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Abstract

In this thesis we modify the well known SIR model, which describes the spread of diseases, by considering the contact intensity between individuals and their mobility. In a first step we introduce a model with contact intensity structure and investigate the existence and uniqueness of solutions with the help of the theorem of Picard-Lindelöf. In the next model we include a mobility structure in one and two dimensions, which is based on the location of residence and a mobility radius. In both cases we can prove the existence of a traveling wave under certain requirements and find a minimal wave speed. Finally, we combine the contact intensity and the mobility structure in one epidemiological model.

Zusammenfassung

In dieser Arbeit modifizieren wir das bekannte SIR Modell, welches die Verbreitung von Krankheiten beschreibt, durch die Berücksichtigung der Kontaktintensität zwischen Individuen und deren MÖbilität. Im ersten Schritt führen wir ein Modell mit Kontaktintensität ein und untersuchen das resultierende System auf eindeutige Lösungen, wobei wir den Satz von Picard-Lindelöf verwenden. Das nächste Modell beinhaltet eine Mobilitätsstruktur im ein- und zweidimensionalen Fall, welche auf dem Wohnort und einem Mobilitätsradius beruht. In beiden Fällen können wir die Existenz einer Wanderwelle unter bestimmten Voraussetzungen zeigen und eine minimale Wellengeschwindigkeit finden. Abschließend vereinen wir sowohl die Kontaktintensität als auch die Mobilitätsstruktur in einem epidemischen Modell.

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1. Introduction

Nowadays, and throughout history, there are a lot of infectious diseases spreading within animal and human populations. Since often such diseases cause a lot of harm to people, we not only want to understand the disease from a medical point of view and find some treatments, but we also aim to find some models to predict the dynamics of the spread. On one hand mathematical models can help us to give some predictions about what will happen in future and on the other hand they tell us what measures are useful to prevent an outbreak. By an infectious disease we understand an illness caused by a pathogenic microbial agent, i.e., by a bacterial, viral, fungal or parasitic agent, see also [8, ch. 1, pp. 1-2]. A special case of infectious diseases are communicable diseases, which means that the disease is transmitted by direct or indirect contact of an infectious individual to another. Examples of communicable diseases are Ebola, Influenza, SARS, HIV, Tuberculosis, Hepatitis, Malaria and the new Covid-19. Our goal is to develop an epidemiological model with contact intensity and mobility structure for the spread of a communicable disease within a population. Let us start by giving a description what epidemiology is about: “Epidemiology is the subject that studies the patterns of health and illness and associated factors at the population level.”, [8, ch. 1, p. 1]. A common kind of epidemiological models are compartmental models, where the population is divided into different classes. The SIR model, or also called Kermack-McKendrick model, is an popular compartment model and we use it as a basis for our model with contact intensity and mobility structure.

1.1. The SIR model

The SIR model was first invented in 1927 by W.O. Kermack and A.G. McKendrick in their works [4], [5] and [6]. We follow the approach of [8, pp. 9-16] and [2, pp. 350-356], but there is a lot of further literature about this topic, e.g., [1] and [3]. In order to state the SIR model we divide the population into the following three compartments:

- Susceptible: The susceptible individuals of a population are the healthy ones,

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but they can get infected by contact to an infected individual. The number of susceptible individuals at time $t \in \mathbb{R}$, $t \geq 0$, is denoted by $S(t)$.

- Infected: The infected individuals within a population are also assumed to be infectious and thus, can infect other individuals. The number of infected individuals is given by $I(t)$ for $t \in \mathbb{R}$, $t \geq 0$.
- Removed: The removed individuals have already been infected, but are not infectious anymore. This state can either be reached through immunization, death or quarantine. The number of recovered individuals at time $t \in \mathbb{R}$, $t \geq 0$, is $R(t)$.

