\}$, then $\boldsymbol{x^*}$ is an unstable equilibrium of the nonlinear system (1.1).*

Theorem 1.9.2: Routh-Hurwitz criterion for $n = 2$[14]

For the quadratic polynomial $\lambda^2 + a_1\lambda + a_2 = 0$, all roots satisfy $\mathrm{Re}(\lambda) < 0$ if and only if:

$$a_1 > 0 \quad \text{and} \quad a_2 > 0.$$

1.10 Traveling wave [20, 32, 34]

Consider a general reaction-diffusion system of the form:

$$\mathbf{u_t = D u_{xx} + f(u)}, \qquad \boldsymbol{x} \in \mathbb{R}, \quad \boldsymbol{t \geq 0}, \tag{1.4}$$

where:

- $\mathbf{u} = (u_1, u_2, \ldots, u_N) \in \mathbb{R}^N$,
- $D = \mathrm{diag}(d_1, d_2, \ldots, d_N)$ with $d_i > 0$ for $i = 1, \ldots, N$,
- $\mathbf{f}(\mathbf{u}) = (f_1(\mathbf{u}), f_2(\mathbf{u}), \ldots, f_N(\mathbf{u}))$ is the reaction term.

Definition 1.10.1

*A **traveling wave solution** is a special type of solution that propagates with constant speed and shape. It has the form:*

$$\mathbf{u}(x, t) = \mathbf{u}(\xi), \qquad \xi = x + ct,$$

where $c > 0$ is the wave speed.

Substituting this form into (1.4) and applying the chain rule, we obtain:

$$D\mathbf{u}''(\xi) - c\mathbf{u}'(\xi) + \mathbf{f}(\mathbf{u}(\xi)) = 0, \qquad \xi \in \mathbb{R}. \tag{1.5}$$

1.10.1 Linearization and the minimum wave speed

To determine the minimum wave speed, we linearize system (1.5) around the inital equilibrium point $\mathbf{E}$ (usually a disease-free equilibrium). We look for solutions of the form:

$$\mathbf{u}(\xi) = e^{\lambda\xi}\boldsymbol{\eta}, \qquad \lambda > 0, \quad \boldsymbol{\eta} = (\eta_1, \ldots, \eta_N) \gg 0.$$

Substituting into the linearized version of (1.5) yields:

$$\operatorname{diag}(d_i\lambda^2 - c\lambda)\boldsymbol{\eta} + \mathbf{f}'(\mathbf{E})\boldsymbol{\eta} = 0,$$

where $\mathbf{f}'(\mathbf{E})$ is the Jacobian matrix of $\mathbf{f}$ evaluated at $\mathbf{E}$. This can be rewritten as the eigenvalue problem:

$$\frac{1}{\lambda}A_\lambda\boldsymbol{\eta} = c\boldsymbol{\eta},$$

with

$$A_\lambda = \operatorname{diag}(d_i\lambda^2) + \mathbf{f}'(\mathbf{E}).$$

Let $\Psi(A_\lambda)$ denote the spectral radius of A_λ. Define the function:

$$\Phi(\lambda) = \frac{1}{\lambda}\Psi(A_\lambda) > 0, \qquad \lambda > 0.$$

The minimum wave speed is then given by:

$$\boxed{\boldsymbol{c^* = \inf_{\lambda>0} \Phi(\lambda) > 0.}}$$

1.11 Leibniz rule for differentiation under the integral sign[18]

Theorem 1.11.1: Leibniz Rule

Let $a(x)$ and $b(x)$ be differentiable functions, and let $f(x, y)$ be a function such that $\dfrac{\partial f}{\partial x}$ exists and is continuous. Then:

$$\frac{d}{dx}\int_{a(x)}^{b(x)} f(x,y)\,dy = f(x,b(x))\cdot b'(x) - f(x,a(x))\cdot a'(x) + \int_{a(x)}^{b(x)} \frac{\partial}{\partial x}f(x,y)\,dy.$$

In particular, for the special cases used in this thesis:

- If $a(x) = -\infty$ (constant) and $b(x) = x$:

$$\frac{d}{dx}\int_{-\infty}^{x} f(x,y)\,dy = f(x,x) + \int_{-\infty}^{x} \frac{\partial}{\partial x} f(x,y)\,dy.$$

- If $a(x) = x$ and $b(x) = \infty$ (constant):

$$\frac{d}{dx}\int_{x}^{\infty} f(x,y)\,dy = -f(x,x) + \int_{x}^{\infty} \frac{\partial}{\partial x} f(x,y)\,dy.$$

1.12 Schauder fixed point

The following theorem is a fundamental result in functional analysis used to prove the existence of fixed points for continuous and compact maps on convex sets.

Theorem 1.12.1: Schauder fixed point [27]

Let X be a Banach space and let K be a non-empty, closed, bounded, and convex subset of X. If $F : K \to K$ is a continuous and compact map (i.e., $F(K)$ is relatively compact in X), then F has at least one fixed point. That is, there exists $u \in K$ such that:

$$F(u) = u.$$

1.13 Arzelá-Ascoli

The Arzelà-Ascoli theorem characterizes compactness in spaces of continuous functions.

Theorem 1.13.1: Arzelà-Ascoli [26]

Let $\{f_n\}$ be a sequence of continuous functions defined on a compact interval $[a,b] \subset \mathbb{R}$. If the sequence is:

1. ***Uniformly bounded:*** *There exists $M > 0$ such that $|f_n(x)| \leq M$ for all n and all $x \in [a,b]$;*
2. ***Equicontinuous:*** *For every $\epsilon > 0$, there exists $\delta > 0$ such that for all n and all $x, y \in [a,b]$ with $|x - y| < \delta$, we have $|f_n(x) - f_n(y)| < \epsilon$;*

then there exists a subsequence $\{f_{n_k}\}$ that converges uniformly on $[a,b]$.

Chapter 2

The Kermack-McKendrick Epidemic Model

Mathematical modeling of epidemics [3, 22] is the use of mathematical structures to describe and predict how infectious diseases spread through populations. These models divide the population into epidemiological compartments according to the state of the disease and describe the changes between them over time. In **1927**, William Ogilvy Kermack **(W.O.Kermack)** and Anderson Gray McKendrick **(A.G.McKendrick)** [31] described the dynamics of the disease transmission using a system of **O**rdinary **D**ifferential **E**quations **ODEs**.

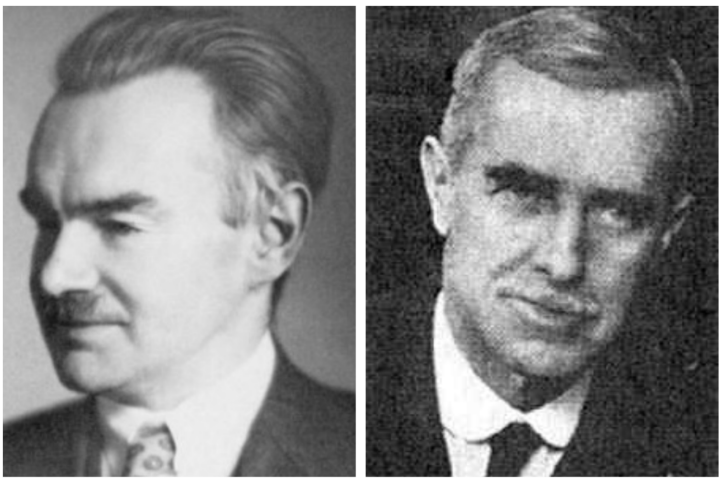

Figure 2.1: W.O.Kermack (1898-1970)(left), A.G.McKendrick (1876-1943)(right).

Among the mathematical models of epidemics, the **SIR** model (**S**: Susceptible, **I**: Infected and **R**: Recovered) remains one of the most historically important models. It was first proposed by **W.O.Kermack** and **A.G.McKendrick** in **1927** [31], and developed by Ronald Ross, William Hamer, and others in the early twentieth century [25]. This model studied the spread and evolution of an infectious disease in a population in which a pathogen is present and actively spreading. The model is divided into three compartments: the susceptible individuals **S** who are healthy, the infected individuals **I** who are capable

of transmitting the disease to the healthy population and the recovered individuals **R** who are removed from the infected population with curing and gaining immunity. This model focuses only on the temporal dynamics of the infection cycle, therefore it is suitable for the description of a well-localised epidemic outbreak. Since then, multiple extensions have been studied: **SIS** (Susceptible, Infected and Susceptible), **SIR** (Susceptible, Infected and Recovered), **SEIS** (Susceptible, Exposed, Infected and Susceptible), **SEIR** (Susceptible, Exposed, Infected and Recovered), etc [7, 8].

2.1 SIR model without demography

The SIR model without demography is the classical model, which has been fundamental to our understanding of disease dynamics in closed populations. It divides the total population **(N)** into three compartments **(S, I, and R)**. In this model demographic processes are not considered, which means that births, migration and natural deaths are ignored, and the total population is constant. Therefore, the transmission between infected and susceptible individuals occurs by direct contact.

2.1.1 Mathematical formula of the model

This model is written as a system of three non-linear **ODEs**. These equations compute the frequency of individuals in each compartment at a given time **(t)** in the total population **(N)**, and describe the transmission dynamics of the disease through direct contact between the susceptible and the infected individuals.

Here is a schematic diagram to picture this process:

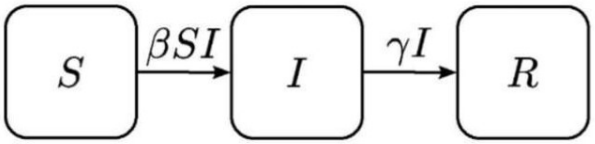

Figure 2.2: Schematic diagram of the SIR model without demography.

As shown in figure (2.2), where $\boldsymbol{\beta}$ and $\boldsymbol{\gamma}$ are positive parameters, the system of **ODEs**

is written as follows:

$$\begin{cases} \dfrac{dS}{dt} = & -\beta SI, \\ \dfrac{dI}{dt} = & \beta SI - \gamma I, \\ \dfrac{dR}{dt} = & \gamma I, \end{cases} \tag{2.1}$$

with the following initial conditions: $\boldsymbol{S(0) = S_0}$, $\boldsymbol{I(0) = I_0}$, $\boldsymbol{R(0) = R_0}$ and $\boldsymbol{N(0) = N_0}$, where $\boldsymbol{N_0}$ is the initial total population size.
Here is the interpretation of the model:

- $\boldsymbol{N(t)}$: The total population size at time **(t)**.
- $\boldsymbol{S(t)}$: Susceptible individuals at time **(t)** who are healthy but can become infected.
- $\boldsymbol{I(t)}$: Infected individuals at time **(t)** who carry the infection and are capable of transmitting it.
- $\boldsymbol{R(t)}$: Recovered individuals at time **(t)** who have recovered and gained immunity.
- $\boldsymbol{dS/dt}$: The change of the susceptible population at a given time **(t)**.
- $\boldsymbol{dI/dt}$: The change of the infected population at a given time **(t)**.
- $\boldsymbol{dR/dt}$: The change of the recovered population at a given time **(t)**.
- $\boldsymbol{\beta}$: The transmission rate of the disease through interactions between susceptible and infected individuals.
- $\boldsymbol{\gamma}$: The recovery rate at which the infected individuals are recovered from the disease and gained immunity or removed due to mortality caused by the disease.
- $\boldsymbol{\beta SI}$ **(Incidence term)**: The infection term, which represents the number of susceptible individuals becoming infected at a given time **(t)**.

2.1.2 Analysis of the model

Theorem 2.1.1

The system described by (2.1) admits a unique solution.

Proof

Since the functions defining system (2.1) are of class $\boldsymbol{C^1}$*, they are locally Lipschitz continuous on* $\mathbb{R}^{\mathbf{3}}_{+}$*. Hence, by the Cauchy–Lipschitz theorem (1.3.1), for any given*

initial condition, there exists a unique local solution to the initial value problem associated with system (2.1).

We add the three equations of system (2.1) to obtain the total population:

$$\begin{aligned}\frac{dN}{dt} &= \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \\ &= (-\beta SI) + (+\beta SI - \gamma I) + (\gamma I) \\ &= 0\end{aligned}$$

Since $\dfrac{dN}{dt} = 0$, it then follows that $N(t) = N_0$, where N_0 is a constant representing the initial total population size. Therefore, in the absence of demography effects, the total population remains constant over time.

Proposition 2.1.1. *The set :*

$$\boldsymbol{\Omega = \left\{(S, I, R) \in \mathbb{R}^3_+ \ : \ S + I + R = N\right\}},$$

is positively invariant.

Proof

The total population $\boldsymbol{N}$ *is divided into three epidemiological compartments:*

$$\boldsymbol{N(t) = S(t) + I(t) + R(t).}$$

Differentiating $\boldsymbol{N}$ *with respect to* t *and substituting from system (2.1), we obtain:*

$$\boldsymbol{\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = (-\beta SI) + (\beta SI - \gamma I) + (\gamma I) = 0.}$$

By a straightforward computation, we find:

$$\boldsymbol{N(t) = N(0) = N_0, \quad \forall t \geq 0.}$$

Consequently, the total population remains constant over time, which shows that the set $\boldsymbol{\Omega = \left\{(S, I, R) \in \mathbb{R}^3_+ \ : \ S + I + R = N_0\right\}}$ *is positively invariant.*

2.1.3 Equilibrium points

The equilibrium points of system (2.1) satisfy:

$$\frac{dS}{dt} = 0, \quad \frac{dI}{dt} = 0, \quad \frac{dR}{dt} = 0.$$

So we solve:

$$\begin{cases} -\beta SI = 0, \\ \beta SI - \gamma I = 0, \\ \gamma I = 0, \end{cases} \tag{2.2}$$

from the third equation of (2.2), we obtain $\boldsymbol{I^* = 0}$ (since $\gamma > 0$).
Substituting $\boldsymbol{I^* = 0}$ in the first two equations of (2.2) yields trivial identities $\mathbf{(0 = 0)}$, providing no further condition on $\boldsymbol{S^*}$.

Using the conservation of the population $\boldsymbol{N = S + I + R}$ with $\boldsymbol{I^* = 0}$ yields: $\boldsymbol{N = S^* + R^*}$.
In the absence of infection, no individuals enter the recovered class, consequently $\boldsymbol{R^* = 0}$ and $\boldsymbol{S^* = N}$.
Collecting these results, we obtain the following equilibrium point:

$$\boxed{E_0 = (N, 0, 0)}$$

Since $\boldsymbol{I^* = 0}$, this point represents the disease-free equilibrium **(DFE)**.

Remark 2.1.1

In the absence of demography, the SIR model admits only one equilibrium point wich is the disease-free equilibrium ***DFE****, since any endemic equilibrium* ***EE*** *requires* $\boldsymbol{I > 0}$*, which is not possible at steady state unless parameters are modified.*

- **Disease-free equilibrium (DFE):** a state where no individuals in the population are infected, which means that the disease is absent.
- **Endemic equilibrium (EE):** a state where the disease persists in the population over time.

2.1.4 The basic reproduction number

Following the next generation method (1.7.1), the basic reproduction number of model (2.1) is calculated as follows:

- **Step 1 (Identifying the infected variables):** In the **SIR** model, the only infected variable is **I**.

- **Step 2:** Writing the equation corresponding to the infected variable in the form:

$$\frac{\boldsymbol{dI}}{\boldsymbol{dt}} = \boldsymbol{\mathcal{F}(x) - \mathcal{V}(x)}.$$

From the model:

$$\frac{\boldsymbol{dI}}{\boldsymbol{dt}} = \boldsymbol{\beta SI - \gamma I}.$$

We have: $\boldsymbol{\mathcal{F} = \beta SI}$ (new infections), and $\boldsymbol{\mathcal{V} = \gamma I}$ (recovery).

- **Step 3 (Linearizing around the DFE):**
At the DFE:

$$\boldsymbol{E_0 = (N, 0, 0)},$$

we compute the derivatives:

$$\boldsymbol{F = \left.\frac{\partial(\beta SI)}{\partial I}\right|_{E_0} = \beta N}.$$

$$\boldsymbol{V = \left.\frac{\partial(\gamma I)}{\partial I}\right|_{E_0} = \gamma}.$$

- **Step 4 (Next generation matrix):** With only one infected compartment, the next generation matrix reduces to:

$$\begin{aligned} K &= FV^{-1} \\ &= \frac{F}{V} \\ &= \frac{\beta N}{\gamma}. \end{aligned}$$

Since the next generation matrix reduces to a scalar, its spectral radius is equal to its unique eigenvalue, yielding:

$$\boxed{\mathcal{R}_0 = \frac{\beta N}{\gamma}.}$$

2.1.5 Stability analysis

Stability of the Disease Free Equilibrium

The Jacobian matrix evaluated at the **DFE ($\boldsymbol{E_0}$)** is:

$$J(E_0) = \begin{pmatrix} 0 & -\beta N & 0 \\ 0 & \beta N - \gamma & 0 \\ 0 & \gamma & 0 \end{pmatrix}.$$

The characteristic equation $\boldsymbol{\det(J(E_0) - \lambda I) = 0}$ yields:

$$\lambda^2\big[(\beta N - \gamma) - \lambda\big] = 0.$$

The eigenvalues are:

$$\boldsymbol{\lambda_1 = \lambda_2 = 0} \text{ (with multiplicity 2)},$$

and

$$\boldsymbol{\lambda_3 = \beta N - \gamma = \gamma(\mathcal{R}_0 - 1)}.$$

Remark 2.1.2

*The Jacobian matrix at the **DFE** has two zero eigenvalues. Consequently, the linearization theorem (1.9.1) cannot be used to determine the stability of $\boldsymbol{E_0}$. Therefore, we must use a different method.*

To determine the stabilty of $\boldsymbol{E_0}$, we examine the behavior of the system near the equilibrium point. Assume a small perturbation near the equilibrium, where the susceptible population $\boldsymbol{S}$ is close to $\boldsymbol{N}$ and the infected population $\boldsymbol{I}$ is small but strictly positive. Substituting $\boldsymbol{S \approx N}$ into the infected equation of system (2.1) gives:

$$\frac{\boldsymbol{dI}}{\boldsymbol{dt}} \approx \boldsymbol{\beta N I - \gamma I = I(\beta N - \gamma)},$$

this differential equation has the following solution:

$$\boldsymbol{I(t) \approx I_0 e^{(\beta N - \gamma)t} = I_0 e^{\gamma(\frac{\beta N}{\gamma} - 1)t}}.$$

Since $\boldsymbol{\mathcal{R}_0 = \dfrac{\beta N}{\gamma}}$, hence:

$$\boxed{\boldsymbol{I(t) \approx I_0 e^{\gamma(\mathcal{R}_0 - 1)t}}}.$$

Consequently:

- If $\boldsymbol{\mathcal{R}_0 < 1}$, then $\boldsymbol{I(t) \to 0}$ as $\boldsymbol{t \to \infty}$. The disease free equilibrium $\boldsymbol{E_0}$ is **locally asymptotically stable**.

- If $\boldsymbol{\mathcal{R}_0 > 1}$, then $\boldsymbol{I(t) \to \infty}$ (grows exponentially) as $\boldsymbol{t \to \infty}$. The disease free equilibrium $\boldsymbol{E_0}$ is **unstable**.

- If $\boldsymbol{\mathcal{R}_0 = 1}$, then $\boldsymbol{I(t) \approx I_0}$, this approximation gives no growth or decay. This is the epidemic threshold case.

2.2 SIR model with demography

Demography is an addition to the classical **SIR** model that is described in detail by **Matt J.Keeling** and **Pejman Rohani** [21]. The **SIR** model with demography [3] also divides the population into three main compartments **S** (susceptible), **I** (infected), and **R** (recovered) individuals. It incorporates demographic processes (births, migration and natural deaths), assuming that all individuals entering the population, whether by birth or migration, are susceptible since they are not yet infected. It also assumes that individuals from each compartment may die naturally.

2.2.1 Mathematical formula of the model

The interactions between the compartments and the demographic processes are described by a system of **ODEs** representing the temporal evolution of population in each compartment.

To understand this process, here is a schematic diagram shows the interactions between the compartments:

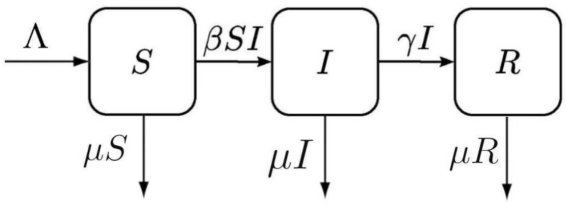

Figure 2.3: Schematic diagram of the SIR model with demography.

As shown in figure (2.3) where $\boldsymbol{\Lambda, \mu, \beta,}$ and $\boldsymbol{\gamma}$ are positive parameters, the system of **ODEs** is written as follows:

$$\begin{cases} \dfrac{dS}{dt} = & \Lambda - \beta SI - \mu S, \\ \dfrac{dI}{dt} = & \beta SI - \gamma I - \mu I, \\ \dfrac{dR}{dt} = & \gamma I - \mu R, \end{cases} \tag{2.3}$$

with the following initial conditions: $\boldsymbol{S(0) = S_0}$, $\boldsymbol{I(0) = I_0}$, $\boldsymbol{R(0) = R_0}$, and $\boldsymbol{N(0) = N_0}$ where $\boldsymbol{N_0}$ is the initial total population size.
The interpretation of the parameters $\boldsymbol{\beta, \gamma}$ and the compartments $\boldsymbol{S, I, R}$ is the same as in Section (2.1) The only differences are the addition of:

- $\boldsymbol{\Lambda}$: The recruitment rate (births or migration).
- $\boldsymbol{\mu}$: The natural death rate for all compartments.