We make the following assumptions:

- The total population $N = S(t) + I(t) + R(t)$ is constant, i.e., $\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$. This assumption means that there are no births and deaths and that there is no immigration or emigration. This is reasonable, because we expect the disease to spread quickly compared to the lifespan of the individuals, thus, we can ignore demographic effects on the population.
- The sizes of the compartments $S(t)$, $I(t)$ and $R(t)$ are nonnegative for all $t \in \mathbb{R}$, $t \geq 0$.
- An individual can only be in one of the three compartments per time.
- The rate at which infected individuals have contact to susceptible individuals per unit time, that also results in a transmission, is given by βSI with $\beta > 0$ constant.
- The rate at which infected individuals are removed from the infected class by recovering, dying or isolation is given by γI with $\gamma > 0$ a disease specific constant.
- As in the description of the removed compartment suggested, we suppose that once an individual recovered from the disease, they are immune to any further infection. Therefore, every individual reaching the removed compartment stays there.

The SIR model is given by the following system of ordinary differential equations

$$\frac{dS}{dt} = -\beta SI, \quad S(0) = S_0, \quad (1.1.1)$$

$$\frac{dI}{dt} = \beta SI - \gamma I, \quad I(0) = I_0, \quad (1.1.2)$$

$$\frac{dR}{dt} = \gamma I, \quad R(0) = R_0. \quad (1.1.3)$$

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In order to understand the epidemiological meaning of the term γI , we assume that there is no inflow into the infected compartment and that there is a certain number of individuals I_0 infected. The differential equation describing the dynamics if a fraction γ is leaving the infected compartment in unit time is given by

$$\frac{dI}{dt} = -\gamma I, \quad I(0) = I_0,$$

with the solution

$$I(t) = I_0 e^{-\gamma t}.$$

Therefore, the amount of individuals who are still infected t time units after infection is $e^{-\gamma t}$. In other words, this is the probability of still being infected at time t . The fraction of individuals who have left the infected compartment is given by $F(t) = 1 - e^{-\gamma t}$, which is a probability distribution for $t \geq 0$. Thus, $f(t) = \frac{dF}{dt} = \gamma e^{-\gamma t}$ is a probability density function. The average time spent in the infected compartment is the mean of $f(t)$, i.e.,

$$\int_{-\infty}^{\infty} t \gamma e^{-\gamma t} dt = \frac{1}{\gamma}.$$

If we know the duration of the infectious period, which is the case for many diseases, we can calculate γ .

Remark 1.1.1. Note that the system (1.1.1) – (1.1.3) is determined only by the first two equations, since we assume N to be constant. Thus, for the analysis we can either work with the whole system or we can neglect the third equation.

1.1.1. Dynamics of the SIR model and the basic reproduction number

We aim to predict the spread of the disease described by the system (1.1.1) – (1.1.3), i.e., we want to analyze the dynamics and want to know if or when there is an outbreak. In mathematical terms an outbreak corresponds to the increase of the size of the infected compartment. Thus, we observe the changes of the sizes of the compartments by time.

Initially, $S_0 > 0$, $I_0 > 0$ and $R_0 = 0$ holds. The number of susceptible individuals is large at the beginning, almost the whole population. On the contrary, the size of the infected compartment is very small for $t = 0$. Since $S(t)' < 0$ for all $t \in \mathbb{R}$, $t \geq 0$,

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and S is nonnegative, the number of susceptible individuals decreases monotonically and $\lim_{t \rightarrow \infty} S(t) = S_\infty$ exists. We will see later on, that in the case of an outbreak, not all individuals get infected, that is, $S_\infty > 0$. Because $(S(t) + I(t))' < 0$, $S(t) + I(t)$ is nonnegative and S_∞ exists, also $\lim_{t \rightarrow \infty} I(t) = I_\infty$ exists. We know that $R(t)' > 0$ holds for all $t \geq 0$, R is nonnegative and bounded by N , i.e., the size of the removed compartment is monotonically increasing until there are no infected individuals left and therefore, we have existence of $\lim_{t \rightarrow \infty} R(t) = R_\infty$. Since

$$\frac{dI}{dt} = \beta SI - \gamma I = (\beta S - \gamma) I \begin{cases} < 0 & \iff \frac{\beta S}{\gamma} < 1 & \iff S < \frac{\gamma}{\beta}, \\ > 0 & \iff \frac{\beta S}{\gamma} > 1 & \iff S > \frac{\gamma}{\beta}, \end{cases}$$

holds, the number of infected individuals increases as long as $S > \frac{\gamma}{\beta}$. For $S = \frac{\gamma}{\beta}$, I attains its maximum and if $S < \frac{\gamma}{\beta}$ it decreases. Consequently, if initially there are too little susceptible individuals, the number of infected individuals never increases and there is no spread of the disease. In other words whether there is an epidemic or not depends on the value of $\frac{\beta S_0}{\gamma} \approx \frac{\beta N}{\gamma}$. If we normalize the size of the total population, i.e., $N = 1$, and the sizes of the compartments, we can simplify this threshold by $\frac{\beta}{\gamma}$. It is called the basic reproduction number and denoted by \mathcal{R}_0 :