2.2.2 Analysis of the model

Theorem 2.2.1

The system described by (2.3) admits a unique solution.

Proof

Since the functions of system (2.3) are of class $\boldsymbol{C^1}$, they are locally Lipschitz on $\mathbb{R}^{\mathbf{3}}_{+}$. By the Cauchy-Lipschitz theorem (1.3.1), we deduce the existence and uniqueness of the solution to the initial value problem associated with system (2.3)

We add the three equations of system (2.3) to obtain the total population :

$$\begin{aligned} \frac{dN}{dt} &= \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \\ &= (\Lambda - \beta SI - \mu S) + (\beta SI - \gamma I - \mu I) + (\gamma I - \mu R) \\ &= \Lambda - \mu S - \mu I - \mu R \\ &= \Lambda - \mu(S + I + R). \end{aligned}$$

Since $N = S + I + R$, we have $\dfrac{dN}{dt} = \Lambda - \mu N$, therefore the total population is not constant.

Proposition 2.2.1. *The set :*

$$\boldsymbol{\Omega = \left\{ (S, I, R) \in \mathbb{R}^{3}_{+} \ : \ S + I + R \leq \max\left(N(0), \frac{\Lambda}{\mu} \right) \right\},}$$

is positively invariant.

Proof

The total population $\boldsymbol{N}$ is divided into three epidemiological compartments mentioned previously, which can be expressed as:

$$\boldsymbol{N(t) = S(t) + I(t) + R(t).}$$

Differentiating $\boldsymbol{N}$ with respect to $\boldsymbol{t}$ and substituting from system (2.3), we obtain:

$$\boldsymbol{\frac{dN}{dt} = \Lambda - \mu N(t).}$$

Solving this linear differential equation, we get:

$$\boldsymbol{N(t) = N(0)e^{-\mu t} + \frac{\Lambda}{\mu}\left(1 - e^{-\mu t}\right).}$$

Consequently, as $\boldsymbol{t \to \infty}$*, we have* $\boldsymbol{N(t) \to \frac{\Lambda}{\mu}}$*, which shows that the set:*

$$\boldsymbol{\Omega = \left\{(S, I, R) \in \mathbb{R}^3_+ \ : \ S + I + R \leq \max\left(N(0), \frac{\Lambda}{\mu}\right)\right\},}$$

is positively invariant.

2.2.3 Equilibrium points

The equilibrium points of system (2.3) satisfy:

$$\frac{dS}{dt} = 0, \quad \frac{dI}{dt} = 0, \quad \frac{dR}{dt} = 0.$$

So we solve:

$$\begin{cases} \Lambda - \beta SI - \mu S = 0, \\ \beta SI - \gamma I - \mu I = 0, \\ \gamma I - \mu R = 0. \end{cases} \tag{2.4}$$

From the second equation of (2.4):

$$\beta SI - (\gamma + \mu)I = 0 \quad \Longrightarrow \quad I\big[\beta S - (\gamma + \mu)\big] = 0.$$

This gives two distinct cases:

- **Case 1:** $I = 0$.
- **Case 2:** $S = \dfrac{\gamma + \mu}{\beta}$, with $I > 0$.

Case 1: Disease-Free Equilibrium (DFE)

Substituting $I = 0$ into the first and third equations of (2.4):

- First equation: $\Lambda - \mu S = 0 \quad \Longrightarrow \quad S = \dfrac{\Lambda}{\mu}$.
- Third equation: $-\mu R = 0 \quad \Longrightarrow \quad R = 0$.

Hence the disease-free equilibrium is:

$$\boxed{E_0 = \left(\frac{\Lambda}{\mu}, 0, 0\right)}$$

Case 2: Endemic Equilibrium (EE)

When $I \neq 0$, we obtain from the second equation:

$$S = \frac{\gamma + \mu}{\beta}.$$

Substituting S into the first equation of (2.4):

$$\Lambda - (\gamma + \mu)I - \mu \cdot \frac{\gamma + \mu}{\beta} = 0,$$

which yields:

$$I = \frac{\Lambda}{\gamma + \mu} - \frac{\mu}{\beta} = \frac{\Lambda\beta - \mu(\gamma + \mu)}{\beta(\gamma + \mu)}.$$

Substituting I into the third equation of (2.4):

$$\gamma I - \mu R = 0.$$

Which yields:

$$R = \frac{\gamma I}{\mu} = \frac{\gamma}{\mu}\left(\frac{\Lambda}{\gamma + \mu} - \frac{\mu}{\beta}\right).$$

Thus the endemic equilibrium is:

$$\boxed{E^* = \left(\frac{\gamma + \mu}{\beta}, \frac{\Lambda\beta - \mu(\gamma + \mu)}{\beta(\gamma + \mu)}, \frac{\gamma}{\mu}\left(\frac{\Lambda}{\gamma + \mu} - \frac{\mu}{\beta}\right)\right).}$$

For this equilibrium to be biologically meaningful, all components must be positive. Since $S > 0$ and $R > 0$ whenever $I > 0$, the necessary and sufficient condition is:

$$\boxed{I > 0 \iff \frac{\Lambda\beta}{\mu(\gamma + \mu)} > 1.}$$

2.2.4 The basic reproduction number

Following the next generation method (1.7.1), the basic reproduction number of model (2.3) is calculated as follows:

- **Step 1 (Identifying the infected variables):** In the **SIR** model, the only infected variable is **I**.

- **Step 2:**
  Writing the equation corresponding to the infected variable in the form:

$$\frac{\boldsymbol{dI}}{\boldsymbol{dt}} = \boldsymbol{\mathcal{F}}(\boldsymbol{x}) - \boldsymbol{\mathcal{V}}(\boldsymbol{x}).$$

  From the model (2.3):

$$\frac{\boldsymbol{dI}}{\boldsymbol{dt}} = \boldsymbol{\beta SI} - \boldsymbol{\gamma I} - \boldsymbol{\mu I}.$$

  We have: $\boldsymbol{\mathcal{F}} = \boldsymbol{\beta SI}$ (new infections), and $\boldsymbol{\mathcal{V}} = \boldsymbol{(\gamma + \mu)I}$ (transfers out).

- **Step 3 (Linearizing around the DFE):**
  At the DFE:

$$\boldsymbol{E_0} = \left(\frac{\boldsymbol{\Lambda}}{\boldsymbol{\mu}}, \boldsymbol{0}, \boldsymbol{0}\right),$$

  we compute the derivatives:

$$\boldsymbol{F} = \left.\frac{\boldsymbol{\partial(\beta SI)}}{\boldsymbol{\partial I}}\right|_{\boldsymbol{E_0}} = \boldsymbol{\beta} \cdot \frac{\boldsymbol{\Lambda}}{\boldsymbol{\mu}} = \frac{\boldsymbol{\beta\Lambda}}{\boldsymbol{\mu}}.$$

$$\boldsymbol{V} = \left.\frac{\boldsymbol{\partial((\gamma + \mu)I)}}{\boldsymbol{\partial I}}\right|_{\boldsymbol{E_0}} = \boldsymbol{\gamma + \mu}.$$

- **Step 4 (Next generation matrix):**
  With only one infected compartment, the next generation matrix reduces to:

$$\begin{aligned} K &= FV^{-1} \\ &= \frac{F}{V} \\ &= \frac{\beta\Lambda}{\mu(\gamma + \mu)}. \end{aligned}$$

  Since the next generation matrix reduces to a scalar, its spectral radius is equal to its unique eigenvalue, yielding:

$$\boxed{\mathcal{R}_0 = \frac{\beta\Lambda}{\mu(\gamma + \mu)}.}$$

Remark 2.2.1

Noting that: $\boldsymbol{\mathcal{R}_0 = \dfrac{\beta\Lambda}{\mu(\gamma+\mu)}}$*, the endemic equilibrium* $\boldsymbol{E^*}$ *can be rewritten as:*

$$\boxed{E^* = \left(\frac{\gamma+\mu}{\beta}, \frac{\mu(\mathcal{R}_0-1)}{\beta}, \frac{\gamma(\mathcal{R}_0-1)}{\beta}\right).}$$

Consequently, $\boldsymbol{E^*}$ *is biologically meaningful (all components are positive)* ***if and only if*** $\boldsymbol{\mathcal{R}_0 > 1}$.

2.2.5 Stability analysis

Stability of the Disease Free Equilibrium

The Jacobian matrix of system (2.3) evaluated at the **DFE** is:

$$J(E_0) = \begin{pmatrix} -\mu & -\dfrac{\beta\Lambda}{\mu} & 0 \\ 0 & \dfrac{\beta\Lambda}{\mu} - (\gamma+\mu) & 0 \\ 0 & \gamma & -\mu \end{pmatrix},$$

The characteristic equation $\boldsymbol{\det(J(E_0) - \lambda I) = 0}$ yields:

$$(-\mu-\lambda)^2\left(\frac{\beta\Lambda}{\mu} - (\gamma+\mu) - \lambda\right) = 0.$$

The eigenvalues are:

$$\boldsymbol{\lambda_1 = \lambda_2 = -\mu} \text{ (with multiplicity 2)},$$

and

$$\boldsymbol{\lambda_3 = \frac{\beta\Lambda}{\mu} - (\gamma+\mu) = (\gamma+\mu)(R_0-1)}.$$

Theorem 2.2.2: Stability of the DFE

The disease-free equilibrium $\boldsymbol{E_0}$ *is locally asymptotically stable if* $\boldsymbol{\mathcal{R}_0 < 1}$ *and unstable if* $\boldsymbol{\mathcal{R}_0 > 1}$.

Proof

Since $\boldsymbol{\lambda_1 = \lambda_2 = -\mu < 0}$*, the stability is determined by* $\boldsymbol{\lambda_3}$*. When* $\boldsymbol{\mathcal{R}_0 < 1}$*, we have* $\boldsymbol{\lambda_3 < 0}$ *and all eigenvalues have negative real parts, implying local asymptotic stability. On the other hand, when* $\boldsymbol{\mathcal{R}_0 > 1}$*, we have* $\boldsymbol{\lambda_3 > 0}$ *and the* ***DFE*** *becomes unstable.*

Stability of the Endemic Equilibrium

The Jacobian matrix of system (2.3) evaluated at the **EE** is:

$$J(E^*) = \begin{pmatrix} -\beta I^* - \mu & -\beta S^* & 0 \\ \beta I^* & \beta S^* - (\gamma + \mu) & 0 \\ 0 & \gamma & -\mu \end{pmatrix}.$$

Substituting the equilibrium values $S^* = \dfrac{\gamma + \mu}{\beta}$ and $I^* = \dfrac{\mu(\mathcal{R}_0 - 1)}{\beta}$, and noting that $\beta S^* - (\gamma + \mu) = 0$, we obtain:

$$J(E^*) = \begin{pmatrix} -\mu\mathcal{R}_0 & -(\gamma + \mu) & 0 \\ \mu(\mathcal{R}_0 - 1) & 0 & 0 \\ 0 & \gamma & -\mu \end{pmatrix}.$$

The characteristic equation $\boldsymbol{\det(J(E^*) - \lambda I) = 0}$ yields:

$$(-\mu - \lambda)\left[\lambda^2 + \mu\mathcal{R}_0\lambda + \mu(\mathcal{R}_0 - 1)(\gamma + \mu)\right] = 0.$$

The eigenvalues are:

$$\boldsymbol{\lambda_1 = -\mu},$$

and

$$\boldsymbol{\lambda_{2,3} = \frac{-\mu R_0 \pm \sqrt{(\mu R_0)^2 - 4\mu(\gamma + \mu)(R_0 - 1)}}{2}}.$$

Theorem 2.2.3: Stability of the EE

The endemic equilibrium $\boldsymbol{E^*}$ *is locally asymptotically stable if* $\boldsymbol{\mathcal{R}_0 > 1}$ *and doesn't exist (not biologically meaningful) if* $\boldsymbol{\mathcal{R}_0 \leq 1}$.

Proof

Since the eigenvalues are $\boldsymbol{\lambda_1 = -\mu < 0}$ *and the roots* $\boldsymbol{\lambda_2, \lambda_3}$ *of the quadratic factor:* $\boldsymbol{\lambda^2 + a_1\lambda + a_2 = 0}$, *where*

$$\boldsymbol{a_1 = \mu\mathcal{R}_0}, \qquad \boldsymbol{a_2 = \mu(\mathcal{R}_0 - 1)(\gamma + \mu)}.$$

When $\boldsymbol{\mathcal{R}_0 > 1}$, *we have:*

- $\boldsymbol{a_1 = \mu\mathcal{R}_0 > 0}$,

- $a_2 = \mu(\mathcal{R}_0 - 1)(\gamma + \mu) > 0.$

By the ***Routh-Hurwitz*** *criterion for quadratic polynomials (1.9.2), all roots of* $\lambda^2 + a_1\lambda + a_2 = 0$ *have negative real parts if and only if* $a_1 > 0$ *and* $a_2 > 0$. *Since these conditions are satisfied for* $\mathcal{R}_0 > 1$, *the eigenvalues* λ_2 *and* λ_3 *have negative real parts.*
Consequently, all eigenvalues of $J(E^*)$ *have negative real parts. Therefore, the endemic equilibrium* E^* *is locally asymptotically stable whenever* $\mathcal{R}_0 > 1$. *On the other hand, when* $\mathcal{R}_0 \leq 1$, *the endemic equilibrium doesn't exist.*

Chapter 3

Travelling Waves Of The Diffusive SIR Model

The **Kermack–McKendrick SIR** model describes the temporal evolution of a population assumed to be well-mixed and spatially homogeneous. However, this framework ignores spatial structures that play an important role in describing the spread of communicable diseases. The importance of these factors has been witnessed in recent global epidemic outbreaks of **SARS**, **H1N1**, and **avian influenza** [4, 5]. Following **H. Wang** et al.[9], we extend the basic model by incorporating diffusion terms to represent the random movement of individuals **(notably infectious agents or the host population)**, transforming the system into reaction–diffusion equations.

3.1 The mass action incidence model

The diffusive **SIR** model without demography is the classical spatial extension, which has been fundamental to our understanding of disease dynamics in populations with random movement, where the transmission follows mass-action incidence. This model was studied by **Kallen** [17], **Hosono** and **Ilyas** [12], who established the existence of traveling wave solutions (solutions that propagate with constant shape and speed). Their work showed that the spatial propagation of an epidemic can be characterized by a traveling wave connecting an initial disease-free state to another disease-free state, with the minimum wave speed.

3.1.1 Mathematical formula of the model

This model divides the total population into three compartments (Susceptible, Infected and Recovered) , ignoring the recovered individuals **R** in the transmission dynamics. In this model, demographic processes are not considered, which means that births, migration and natural deaths are ignored, and the total population is not constant. Therefore, transmission between infected and susceptible individuals occurs by direct contact with

mass-action incidence.
The model is written as a system of two non-linear reaction–diffusion equations:

$$\begin{cases} \partial_t S = d_1 \partial_{xx} S - \beta SI, \\ \partial_t I = d_2 \partial_{xx} I + \beta SI - \gamma I, \end{cases} \tag{3.1}$$

with the following initial conditions: $\boldsymbol{S(0) = S_0}$, $\boldsymbol{I(0) = I_0}$, and $\boldsymbol{N(0) = N_0}$ where $\boldsymbol{N_0}$ is the initial total population size. Here is the interpretation of the model:

- $\boldsymbol{N(t)}$: The total population size at time **(t)**.
- $\boldsymbol{S(t)}$: Susceptible individuals at time **(t)** who are healthy but can become infected.
- $\boldsymbol{I(t)}$: Infected individuals at time **(t)** who carry the infection and are capable of transmitting it.
- $\boldsymbol{\partial_t S}$: The change of susceptible individuals at a given position $\boldsymbol{(x)}$ and time $\boldsymbol{(t)}$.
- $\boldsymbol{\partial_t I}$: The change of infected individuals at a given position $\boldsymbol{(x)}$ and time $\boldsymbol{(t)}$.
- $\boldsymbol{d_1}$: The diffusion rate of susceptible individuals.
- $\boldsymbol{d_2}$: The diffusion rate of infected individuals.
- $\boldsymbol{d_1 \partial_{xx} S}$: The diffusion term, describes how susceptible individuals randomly spread from area to area.
- $\boldsymbol{d_2 \partial_{xx} I}$: The diffusion term, describes how infected individuals randomly spread from area to area.
- $\boldsymbol{\beta}$: The transmission rate of the disease through interactions between susceptible and infected individuals.
- $\boldsymbol{\gamma}$: The recovery rate at which infected individuals are recovered from the disease and gained immunity.
- $\boldsymbol{\beta SI}$ **(Incidence term)**: The infection term, which represents the number of susceptible individuals becoming infected at a given time **(t)**.

3.1.2 Existence and uniqueness

Theorem 3.1.1: Existence and Uniqueness

Let

$$Y = C(\overline{\Omega}, \mathbb{R}^3)$$

be the Banach space endowed with the supremum norm, and consider the diffusive SIR system with initial condition

$$u_0 = (S_0, I_0, R_0) \in Y.$$

Since the nonlinear operator $F : Y \to Y$ is locally Lipschitz on (Y) [29, Lemma 3.1], it follows from [6, Proposition 4.16] that for every $u_0 \in Y$, there exists a unique maximal solution

$$u(\cdot, u_0) \in C([0, T_0), Y),$$

where $T_0 \in (0, \infty]$. Moreover, either $T_0 = \infty$ or

$$\limsup_{t \to T_0^-} |u(t, u_0)|_Y = \infty.$$

Proof

The result follows from the local Lipschitz continuity of (F) on (Y) established in [29, Lemma 3.1] and the classical semilinear evolution equation theory in [6, Proposition 4.16].

3.1.3 Equilibrium points and basic reproduction number

We consider the spatially homogeneous system (no diffusion terms) since, at equilibrium the spatial derivatives are zero. Hence we look at the following **ODE** system :

$$\begin{cases} \dfrac{dS}{dt} = -\beta SI, \\ \dfrac{dI}{dt} = \beta SI - \gamma I. \end{cases}$$

The equilibrium points satisfy:

$$\begin{cases} \dfrac{dS}{dt} = 0, \\ \dfrac{dI}{dt} = 0. \end{cases} \tag{3.2}$$

From the second equation of system (3.2):

$$\beta SI - \gamma I = 0 \Longrightarrow I(\beta S - \gamma) = 0,$$

this gives two distinct cases:

- **Case 1:** $I = 0$.
- **Case 2:** $S = \dfrac{\gamma}{\beta}$, with $I > 0$.

Case 1: Disease-Free Equilibrium (DFE)

If $I = 0$, the second equation is satisfied for any $S \geq 0$. Also, the first equation is satisfied (since $I = 0$). Therefore, there are infinitely many disease-free equilibria:

$$\boxed{E_0 = (S_0, 0), \text{ with } S_0 \geq 0,}$$

any point with no infected individuals is an equilibrium.

Case 2: Endemic Equilibrium (EE)

If $S^* = \dfrac{\gamma}{\beta}$, with $I > 0$. Substituting into the first equation of (3.2) gives:

$$\frac{dS}{dt} = -\beta \cdot \frac{\gamma}{\beta} \cdot I = -\gamma I \neq 0, \text{ (since } I > 0 \text{ and } \gamma > 0),$$

therefore, no endemic equilibrium exists in the spatially homogeneous system. Following the next-generation method (1.7.1), the basic reproduction number is given by:

$$\boxed{\boldsymbol{R_0 = \frac{\beta S_0}{\gamma}.}}$$

3.1.4 Traveling wave

To investigate the spatial spread of the epidemic, we seek the traveling waves of the form:

$$S(x,t) = S(\xi), \quad I(x,t) = I(\xi),$$

where

$$\xi = x + ct,$$

and $\boldsymbol{c > 0}$ denotes the traveling wave speed. Applying the chain rule gives the following:

$$\frac{\partial S}{\partial t} = cS'(\xi), \quad \frac{\partial^2 S}{\partial x^2} = S''(\xi),$$

and similarly:

$$\frac{\partial I}{\partial t} = cI'(\xi), \quad \frac{\partial^2 I}{\partial x^2} = I''(\xi),$$

substituting these expressions into the reaction–diffusion system (3.1) yields:

$$\begin{cases} cS' = d_1 S'' - \beta SI, \\ cI' = d_2 I'' + \beta SI - \gamma I, \end{cases}$$

rearranging:

$$\begin{cases} d_1 S'' - cS' - \beta SI = 0, \\ d_2 I'' - cI' + \beta SI - \gamma I = 0. \end{cases}$$