Definition 1.1.1. The *basic reproduction number* \mathcal{R}_0 is the number of secondary cases caused by a single infected individual within a susceptible population.

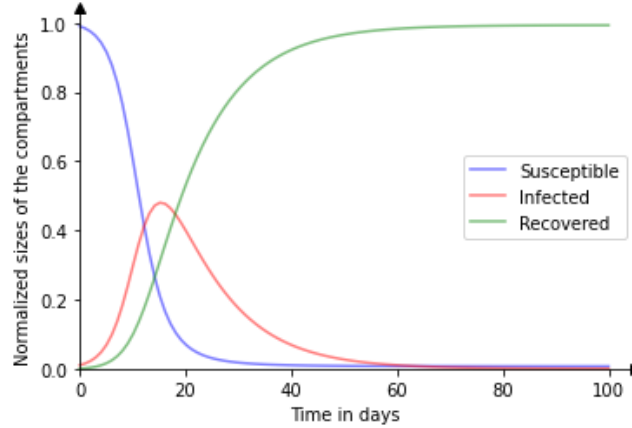


Figure 1.1.: The plot shows the SIR model with $S_0 = 0.99$, $I_0 = 0.01$, $R_0 = 0$, $\beta = 0.5$ and $\gamma = \frac{1}{10}$. Since $\mathcal{R}_0 = \frac{\beta}{\gamma} > 1$, the outbreak of the disease is visible. It is plotted with Python 3.8 and the code can be found in Section A.1.

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Next we show that $S_\infty > 0$, calculate the maximum of $I(t)$ provided it exists and determine the value for I_∞ . In order to prove $S_\infty > 0$, we divide (1.1.1) by (1.1.3) and obtain

$$\frac{dS}{dR} = -\frac{\beta}{\gamma}S.$$

Solving this equation and bounding R from above by $N = 1$ yields

$$S(R(t)) = S_0 e^{-\frac{\beta}{\gamma}R} \geq S_0 e^{-\frac{\beta}{\gamma}} > 0. \quad (1.1.4)$$

We conclude that $S_\infty > 0$ and hence, that there are always susceptible individuals left at the end of an epidemic who escape the disease. Biologically this is reasoned by the fact that the pathogen can hardly find a new host, if enough individuals were infected already. We call S_∞ the *final size of the epidemic*. We can find this lower bound as well by the calculation

$$\begin{aligned} (S(t) + I(t))' &= -\gamma I(t) \\ \implies S(t) + I(t) - S(0) - I(0) &= -\gamma \int_0^t I(\tau) d\tau \\ \implies \int_0^t I(\tau) d\tau &\leq \frac{N}{\gamma} = \frac{1}{\gamma}, \end{aligned}$$

$$\begin{aligned} \frac{S(t)'}{S(t)} &= -\beta I(t) \\ \implies \ln(S(0)) - \ln(S(t)) &= \beta \int_0^t I(\tau) d\tau \leq \frac{\beta}{\gamma} \\ \implies \frac{S(0)}{S(t)} &\leq e^{\frac{\beta}{\gamma}} \\ \iff S(t) &\geq S(0)e^{-\frac{\beta}{\gamma}} > 0, \end{aligned}$$

which equals the result (1.1.4). For the calculation of the maximum value of $I(t)$, in case it exists, i.e., for $\mathcal{R}_0 > 1$, we look at the SI -plane. Therefore, we divide (1.1.2) by (1.1.1)