Following **Wang et al.** [9], the traveling waves is assumed to connect two equilibrium states at spatial infinity. Therefore, the boundary conditions are written as follows:

$$S(-\infty) = S_{-\infty}, \quad I(-\infty) = 0,$$

and

$$S(+\infty) = S_{+\infty}, \quad I(+\infty) = 0,$$

the quantity $S_{-\infty}$ represents the density of susceptible population ahead of the epidemic wave before the infection reaches the population, while $S_{+\infty}$ denotes the density of susceptible population after the passage of the wave. In particular, for traveling waves analysis, the two equilibrium states connected by the wave are:

$$E_0 = (S_{-\infty}, 0), \qquad E_1 = (S_{+\infty}, 0),$$

and the basic reproduction number is written as follows:

$$R_0 = \frac{\beta S_{-\infty}}{\gamma}.$$

3.1.5 Wave speed

To determine the propagation speed of the epidemic wave, we linearize the infected equation around the disease-free equilibrium

$$E_0 = (S_{-\infty}, 0).$$

Near the disease-free state, the infected equation becomes:

$$d_2 I'' - cI' + (\beta S_{-\infty} - \gamma)I = 0.$$

Assuming an exponential solution of the form

$$I(\xi) = e^{\lambda\xi},$$

substituting into the previous equation yields:

$$d_2\lambda^2 - c\lambda + (\beta S_{-\infty} - \gamma) = 0.$$

For real solutions to exist, the discriminant must satisfy

$$\Delta = c^2 - 4d_2(\beta S_{-\infty} - \gamma) \geq 0.,$$

hence:

$$c \geq 2\sqrt{d_2(\beta S_{-\infty} - \gamma)}.$$

Using the basic reproduction number $\boldsymbol{R_0 = \dfrac{\beta S_{-\infty}}{\gamma}}$, we can also write:

$$\boxed{\boldsymbol{c^* = 2\sqrt{d_2\gamma(R_0 - 1)}.}}$$

In particular, with the aid of **Dunbar** [1, 2], **Hossono** and **Ilyas** [13] proved that if the basic reproduction number $\boldsymbol{\mathcal{R}_0 = \dfrac{\beta S_{-\infty}}{\gamma} > 1}$, then for each $\boldsymbol{c \geq c^*}$ system (3.1) has a traveling wave solution $\boldsymbol{(S(x+ct), I(x+ct))}$. On the other hand, there is no traveling solution for (3.1) if $\boldsymbol{\mathcal{R}_0 = \dfrac{\beta S_{-\infty}}{\gamma} \leq 1}$.

3.2 The standard incidence model (SI)

In classical epidemic models, the incidence rate(the rate at which new infections occur) is often assumed to be proportional to the product of susceptible and infected populations. This is known as mass-action incidence. However, for many realistic human diseases, the number of contacts per individual does not increase linearly with population density due to behavioral or social constraints.

3.2.1 Mathematical formula of the model

This model divides the total population into three compartments (Susceptible, Infected and Recovered), neglecting recovered individuals **R**. Demographic processes such as births and natural deaths are also ignored. The transmission of the disease follows the fraction incidence, where the infection rate depends on the fraction of infected individuals within the population.

The model is written as a system of two non-linear reaction–diffusion equations:

$$\begin{cases} \partial_t S = d_1 \partial_{xx} S - \dfrac{\beta SI}{S+I}, \\ \partial_t I = d_2 \partial_{xx} I + \dfrac{\beta SI}{S+I} - \gamma I, \end{cases} \tag{3.3}$$

with the following initial conditions: $\boldsymbol{S(0) = S_0}$, $\boldsymbol{I(0) = I_0}$, and $\boldsymbol{N(0) = N_0}$ where $\boldsymbol{N_0}$ is the initial total population size.
The interpretation of the parameters $\boldsymbol{d_1, d_2, \beta, \gamma}$ and the diffusion terms is the same as in section (3.1). The only difference is the incidence term, which is now given by the fraction incidence $\dfrac{\boldsymbol{\beta SI}}{\boldsymbol{S+I}}$. This term represents the number of susceptible individuals becoming infected at a given time $\mathbf{(t)}$.

3.2.2 Existence and uniqueness

Theorem 3.2.1: Existence and Uniqueness

Let

$$Y = C(\overline{\Omega}, \mathbb{R}^3)$$

be the Banach space endowed with the supremum norm, and consider the diffusive SIR system with initial condition

$$u_0 = (S_0, I_0, R_0) \in Y.$$

Since the nonlinear operator $F : Y \to Y$ is locally Lipschitz on (Y) [29, Lemma 3.1], it follows from [6, Proposition 4.16] that for every $u_0 \in Y$, there exists a unique maximal solution

$$u(\cdot, u_0) \in C([0, T_0), Y),$$

where $T_0 \in (0, \infty]$. Moreover, either $T_0 = \infty$ or

$$\limsup_{t \to T_0^-} |u(t, u_0)|_Y = \infty.$$

Proof

The result follows from the local Lipschitz continuity of (F) on (Y) established in [29, Lemma 3.1] and the classical semilinear evolution equation theory in [6, Proposition 4.16].

3.2.3 Equilibrium points and basic reproduction number

We consider the spatially homogeneous system (no diffusion terms) since at equilibrium the spatial derivatives are zero. Hence we look at the following **ODE system** :

$$\begin{cases} \dfrac{dS}{dt} = -\dfrac{\beta SI}{S+I}, \\ \dfrac{dI}{dt} = \dfrac{\beta SI}{S+I} - \gamma I. \end{cases}$$

The equilibrium points satisfy:

$$\begin{cases} \dfrac{dS}{dt} = 0, \\ \dfrac{dI}{dt} = 0. \end{cases} \tag{3.4}$$

From the first equation of system (3.4):

$$-\frac{\beta SI}{S+I} = 0 \quad \Longrightarrow \quad SI = 0,$$

this gives two distinct cases:

- **Case 1**: $I = 0$.
- **Case 2**: $S = 0$, with $I > 0$.

Case 1: Disease-Free Equilibrium (DFE)

If $I = 0$, the second equation of (3.4) is satisfied (since both terms are zero). The first equation is also satisfied. Therefore, there are infinitely many disease-free equilibria :

$$\boxed{E_0 = (S_0, 0), \quad S_0 \geq 0,}$$

any point with no infected individuals is an equilibrium.

Case 2: Endemic Equilibrium (EE)

If $S = 0$, the first equation of (3.4) is satisfied. Substituting $S = 0$ into the second equation :

$$\frac{\beta \cdot 0 \cdot I}{0+I} - \gamma I = -\gamma I \neq 0, \text{ (since } I > 0 \text{ and } \gamma > 0).$$

Therefore, no endemic equilibrium exists in the spatially homogeneous system. Following the next-generation method (1.7.1), the basic reproduction number is given by:

$$\boxed{\boldsymbol{R_0 = \frac{\beta}{\gamma}.}}$$

Remark 3.2.1

Unlike the mass-action incidence model where $\boldsymbol{\mathcal{R}_0 = \dfrac{\beta S_0}{\gamma}}$ *depends on the initial susceptible population* $\boldsymbol{S_0}$*, the basic reproduction number for the fraction incidence model is independent of* $\boldsymbol{S_0}$*.*

3.2.4 Traveling wave

To investigate the spatial spread of the epidemic, we seek traveling wave solutions of the form:

$$S(x,t) = S(\xi), \quad I(x,t) = I(\xi),$$

where

$$\xi = x + ct,$$

and $\boldsymbol{c > 0}$ denotes the traveling wave speed.
Applying the chain rule gives the following:

$$\frac{\partial S}{\partial t} = cS'(\xi), \quad \frac{\partial^2 S}{\partial x^2} = S''(\xi),$$

and similarly:

$$\frac{\partial I}{\partial t} = cI'(\xi), \quad \frac{\partial^2 I}{\partial x^2} = I''(\xi),$$

Substituting these expressions into the reaction-diffusion system (3.3) yields:

$$\begin{cases} cS' = d_1 S'' - \dfrac{\beta SI}{S+I}, \\ cI' = d_2 I'' + \dfrac{\beta SI}{S+I} - \gamma I. \end{cases}$$

Rearranging:

$$\begin{cases} d_1 S'' - cS' - \dfrac{\beta SI}{S+I} = 0, \\ d_2 I'' - cI' + \dfrac{\beta SI}{S+I} - \gamma I = 0. \end{cases}$$

Following **Wang et al.** [9], the traveling waves are assumed to connect two equilibrium states at spatial infinity. Therefore, the boundary conditions are written as follows:

$$S(-\infty) = S_{-\infty}, \quad I(-\infty) = 0,$$

and

$$S(+\infty) = S_{+\infty}, \quad I(+\infty) = 0.$$

The quantity $S_{-\infty}$ represents the density of susceptible population ahead of the epidemic wave before the infection reaches the population, while $S_{+\infty}$ denotes the density of susceptible population after the passage of the wave. In particular, for traveling wave analysis, the two equilibrium states connected by the wave are:

$$E_0 = (S_{-\infty}, 0), \text{ and } E_1 = (S_{+\infty}, 0).$$

3.2.4 Wave speed

To determine the propagation speed of the epidemic wave, we linearize the infected equation around the disease-free equilibrium

$$E_0 = (S_{-\infty}, 0).$$

Near the disease-free state, we have $S \approx S_\infty$, and for small I, we have $S + I \approx S_{-\infty}$, so:

$$\frac{\beta SI}{S+I} \approx \frac{\beta S_{-\infty} I}{S_{-\infty}} = \beta I.$$

Therefore, the infected equation becomes:

$$d_2 I'' - cI' + (\beta - \gamma)I = 0.$$

Assuming an exponential solution of the form:

$$I(\xi) = e^{\lambda \xi},$$

substituting into the previous equation yields:

$$d_2\lambda^2 - c\lambda + (\beta - \gamma) = 0.$$

For real solutions to exist, the discriminant must satisfy:

$$\Delta = c^2 - 4d_2(\beta - \gamma) \geq 0.$$

Hence,

$$c \geq 2\sqrt{d_2(\beta - \gamma)}.$$

Using the basic reproduction number $\mathcal{R}_0 = \dfrac{\beta}{\gamma}$, we can also write :

$$\boxed{\boldsymbol{c^* = 2\sqrt{d_2\gamma(\mathcal{R}_0 - 1)}.}}$$

In a more recent work, as in section (3.1) Wang et al.[33] proved a similar result for the diffusive Kermack–McKendrick SIR model with the fraction incidence, traveling waves exist if and only if $\boldsymbol{\mathcal{R}_0 = \frac{\beta}{\gamma} > 1}$.

3.3 The standard incidence model (SIR)

We now extend the previous fraction incidence model and examine a more general diffusive **Kermack–McKendrick SIR** model by including the recovered compartment **R**, with the assumption that some of the infective individuals will be removed from the population due to death caused by disease or quarantine, while others will recover and return to the community.

3.3.1 Mathematical formula of the model

This model divides the total population into three compartments (Susceptible, Infected, and Recovered). Hence, the incidence term now depends on the total population $\boldsymbol{N = S + I + R}$, i.e., $\boldsymbol{\frac{\beta SI}{S+I+R}}$. The model is written as a system of three non-linear reaction-diffusion equations:

$$\begin{cases} \partial_t S = d_1 \partial_{xx} S - \dfrac{\beta SI}{S+I+R}, \\ \partial_t I = d_2 \partial_{xx} I + \dfrac{\beta SI}{S+I+R} - \gamma I - \delta I, \\ \partial_t R = d_3 \partial_{xx} R + \gamma I, \end{cases} \tag{3.5}$$

with the following initial conditions: $\boldsymbol{S(0) = S_0}$, $\boldsymbol{I(0) = I_0}$, $\boldsymbol{R(0) = R_0}$, and $\boldsymbol{N(0) = N_0}$ where $\boldsymbol{N_0}$ is the initial total population size.
The interpretation of the parameters and diffusion terms is the same as in sections(3.1) and (3.2). The only differences are the incidence term $\boldsymbol{\frac{\beta SI}{S+I+R}}$, which now depends on the total population, and the addition of the recovered compartment **R** with its diffusion term $\boldsymbol{d_3 \partial_{xx} R}$ and the death caused by disease rate $\boldsymbol{\delta}$ for infected individuals.

3.3.2 Existence and uniqueness

Theorem 3.3.1: Existence and Uniqueness

Let

$$Y = C(\overline{\Omega}, \mathbb{R}^3)$$

be the Banach space endowed with the supremum norm, and consider the diffusive SIR system with initial condition

$$u_0 = (S_0, I_0, R_0) \in Y.$$

Since the nonlinear operator $F : Y \to Y$ is locally Lipschitz on (Y) [29, Lemma 3.1], it follows from [6, Proposition 4.16] that for every $u_0 \in Y$, there exists a unique maximal solution

$$u(\cdot, u_0) \in C([0, T_0), Y),$$

where $T_0 \in (0, \infty]$. Moreover, either $T_0 = \infty$ or

$$\limsup_{t \to T_0^-} |u(t, u_0)|_Y = \infty.$$

Proof

The result follows from the local Lipschitz continuity of (F) on (Y) established in [29, Lemma 3.1] and the classical semilinear evolution equation theory in [6, Proposition 4.16].

3.3.3 Equilibrium points and basic reproduction number

Following the same reasoning as in sections (3.1) and (3.2), the model (3.5) has infinitely many disease-free equilibria of the form:

$$\mathbf{(S,\ 0,\ R)}, \qquad S \geq 0, \quad R \geq 0,$$

and no endemic equilibrium when $\boldsymbol{I > 0}$.
Following the next-generation method (1.7.1) around the disease-free equilibrium, the basic reproduction number is given by:

$$\boxed{\boldsymbol{\mathcal{R}_0 = \frac{\beta}{\gamma + \delta}.}}$$

3.3.4 Traveling wave solutions

A traveling wave solution is a type of solution of the form $\boldsymbol{(S(x+ct), I(x+ct), R(x+ct)}$. It describes the transition of an outbreak from the initial disease-free equilibrium to another disease-free state. To investigate the spatial spread of the epidemic, we seek

traveling wave solutions of the form:

$$S(x,t) = S(\xi), \quad I(x,t) = I(\xi), \qquad R(x,t) = R(\xi),$$

where

$$\xi = x + ct,$$

and $c > 0$, denotes the traveling wave speed.
Applying the chain rule gives the following:

$$\frac{\partial S}{\partial t} = cS'(\xi), \quad \frac{\partial^2 S}{\partial x^2} = S''(\xi),$$

$$\frac{\partial I}{\partial t} = cI'(\xi), \quad \frac{\partial^2 I}{\partial x^2} = I''(\xi),$$

and

$$\frac{\partial R}{\partial t} = cR'(\xi), \quad \frac{\partial^2 R}{\partial x^2} = R''(\xi).$$

Substituting these expressions into the reaction-diffusion system (3.5) yields the following system of ordinary differential equations:

$$\begin{cases} cS' = d_1 S'' - \dfrac{\beta SI}{S+I+R}, \\ cI' = d_2 I'' + \dfrac{\beta SI}{S+I+R} - (\gamma+\delta)I, \\ cR' = d_3 R'' + \gamma I. \end{cases} \tag{3.6}$$

Following **Wang et al.** [9], the traveling waves are assumed to connect two equilibrium states at spatial infinity. Therefore, the boundary conditions are written as follows:

$$S(-\infty) = S_{-\infty}, \quad I(-\infty) = 0, \qquad R(-\infty) = 0$$

and

$$S(+\infty) = S_{+\infty}, \quad I(+\infty) = 0, \qquad R(+\infty) = R_{+\infty}.$$

3.3.5 Wave speed

One of the authors [32] showed that, traveling wave speeds can be obtained from the eigenvalues of the parameterized Jacobian matrix of the system linearized at the initial equilibrium point. As a result, the minimal wave speed is simply the minimum among these eigenvalues.
Applying the method described in (1.10), we linearize the system around the initial disease-free equilibrium $\boldsymbol{(S_{-\infty}, 0, 0)}$:

$$f(S_{-\infty},0,0)=\begin{pmatrix}0 & -\beta & 0\\ 0 & \beta-\gamma-\delta & 0\\ 0 & \gamma & 0\end{pmatrix}.$$

For a traveling wave solution of the form $e^{\lambda\xi}$, we consider the matrix:

$$A_\lambda=\begin{pmatrix}d_1\lambda^2 & -\beta & 0\\ 0 & d_2\lambda^2+\beta-\gamma-\delta & 0\\ 0 & \gamma & d_3\lambda^2\end{pmatrix}.$$

The eigenvalues of A_λ are $\boldsymbol{d_1\lambda^2}$, $\boldsymbol{d_2\lambda^2+\beta-\gamma-\delta}$, and $\boldsymbol{d_3\lambda^2}$. The minimum wave speed is obtained by minimizing the largest eigenvalue over $\lambda>0$:

$$c^*=\inf_{\lambda>0}\frac{d_2\lambda^2+\beta-\gamma-\delta}{\lambda}=2\sqrt{d_2(\beta-\gamma-\delta)}.$$

3.3.6 Existence of traveling wave

It is well known that $\mathcal{R}_0=\frac{\beta}{\gamma+\delta}>1$ is the basic reproduction number for the ordinary differential system without diffusion [23, 24], the wave speed satisfies $c>c^*=2\sqrt{d_2(\beta-\gamma-\delta)}$ and the technical condition $d_3<2d_2$ holds.

Linearizing the equation of infected individuals around the disease-free equilibrium $(S_{-\infty},0,0)$ gives the characteristic function:

$$f(\lambda):=-d_2\lambda^2+c\lambda-(\beta-\gamma-\delta).$$

We denote by λ_0 the smaller positive root of $f(\lambda)=0$:

$$\lambda_0:=\frac{c-\sqrt{c^2-4d_2(\beta-\gamma-\delta)}}{2d_2}>0.$$

The condition $d_3<2d_2$, implies:

$$c-d_3\lambda_0>0,$$

this condition ensures that the recovered individuals do not diffuse too rapidly compared to infected individuals. This condition is required for the construction of super-solutions and sub-solutions.

Let $\alpha_1,\alpha_2,\alpha_3$ be three sufficiently large positive constants. For $i=1,2,3$, we define the second-order differential operator D_i as follows:

$$D_ih:=-d_ih''+ch'+\alpha_ih,\qquad \forall h\in C^2(\mathbb{R}).$$

For each i, the equation $f_i(\lambda):=-d_i\lambda^2+c\lambda+\alpha_i=0$ has two roots:

$$\lambda_i^{\pm} = \frac{c \pm \sqrt{c^2 + 4d_i\alpha_i}}{2d_i}, \qquad \text{with } \lambda_i^- < 0 < -\lambda_i^- < \lambda_i^+.$$

We also set:

$$\rho_i := d_i(\lambda_i^+ - \lambda_i^-) = \sqrt{c^2 + 4d_i\alpha_i}.$$

The inverse operator D_i^{-1} is defined by the integral representation:

$$(D_i^{-1}h)(x) := \frac{1}{\rho_i}\int_{-\infty}^{x} e^{\lambda_i^-(x-y)}h(y)\,dy + \frac{1}{\rho_i}\int_{x}^{\infty} e^{\lambda_i^+(x-y)}h(y)\,dy, \tag{3.7}$$

for $h \in C_{\mu^-,\mu^+}(\mathbb{R})$ with $\mu^- > \lambda_i^-$ and $\mu^+ < \lambda_i^+$, where:

$$(D_i^{-1}h) := \left\{ h \in C(\mathbb{R}) : \sup_{x\le 0}|h(x)e^{-\mu^- x}| + \sup_{x\ge 0}|h(x)e^{-\mu^+ x}| < \infty \right\}.$$

From the integral representation(3.7), and sing the Leibniz rule (1.11) we obtain the following derivatives of $D_i^{-1}h$:

$$(D_i^{-1}h)'(x) = \frac{\lambda_i^-}{\rho_i}\int_{-\infty}^{x} e^{\lambda_i^-(x-y)}h(y)\,dy + \frac{\lambda_i^+}{\rho_i}\int_{x}^{\infty} e^{\lambda_i^+(x-y)}h(y)\,dy,$$

$$(D_i^{-1}h)''(x) = \frac{(\lambda_i^-)^2}{\rho_i}\int_{-\infty}^{x} e^{\lambda_i^-(x-y)}h(y)\,dy + \frac{(\lambda_i^+)^2}{\rho_i}\int_{x}^{\infty} e^{\lambda_i^+(x-y)}h(y)\,dy - \frac{h(x)}{d_i}.$$

We choose $\alpha_1 > \beta$, $\alpha_2 > \gamma + \delta$, and $\alpha_3 > 0$ sufficiently large so that $|\lambda_i^-| = -\lambda_i^- > \lambda_0$ for $i = 1, 2, 3$. Then we select $\mu > \lambda_0$ such that $\mu < -\lambda_i^-$ for all $i = 1, 2, 3$. Consequently:

$$\lambda_0 < \mu < -\lambda_i^- < \lambda_i^+, \qquad i = 1, 2, 3,$$

and

$$\lambda_i^- < -\mu < \mu < \lambda_i^+, \qquad i = 1, 2, 3.$$

We now define the Banach space:

$$B_\mu(\mathbb{R}, \mathbb{R}^n) := \underbrace{C_{-\mu,\mu}(\mathbb{R}) \times \cdots \times C_{-\mu,\mu}(\mathbb{R})}_{n \text{ times}},$$

equipped with the norm:

$$|u|_\mu := \max_{1\le i\le n} \sup_{x\in\mathbb{R}} e^{-\mu|x|}|u_i(x)|, \tag{3.8}$$

where $u = (u_1, \ldots, u_n) \in B_\mu(\mathbb{R}, \mathbb{R}^n)$.

Finally, we define the map $F = (F_1, F_2, F_3)$ on $B_\mu(\mathbb{R}, \mathbb{R}^3)$ as follows:

$$F_1(S, I, R) := D_1^{-1}\left[\alpha_1 S - \frac{\beta SI}{S + I + R}\right],$$
$$F_2(S, I, R) := D_2^{-1}\left[\alpha_2 I + \frac{\beta SI}{S + I + R} - (\gamma + \delta)I\right],$$
$$F_3(S, I, R) := D_3^{-1}\left[\alpha_3 R + \gamma I\right].$$

We now show that if **(S,I,R)** is a fixed point of **F**, then it satisfies the traveling wave ODE system.