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$$\frac{dI}{dS} = -1 + \frac{\gamma}{\beta S},$$

separate the variables and integrate to obtain

$$I(S(t)) = -S(t) + \frac{\gamma}{\beta} \ln(S(t)) + C,$$

where C is a constant. We substitute the initial conditions S_0 and I_0 in order to obtain the value for C , which is

$$C = S_0 + I_0 - \frac{\gamma}{\beta} \ln(S_0).$$

Since we are looking for a maximum, we need $I' = 0$, which is attained for $S = \frac{\gamma}{\beta}$. After inserting C and S , we get the following maximum for I :

$$I_{\max} = -\frac{\gamma}{\beta} + \frac{\gamma}{\beta} \ln\left(\frac{\gamma}{\beta}\right) + S_0 + I_0 - \frac{\gamma}{\beta} \ln(S_0).$$

Taking into account that $S(t)$ decreases, we conclude that in the SI -plane the curve goes from right to left and thus, $I(S(t))$ increases for $S > \frac{\gamma}{\beta}$ and decreases for $S(t) < \frac{\gamma}{\beta}$.

Note that all solutions move from bottom-right upwards, then downwards on the left and they stay below the line $S + I = 1$. We expect the limit of $I(t)$ for $t \rightarrow \infty$ to be zero. In order to prove that, let us assume $I_\infty \neq 0$. Therefore, equation (1.1.3) is strictly positive for all $t \in \mathbb{R} \cup \infty$, $t \geq 0$, and $R_\infty = \infty$. But we already proved that R_∞ exists, which is a contradiction and $I_\infty = 0$. Note that we can conclude $I_\infty = 0$ with the same arguments as above by summing up (1.1.1) and (1.1.2).

In conclusion, we note that the SIR model is not hard to analyze. Unfortunately, it is not very realistic, since it assumes the population to be homogeneously mixed and the individuals to behave alike. In the following chapters we seek to adapt the model and therefore, exchanging β by taking individual behavior into account.

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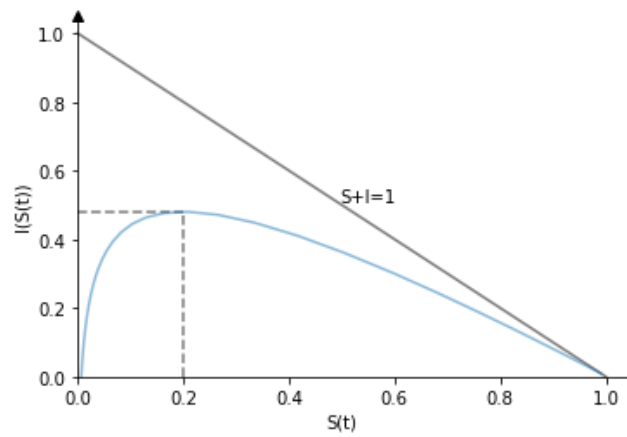


Figure 1.2.: The plot shows the SI -plane of the SIR model with $S_0 = 0.99$, $I_0 = 0.01$, $R_0 = 0$, $\beta = 0.5$ and $\gamma = \frac{1}{10}$. The dashed lines show the point $(I_{\max}, \frac{\gamma}{\beta})$. This plot is created with Python 3.8 as well, see Section A.1.

2. SIR epidemiological model with contact intensity structure

The purpose of this chapter is to make the classical SIR model more realistic. Since individuals behave differently in general, one way to obtain a more realistic model is to include a function, which measures the contact intensity. The idea is that the contact intensity is high, if the individuals tend to have close physical contact to others, for example by shaking hands. It is low if the individuals keep distance to others or wear face coverings and gloves. Instead of total sizes we work with the population densities of the susceptible, infected and removed individuals denoted by $f_S(c, t)$, $f_I(c, t)$ and $f_R(c, t)$. The densities depend on a contact intensity $c \in [0, 1]$ and time $t \in \mathbb{R}$, $t \geq 0$, and are nonnegative for all c and t . The initial conditions are given by $f_S(c, 0) = f_{S_0}(c) > 0$, $f_I(c, 0) = f_{I_0}(c) > 0$, and $f_R(c, 0) = f_{R_0}(c) = 0$ and we have $f_S(c, t) + f_I(c, t) + f_R(c, t) = f_N(c)$ for all $t \in \mathbb{R}$, $t \geq 0$, thus, the total population is still constant w.r.t. time. The intensity of the interaction between the individuals is measured by the kernel $K_1(c, \tilde{c})$ and the SIR epidemiological model with contact intensity structure is given by