Lemma 3.3.1

Let $(S, I, R) \in B_\mu(\mathbb{R}, \mathbb{R}^3)$ be a fixed point of the map $F = (F_1, F_2, F_3)$, then (S, I, R) satisfies the traveling wave ODE system(3.6).

Proof

Since (S, I, R) is a fixed point of F, we have:

$$S = F_1(S, I, R) = D_1^{-1}\left[\alpha_1 S - \frac{\beta SI}{S + I + R}\right].$$

Applying D_1 to both sides and using the property $D_1(D_1^{-1}h) = h$, we obtain:

$$D_1 S = \alpha_1 S - \frac{\beta SI}{S + I + R}.$$

By definition, $D_1 S = -d_1 S'' + cS' + \alpha_1 S$. Substituting this gives:

$$-d_1 S'' + cS' + \alpha_1 S = \alpha_1 S - \frac{\beta SI}{S + I + R}$$

$$\Rightarrow\ cS' = d_1 S'' - \frac{\beta SI}{S + I + R}.$$

This is the first equation of (3.6). The second and third equations are obtained similarly by applying D_2 and D_3 to the fixed point equations for I and R, respectively.

We now construct super and sub-solutions. For $x \in \mathbb{R}$, we define them as follows:

$$\begin{aligned}
S_+(x) &:= S_{-\infty};\\
S_-(x) &:= \max\left\{S_{-\infty}(1 - M_1 e^{\epsilon_1 x}), 0\right\};\\
I_+(x) &:= e^{\lambda_0 x};\\
I_-(x) &:= \max\left\{e^{\lambda_0 x}(1 - M_2 e^{\epsilon_2 x}), 0\right\};\\
R_+(x) &:= \frac{\gamma}{c\lambda_0 - d_3\lambda_0^2} e^{\lambda_0 x};\\
R_-(x) &:= \max\left\{\frac{\gamma}{c\lambda_0 - d_3\lambda_0^2} e^{\lambda_0 x}(1 - M_3 e^{\epsilon_3 x}), 0\right\},
\end{aligned}$$

where $M_1, M_2, M_3, \epsilon_1, \epsilon_2, \epsilon_3$ are six positive constants.
The following lemma provides inequalities that will be used to prove the invariance of the convex set $\mathbf{\Gamma}$

Lemma 3.3.2

Given sufficiently large $M_1, M_2, M_3 > 0$ and sufficiently small $\epsilon_1, \epsilon_2, \epsilon_3 > 0$, the following inequalities hold:

$$-\beta I_+ \geq -d_1 S_-'' + cS_- \quad \text{for } x \leq x_1 := -\epsilon_1^{-1} \ln M_1,$$

$$\frac{\beta S_- I_-}{S_- + I_+ + R_+} - (\gamma + \delta) I_- \geq -d_2 I_-'' + cI_- \quad \text{for } x \leq x_2 := -\epsilon_2^{-1} \ln M_2,$$

$$\gamma I_- \geq -d_3 R_-'' + cR_- \quad \text{for } x \leq x_3 := -\epsilon_3^{-1} \ln M_3.$$

Proof

The proof follows from direct substitution of the definitions of $S_+, S_-, I_+, I_-, R_+, R_-$ and the choice of sufficiently large M_i and sufficiently small ϵ_i. see Wang et al.[9]

With the aid of the super and sub-solutions, we are now ready to define a convex set $\mathbf{\Gamma}$ as follows:

$$\Gamma := \left\{(S, I, R) \in B_\mu(\mathbb{R}, \mathbb{R}^3) : S_- \leq S \leq S_+,\ I_- \leq I \leq I_+,\ R_- \leq R \leq R_+\right\}.$$

To prove the invariance of the convex set Γ under the map F, we shall show that D_i^{-1} is indeed the inverse of D_i and that it preserves the ordering of functions.

Lemma 3.3.3

For $i = 1, 2, 3$, we have:

$$D_i^{-1}(D_i h) = h$$

for any $h \in C^2(\mathbb{R})$ such that $h, h', h'' \in C_{\mu^-,\mu^+}(\mathbb{R})$ with $\mu^- > \lambda_i^-$ and $\mu^+ < \lambda_i^+$. Let

$$g(x) := \max\{e^{\lambda x}(1 - Me^{\epsilon x}), 0\}$$

for some $M > 0$, $\epsilon > 0$ and λ such that $\lambda_i^- < \lambda < \lambda + \epsilon < \lambda_i^+$. Then

$$D_i^{-1}(D_i g) \geq g.$$

Here $D_i g$ is understood as a piecewise defined function:

$$(D_i g)(x) = \begin{cases} f_i(\lambda)e^{\lambda x} - Mf_i(\lambda+\epsilon)e^{(\lambda+\epsilon)x}, & x < x^* := -\epsilon^{-1}\ln M, \\ 0, & x > x^* := -\epsilon^{-1}\ln M. \end{cases}$$

Proof

The proof follows from integration by parts and the definitions of $\lambda_i^{\pm}$ and ρ_i.
For the first part $D_i^{-1}(D_i h) = h$, we substitute the definition of D_i^{-1} into $D_i^{-1}(D_i h)$ and apply integration by parts. Using the fact that $\lambda_i^{\pm}$ are the roots of $f_i(\lambda) = -d_i\lambda^2 + c\lambda + \alpha_i = 0$ see Wang et al [9], we obtain:

$$\int_{-\infty}^{x} e^{\lambda_i^-(x-y)}[-d_i h''(y) + ch'(y) + \alpha_i h(y)]dy = -d_i h'(x) + (-d_i\lambda_i^- + c)h(x),$$

and similarly for the integral from x to ∞. Adding both contributions and using $\rho_i = d_i(\lambda_i^+ - \lambda_i^-)$ gives $D_i^{-1}(D_i h) = h$.
For the second part $D_i^{-1}(D_i g) \geq g$, we consider two cases. If $x \leq x^*$, direct computation using the integral representation yields:

$$[D_i^{-1}(D_i g)](x) = [e^{\lambda x} - Me^{(\lambda+\epsilon)x}] + \frac{\epsilon}{\lambda_i^+ - \lambda_i^-}e^{\lambda x^* + \lambda_i^+(x-x^*)} \geq e^{\lambda x} - Me^{(\lambda+\epsilon)x}.$$

If $x \geq x^*$, we obtain:

$$[D_i^{-1}(D_i g)](x) = \frac{\epsilon}{\lambda_i^+ - \lambda_i^-}e^{\lambda x^* + \lambda_i^-(x-x^*)} \geq 0 = g(x).$$

Thus, $D_i^{-1}(D_i g) \geq g$ holds for all $x \in \mathbb{R}$.

We now prove that the convex set $\mathbf{\Gamma}$ is invariant under the map $F = (F_1, F_2, F_3)$. defined in (3.3.6)

Lemma 3.3.4

The convex set

$$\Gamma = \left\{(S, I, R) \in B_\mu(\mathbb{R}, \mathbb{R}^3) : S^- \leq S \leq S^+,\ I^- \leq I \leq I^+,\ R^- \leq R \leq R^+\right\}$$

satisfies

$$F(\Gamma) \subset \Gamma.$$

That is, for any

$$(S, I, R) \in \Gamma,$$

we have:

$$S^- \leq F_1(S, I, R) \leq S^+,$$
$$I^- \leq F_2(S, I, R) \leq I^+,$$
$$R^- \leq F_3(S, I, R) \leq R^+.$$

Proof

We prove the inequalities for each component separately.

Upper bound for F_1: *Since $S \leq S_+$ and $\frac{\beta SI}{S+I+R} \geq 0$, we have:*

$$\alpha_1 S - \frac{\beta SI}{S + I + R} \leq \alpha_1 S_+.$$

Because S_+ is constant, $D_1 S_+ = \alpha_1 S_+$. Applying D_1^{-1} to both sides and using Lemma (3.3.2) gives $F_1(S, I, R) \leq S_+$.

Lower bound for F_1: *For $x \leq x_1$, using the first inequality of Lemma (3.3.2) and $S \geq S_-$, we obtain:*

$$\alpha_1 S - \frac{\beta SI}{S + I + R} \geq \alpha_1 S_- - \beta I_+ \geq -d_1 S_-'' + cS_-' + \alpha_1 S_- = D_1 S_-.$$

For $x \geq x_1$, $S_-(x) = 0$ and $\alpha_1 > \beta$, so:

$$\alpha_1 S - \frac{\beta SI}{S + I + R} \geq (\alpha_1 - \beta)S \geq 0 = D_1 S_-.$$

Applying D_1^{-1} and using Lemma (3.3.2) yields $F_1(S, I, R) \geq S_-$.

Upper bound for F_2: *Since $I \leq I_+$, $\frac{\beta SI}{S+I+R} \leq \beta I$, and $\alpha_2 > \gamma + \delta$, we have:*

$$\alpha_2 I + \frac{\beta SI}{S+I+R} - (\gamma+\delta)I \leq \alpha_2 I_+ + \beta I_+ - (\gamma+\delta)I_+ = D_2 I_+.$$

Thus, $F_2(S,I,R) \leq I_+$.

Lower bound for F_2**:** *For* $x \leq x_2$*, using the second inequality of Lemma (3.3.2) and the monotonicity of* $\frac{\beta SI}{S+I+R}$ *in* S*, we get:*

$$\alpha_2 I + \frac{\beta SI}{S+I+R} - (\gamma+\delta)I \geq D_2 I_-.$$

For $x \geq x_2$*,* $I_-(x) = 0$ *and* $\alpha_2 > \gamma + \delta$*, so:*

$$\alpha_2 I + \frac{\beta SI}{S+I+R} - (\gamma+\delta)I \geq 0 = D_2 I_-.$$

Hence, $F_2(S,I,R) \geq I_-$.

Upper bound for F_3**:** *Using* $R \leq R_+$ *and* $I \leq I_+$*, we obtain:*

$$\alpha_3 R + \gamma I \leq \alpha_3 R_+ + \gamma I_+ = D_3 R_+.$$

Therefore, $F_3(S,I,R) \leq R_+$.

Lower bound for F_3**:** *For* $x \leq x_3$*, using the third inequality of Lemma (3.3.2) and* $R \geq R_-$*, we have:*

$$\alpha_3 R + \gamma I \geq D_3 R_-.$$

For $x \geq x_3$*,* $R_-(x) = 0$*, so:*

$$\alpha_3 R + \gamma I \geq 0 = D_3 R_-.$$

Thus, $F_3(S,I,R) \geq R_-$*. Combining all the inequalities, we conclude that* $F(\Gamma) \subset \Gamma$.

To apply **Schauder's fixed point** theorem (1.12.1), we must first show that $\mathbf{F}$ is continuous and compact on $\mathbf{\Gamma}$ with respect to the norm $|\cdot|_{\boldsymbol{\mu}}$ defined in (3.8).

Lemma 3.3.5

The map F *is continuous and compact on* Γ *with respect to the norm* $|\cdot|_\mu$ *defined in* (3.8).

Proof

We prove continuity and compactness separately, see Wang et al. [9].

- ***Continuity:*** *The function* $\frac{\beta SI}{S+I+R}$ *has bounded partial derivatives with respect to* S, I, R *(each derivative is bounded by* β*). Since the operators* D_i^{-1} *are linear and continuous, the composition* F_i *is continuous. More precisely, for any* $(S_1, I_1, R_1), (S_2, I_2, R_2) \in \Gamma$*, there exists a constant* $C > 0$ *such that:*

$$|F_i(S_1, I_1, R_1) - F_i(S_2, I_2, R_2)|_\mu \leq C\left(|S_1 - S_2|_\mu + |I_1 - I_2|_\mu + |R_1 - R_2|_\mu\right).$$

  Hence F *is Lipschitz continuous, and therefore continuous.*

- ***Compactness:*** *Let* $\{(S_n, I_n, R_n)\}$ *be a sequence in* Γ*. Since* Γ *is uniformly bounded with respect to* $|\cdot|_\mu$*, the sequences* $\{F_1(S_n, I_n, R_n)\}$*,* $\{F_2(S_n, I_n, R_n)\}$*,* $\{F_3(S_n, I_n, R_n)\}$ *are uniformly bounded and equicontinuous on any compact interval* $[-k, k]$*. By the* ***Arzelà–Ascoli*** *theorem (1.13) and a standard diagonal argument, there exists a subsequence that converges uniformly on compact sets. Moreover, using the norm* $|\cdot|_\mu$*, one can show that this subsequence converges in* $B_\mu(\mathbb{R}, \mathbb{R}^3)$*. Therefore,* F *is compact.*

Proposition 3.3.1 ([9])**.** *The fixed point* $(S, I, R) \in \Gamma$ *obtained from Schauder's fixed point theorem satisfies the following asymptotic properties:*

- ***As*** $x \to -\infty$ ***(ahead of the wave):***

$$S(x) \to S_{-\infty}, \quad I(x) \sim e^{\lambda_0 x}, \quad R(x) \sim \frac{\gamma e^{\lambda_0 x}}{c\lambda_0 - d_3\lambda_0^2},$$

  and $S'(x), I'(x), R'(x), S''(x), I''(x), R''(x) \to 0$*.*

- ***As*** $x \to +\infty$ ***(behind the wave):***

$$S(x) \to S_\infty < S_{-\infty}, \quad I(x) \to 0, \quad R(x) \to \frac{\gamma(S_{-\infty} - S_\infty)}{\gamma + \delta},$$

  and $S'(x), I'(x), R'(x), S''(x), I''(x), R''(x) \to 0$*.*

- ***Monotonicity and bounds:*** $S(x)$ *is decreasing,* $R(x)$ *is increasing, and* $0 \leq I(x) \leq S_{-\infty} - S_\infty$ *for all* $x \in \mathbb{R}$*.*

- ***Integral relation:***

$$\int_{-\infty}^{\infty} (\gamma + \delta) I(x)\, dx = \int_{-\infty}^{\infty} \frac{\beta S(x) I(x)}{S(x) + I(x) + R(x)}\, dx = c(S_{-\infty} - S_\infty).$$

Theorem 3.3.2: Existence of traveling wave

Assume $d_i > 0$ for $i = 1, 2, 3$, $\beta > 0$, $\gamma > 0$, and $\delta \geq 0$. If the technical condition $d_3 < 2d_2$ holds, then:

- ***Existence:*** *For any $S_{-\infty} > 0$, $\mathcal{R}_0 = \frac{\beta}{\gamma+\delta} > 1$, and $c \geq c^* = 2\sqrt{d_2(\beta - \gamma - \delta)}$, there exists a traveling wave solution $(S(x+ct), I(x+ct), R(x+ct))$ of system (3.5) satisfying:*

$$\begin{aligned} &S(-\infty) = S_{-\infty}, \quad && S(\infty) = S_\infty, \\ &I(-\infty) = 0, && I(\infty) = 0, \\ &R(-\infty) = 0, && R(\infty) = \frac{\gamma}{\gamma+\delta}(S_{-\infty} - S_\infty). \end{aligned}$$

Furthermore, $S(x)$ is decreasing, $R(x)$ is increasing, $0 \leq I(x) \leq S_{-\infty} - S_\infty$ for all $x \in \mathbb{R}$, and the following integral relations hold:

$$\int_{-\infty}^{\infty} (\gamma + \delta) I(x)\, dx = \int_{-\infty}^{\infty} \frac{\beta S(x) I(x)}{S(x) + I(x) + R(x)}\, dx = c(S_{-\infty} - S_\infty).$$

Conclusion

This thesis was devoted to the study of traveling wave solutions in diffusive SIR epidemic models. We examined three distinct incidence forms: mass-action incidence, standard incidence without recovered population (SI), and standard incidence with recovered population (SIR).

In Chapter 2, we presented the classical Kermack-McKendrick SIR model, first without demography and then with demographic processes. Then in Chapter 3, we extended the classical framework by incorporating diffusion terms to model the random movement of individuals, and studied traveling wave solutions for three diffusive SIR models.

The main result of this thesis is the proof of existence of traveling wave solutions for the diffusive SIR model with standard incidence. Using Schauder's fixed point theorem and the Arzelà-Ascoli theorem, we showed that a traveling wave exists if and only if $\mathcal{R}_0 > 1$ and $c \geq c^*$.

Our results confirm that the basic reproduction number $\mathcal{R}_0$ plays a crucial role as a threshold parameter.

Bibliography

[1] Dunbar, S.R. Travelling wave solutions of diffusive Lotka-Volterra equations. J. Math. Biol. 17(1), 11–32 (1983).

[2] Dunbar, S.R.: Traveling wave solutions of diffusive Lotka-Volterra equations: a heteroclinic connection in R4. Trans. Am. Math. Soc. 286(2), 557–594 (1984).

[3] F. Brauer, P. van den Driessche, J. Wu (Eds.), *Mathematical Epidemiology*, Springer, 2008.

[4] F. Brauer, van den Driessche, P., Wu, J.: Mathematical Epidemiology. Springer, Berlin (2008).

[5] F. Brauer, Castillo-Chvez, C.: Mathematical Models in Population Biology and Epidemiology, 2nd edn. Springer, Berlin (2012).

[6] G. F. Webb, Theory of Nonlinear Age-Dependent Population Dynamics, CRC Press, 1985.

[7] H.W. Hethcote, "Qualitative analyses of communicable disease models," *Math. Biosci.*, 1976.

[8] H.W. Hethcote, "Qualitative analyses of communicable disease models," *SIAM Rev.*, 2000.

[9] H. Wang, X. Wang. Traveling Wave Phenomena in a Kermack–McKendrick SIR Model.Journal of Dynamics and Differential Equations, 2016, 28: 143–166.

[10] Hemlata Saxena, *First Order and First Degree Differential Equations.*

[11] Hirsch, M. W., Smale, S., and Devaney, R. L. (2004). Differential Equations, Dynamical Systems, and an Introduction to Chaos (2nd ed.). Elsevier/Academic Press.

[12] Hosono, Y., Ilyas, B.: Existence of traveling waves with any positive speed for a diffusive epidemic model. Nonlinear World 1(3), 277–290 (1994).

[13] Hosono, Y., Ilyas, B.: Traveling waves for a simple diffusive epidemic model. Math. Models Methods Appl. Sci. 5(7), 935–966 (1995).

[14] Hurtado, P. J. (n.d.). Linear Differential Equations: Theory and Examples. Section 4.5, Routh-Hurwitz Criteria.

[15] Ivrii, Victor. Partial Differential Equations. Department of Mathematics, University of Toronto, Toronto, Ontario, Canada, 2026.

[16] J. Dieudonné, Foundations of Modern Analysis, Academic Press, New York, 1969.

[17] Källén, A.: Thresholds and travelling waves in an epidemic model for rabies. Nonlinear Anal. TMA 8, 851–856 (1984).

[18] Kaplan, W. (1992). Advanced Calculus (4th ed.). Addison-Wesley.

[19] Lebovitz, N. R. Stable Equilibrium Points. Department of Computer Science, University of Chicago.

[20] Lui, R.: Biological growth and spread modeled by systems of recursions. I. Mathematical theory. Math. Biosci. 93(2), 269–295 (1989).

[21] M.J. Keeling and P. Rohani, *Modeling Infectious Diseases in Humans and Animals*, Princeton University Press, 2008.

[22] M. Martcheva, *An Introduction to Mathematical Epidemiology*, Springer, 2015.

[23] O. Diekmann, J.A.P. Heesterbeek, and J.A.J. Metz, "On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations," *J. Math. Biol.*, vol. 28, pp. 365–382, 1990.

[24] P. van den Driessche and J. Watmough, "Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission," *Mathematical Biosciences*, vol. 180, pp. 29–48, 2002.

[25] R.M. Anderson. Discussion: the Kermack-McKendrick epidemic threshold theorem. Bulletin of mathematical biology, 53(1):1–32, 1991.

[26] Rudin, W. Principles of Mathematical Analysis (3rd ed.). 1976. McGraw-Hill.

[27] Schauder, J. (1930). Der Fixpunktsatz in Funktionalräumen. Studia Mathematica, 2, 171-180.

[28] Sheply L. Ross, *Introduction To Ordinary Differential Equations.*

[29] T. Kuniya, J. Wang, Lyapunov Functions and Global Stability for a Spatially Diffusive SIR Epidemic Model, Applied Analysis, 96,11, 1935–1960, 2017.

[30] Universiteit Utrecht, Chapter 9, *Equilibrium points and fixed points.*

[31] W.O. Kermack and A.G. McKendrick, "A contribution to the mathematical theory of epidemics," *Proc. R. Soc. Lond. B*, vol. 115, pp. 700–721, 1927.

[32] Wang, H.: Spreading speeds and traveling waves for non-cooperative reaction-diffusion systems. J. Nonlinear Sci. 21, 747–783 (2011).

[33] Wang, X.-S., Wang, H., Wu, J.: Traveling waves of diffusive predator-prey systems: disease outbreak propagation. Discret. Contin. Dyn. Syst. A 32, 3303–3324 (2012).

[34] Weinberger, H.F., Lewis, M.A., Li, B.: Analysis of linear determinacy for spread in cooperative models. J. Math. Biol. 45, 183–218 (2002).

[35] Wiggins, S. Introduction to Applied Nonlinear Dynamical Systems and Chaos (2nd ed.). (2003). Springer.