$$\partial_t f_S(c, t) = -f_S(c, t) \int_0^1 K_1(c, \tilde{c}) f_I(\tilde{c}, t) d\tilde{c}, \quad (2.0.1)$$

$$\partial_t f_I(c, t) = f_S(c, t) \int_0^1 K_1(c, \tilde{c}) f_I(\tilde{c}, t) d\tilde{c} - \gamma f_I(c, t), \quad (2.0.2)$$

$$\partial_t f_R(c, t) = \gamma f_I(c, t), \quad (2.0.3)$$

where $\gamma > 0$ is the recovery rate. The kernel K_1 should satisfy $K_1(c, \tilde{c}) = 0$ if and only if $c = 0$, $\tilde{c} = 0$ or $c = \tilde{c} = 0$. This assumption takes care of the case when there is no contact intensity, therefore, no interaction and thus, no infection. The following kernels satisfy this assumption

- $K_1(c, \tilde{c}) = c\tilde{c}$,
- $K_1(c, \tilde{c}) = (c\tilde{c})^p$ with $p > 0$,

2. SIR epidemiological model with contact intensity structure

- $K_1(c, \tilde{c}) = \min(c, \tilde{c})$.

As in the SIR model, we see that also the system (2.0.1) – (2.0.3) is determined by the first two equations. Therefore, we neglect the third equation in the following analysis.

2.1. Discussion of the dynamics

Following the same arguments as in Section 1.1.1, we obtain the dynamics of $f_S(c, t)$, $f_I(c, t)$ and $f_R(c, t)$. We begin with a very large density of susceptible individuals and a small density of infected individuals. For an arbitrary fixed $c \in [0, 1]$ the limit $\lim_{t \rightarrow \infty} f_S(c, t) = f_{S_\infty}(c)$ exists, since $f_S(c, t)$ decreases for $t \in \mathbb{R}$, $t \geq 0$ and $f_S(c, t)$ is nonnegative. Also, $\lim_{t \rightarrow \infty} f_I(c, t)$ exists for a fixed $c \in [0, 1]$. In order to prove this existence, we look at $\partial_t (f_S(c, t) + f_I(c, t))$. The derivative is negative, but the functions themselves are nonnegative. Thus, $f_S(c, t) + f_I(c, t)$ is decreasing to some limit and $f_I(c, t)$ can not diverge. The limit of $f_R(c, t)$ exists by the same argument as in Section 1.1.1. Again, by the same arguments as in Section 1.1.1 we obtain $f_{I_\infty} = 0$.

Remark 2.1.1. The equilibria with $f_I(c, t) = 0$ are called *disease free equilibria*.

In order to derive a lower bound for f_S we divide (2.0.1) by $f_S(c, t)$, which yields

$$\frac{\partial_t f_S(c, t)}{f_S(c, t)} = - \int_0^1 K_1(c, \tilde{c}) f_I(\tilde{c}, t) d\tilde{c}.$$

By integration with respect to t , we obtain

$$\ln(f_S(c, t)) - \ln(f_S(c, 0)) = - \int_0^1 K_1(c, \tilde{c}) \int_0^t f_I(\tilde{c}, \tau) d\tau d\tilde{c}. \quad (2.1.1)$$

We use again the equation resulting from adding (2.0.1) and (2.0.2) to get

$$\begin{aligned} \partial_t (f_S(c, t) + f_I(c, t)) &= -\gamma f_I(c, t) \\ \implies f_S(c, t) + f_I(c, t) - f_S(c, 0) - f_I(c, 0) &= -\gamma \int_0^t f_I(c, \tau) d\tau \\ \implies \int_0^t f_I(c, \tau) d\tau &\leq \frac{1}{\gamma} (f_S(c, 0) + f_I(c, 0)), \end{aligned}$$

where the last inequality holds pointwise for $c \in [0, 1]$. We insert this estimate into (2.1.1) to obtain a lower bound for the density of susceptible individuals

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$$\begin{aligned}
\ln(f_S(c, 0)) - \ln(f_S(c, t)) &= \int_0^1 K_1(c, \tilde{c}) \int_0^t f_I(\tilde{c}, \tau) d\tau d\tilde{c} \\
&\leq \frac{1}{\gamma} \int_0^1 K_1(c, \tilde{c}) (f_S(\tilde{c}, 0) + f_I(\tilde{c}, 0)) d\tilde{c} \\
\implies \frac{f_S(c, 0)}{f_S(c, t)} &\leq e^{\frac{1}{\gamma} \int_0^1 K_1(c, \tilde{c}) (f_S(\tilde{c}, 0) + f_I(\tilde{c}, 0)) d\tilde{c}} \\
\iff f_S(c, t) &\geq f_S(c, 0) e^{-\frac{1}{\gamma} \int_0^1 K_1(c, \tilde{c}) (f_S(\tilde{c}, 0) + f_I(\tilde{c}, 0)) d\tilde{c}} \\
&= f_S(c, 0) e^{-\frac{1}{\gamma} \int_0^1 K_1(c, \tilde{c}) f_N(\tilde{c}) d\tilde{c}} > 0. \tag{2.1.2}
\end{aligned}$$

This lower bound for f_S is analogous to the bound for S in Section 1.1.1.

2.2. Existence and uniqueness of solutions

We aim to prove the existence and uniqueness of solutions of the system (2.0.1) – (2.0.3). Therefor we fix an arbitrary $c \in [0, 1]$ and recall the theory of ordinary differential equations, which can be found in, e.g., [10] and [12]. We consider the ordinary differential equation

$$\frac{du}{dt} = f(u(t)), \quad u(0) = u_0, \tag{2.2.1}$$

with $u(t) \in \mathbb{R}^n$ for $t \in \mathbb{R}$ and $f : \mathbb{R}^n \rightarrow \mathbb{R}^n$. The following theorem guarantees local existence and uniqueness of solutions:

Theorem 2.2.1 (Picard-Lindelöf). *Let $u_0 \in \mathbb{R}^n$ and let $f(u)$ be Lipschitz continuous in a neighborhood U of u_0 with values in \mathbb{R}^n . Then there exists $T > 0$ and a unique $u \in C^1((-T, T))$ solving (2.2.1) for $-T < t < T$. The existence time T only depends on U , on $\sup U|f|$, and on the Lipschitz constant of f in U .*

In the following we sketch the proof of Theorem 2.2.1:

The integral equation of (2.2.1) is given by

$$u(t) = u_0 + \int_0^t f(u(s)) ds. \tag{2.2.2}$$

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For small t , $u_0(t) = u_0$ is an approximate solution and if we plug it into the integral equation we obtain

$$u_1(t) = u_0 + \int_0^t f(u_0(s)) ds.$$

Iterating this procedure leads to a sequence of approximate solutions

$$u_{n+1}(t) = u_0 + \int_0^t f(u_n(s)) ds =: F(u_n)(t).$$

We want to apply the Banach fixed point Theorem A.2.1 to $F : C([0, T], \mathbb{R}^n) \rightarrow C([0, T], \mathbb{R}^n)$ and therefore, we need to prove that F is a contraction for a locally Lipschitz continuous f with Lipschitz constant L . Note that $C([0, T], \mathbb{R}^n)$ is a Banach space equipped with the $L_\infty([0, T])$ norm and hence, the Banach fixed point Theorem is applicable after proving the contraction estimate. For $u, v \in C([0, T], \mathbb{R}^n)$ with $u \neq v$ the estimate

$$\begin{aligned} |F(u)(t) - F(v)(t)| &= \left| \int_0^t (f(u(s)) - f(v(s))) ds \right| \\ &\leq \int_0^t |f(u(s)) - f(v(s))| ds \\ &\leq L \int_0^t |u(s) - v(s)| ds \\ &\leq Lt \|u - v\|_{L^\infty([0, T])} \\ &\leq LT \|u - v\|_{L^\infty([0, T])} \end{aligned}$$

holds, which implies

$$\|F(u) - F(v)\|_{L^\infty([0, T])} \leq LT \|u - v\|_{L^\infty([0, T])}.$$

Hence, for small T the term LT is less than one and F is a contraction. By the Banach fixed point Theorem, F has exactly one fixed point and thus, there locally exists exactly one solution for the initial value Problem (2.2.1). For a global result, we refer to [10, p. 4].

2. SIR epidemiological model with contact intensity structure

In our case, we first show that the right hand side of (2.0.1) – (2.0.2) is Lipschitz continuous w.r.t. $t \in \mathbb{R}$, $t \geq 0$, for arbitrary fixed $c \in [0, 1]$

$$\begin{aligned}
& \left| f_S(c, t) \int_0^1 K_1(c, \tilde{c}) f_I(\tilde{c}, t) d\tilde{c} - g_S(c, t) \int_0^1 K_1(c, \tilde{c}) g_I(\tilde{c}, t) d\tilde{c} \right| \\
& \leq \int_0^1 K_1(c, \tilde{c}) |f_S(c, t) f_I(\tilde{c}, t) - g_S(c, t) g_I(\tilde{c}, t)| d\tilde{c} \\
& = \int_0^1 K_1(c, \tilde{c}) |(f_S(c, t) - g_S(c, t)) f_I(\tilde{c}, t) + g_S(c, t) (f_I(\tilde{c}, t) - g_I(\tilde{c}, t))| d\tilde{c} \\
& \leq \tilde{f} \max_{c \in [0, 1]} \int_0^1 K_1(c, \tilde{c}) d\tilde{c} \left(\|f_S(t) - g_S(t)\|_{L_\infty([0, 1])} + \|f_I(t) - g_I(t)\|_{L_\infty([0, 1])} \right)
\end{aligned}$$

and

$$\begin{aligned}
& \left| f_S(c, t) \int_0^1 K_1(c, \tilde{c}) f_I(\tilde{c}, t) d\tilde{c} - \gamma f_I(c, t) - g_S(c, t) \int_0^1 K_1(c, \tilde{c}) g_I(\tilde{c}, t) + \gamma g_I(c, t) d\tilde{c} \right| \\
& \leq \int_0^1 K_1(c, \tilde{c}) |f_S(c, t) f_I(\tilde{c}, t) - g_S(c, t) g_I(\tilde{c}, t)| d\tilde{c} + \gamma |f_I(c, t) - g_I(c, t)| \\
& = \int_0^1 K_1(c, \tilde{c}) |(f_S(c, t) - g_S(c, t)) f_I(\tilde{c}, t) + g_S(c, t) (f_I(\tilde{c}, t) - g_I(\tilde{c}, t))| d\tilde{c} \\
& \quad + \gamma |f_I(c, t) - g_I(c, t)| \\
& \leq \tilde{f} \max_{c \in [0, 1]} \int_0^1 K_1(c, \tilde{c}) d\tilde{c} \|f_S(t) - g_S(t)\|_{L_\infty([0, 1])} \\
& \quad + \left(\tilde{f} \max_{c \in [0, 1]} \int_0^1 K_1(c, \tilde{c}) d\tilde{c} + \gamma \right) \|f_I(t) - g_I(t)\|_{L_\infty([0, 1])}.
\end{aligned}$$

For the last inequalities we use the estimate

$$\begin{aligned}
& \partial_t (f_S + f_I) = -\gamma f_I < 0 \\
& \implies f_S + f_I \leq f_{S_0} + f_{I_0} = \tilde{f}.
\end{aligned}$$

Now we follow the sketch of the proof and show that $F = (F_S, F_I)$ with

$$\begin{aligned}
f_S(c, t) &= f_{S_0}(c) - \int_0^t f_S(c, \tau) \int_0^1 K_1(c, \tilde{c}) f_I(\tilde{c}, \tau) d\tilde{c} d\tau = F_S(f_S, f_I)(c, t), \\
f_I(c, t) &= f_{I_0}(c) + \int_0^t \left(f_S(c, \tau) \int_0^1 K_1(c, \tilde{c}) f_I(\tilde{c}, \tau) d\tilde{c} - \gamma f_I(c, \tau) \right) d\tau = F_I(f_S, f_I)(c, t)
\end{aligned}$$

2. SIR epidemiological model with contact intensity structure

is a contraction on the Banach space $C([0, 1] \times [0, T], \mathbb{R}^n)$ with the $L_\infty([0, 1] \times [0, T])$ norm. We proceed by proving it for F_S and F_I separately

$$\begin{aligned}
& |F_S(f_S, f_I)(c, t) - F_S(g_S, g_I)(c, t)| \\
& \leq \int_0^t \int_0^1 K_1(c, \tilde{c}) |f_S(c, \tau) f_I(\tilde{c}, \tau) - g_S(c, \tau) g_I(\tilde{c}, \tau)| d\tilde{c} d\tau \\
& \leq \tilde{f}T \max_{c \in [0, 1]} \int_0^1 K_1(c, \tilde{c}) d\tilde{c} \left(\|f_S - g_S\|_{L_\infty([0, 1] \times [0, T])} + \|f_I - g_I\|_{L_\infty([0, 1] \times [0, T])} \right)
\end{aligned}$$

and

$$\begin{aligned}
& |F_I(f_S, f_I)(c, t) - F_I(g_S, g_I)(c, t)| \\
& \leq \int_0^t \left(\int_0^1 K_1(c, \tilde{c}) |f_S(c, \tau) f_I(\tilde{c}, \tau) - g_S(c, \tau) g_I(\tilde{c}, \tau)| d\tilde{c} + \gamma |f_I(c, \tau) - g_I(c, \tau)| \right) d\tau \\
& \leq \tilde{f}T \max_{c \in [0, 1]} \int_0^1 K_1(c, \tilde{c}) d\tilde{c} \|f_S - g_S\|_{L_\infty([0, 1] \times [0, T])} \\
& \quad + \left(\tilde{f}T \max_{c \in [0, 1]} \int_0^1 K_1(c, \tilde{c}) d\tilde{c} + \gamma T \right) \|f_I - g_I\|_{L_\infty([0, 1] \times [0, T])}.
\end{aligned}$$

Thus, for small T , we obtain a contraction and again by the Banach fixed point Theorem we conclude that (2.0.1) – (2.0.2) has locally exactly one solution pointwise for $c \in [0, 1]$.

3. SIR epidemiological model with mobility structure in one dimension

Another way to make the SIR model more realistic is to include a mobility structure. That is, the individuals have a location of residence and an area around this location, where they usually move. If an individual has a large mobility radius, for example because their home is far away from their working place, they meet more other individuals than the ones with small mobility radius. Since there is a space variable included, it is obvious to investigate the existence of an infection wave which travels through space. This approach can also be found in, e.g., [7] and [3, pp. 418-424]. We again work with population densities rather than total sizes. Let $f_S(x, r, t)$, $f_I(x, r, t)$ and $f_R(x, r, t)$ denote the densities of the susceptible, infected and removed individuals depending on the location of residence $x \in \mathbb{R}$, a mobility radius $r \in \mathbb{R}$, $r \geq 0$, and time $t \in \mathbb{R}$, $t \geq 0$. Analogous to Chapter 2 we have the initial conditions $f_S(x, r, 0) = f_{S_0}(x, r) > 0$, $f_I(x, r, 0) = f_{I_0}(x, r) > 0$, and $f_R(x, r, 0) = f_{R_0}(x, r) = 0$ and $f_S(x, r, t) + f_I(x, r, t) + f_R(x, r, t) = f_N(x, r)$ holds for all $t \in \mathbb{R}$, $t \geq 0$. In this case we measure the contact between the individuals due to mobility by the kernel $K_2(x, \tilde{x}, r, \tilde{r})$ and obtain the model

$$\partial_t f_S(x, r, t) = -f_S(x, r, t) \int_0^{r_{\max}} \int_{\mathbb{R}} K_2(x, \tilde{x}, r, \tilde{r}) f_I(\tilde{x}, \tilde{r}, t) d\tilde{x} d\tilde{r}, \quad (3.0.1)$$

$$\partial_t f_I(x, r, t) = f_S(x, r, t) \int_0^{r_{\max}} \int_{\mathbb{R}} K_2(x, \tilde{x}, r, \tilde{r}) f_I(\tilde{x}, \tilde{r}, t) d\tilde{x} d\tilde{r} - \gamma f_I(x, r, t), \quad (3.0.2)$$

$$\partial_t f_R(x, r, t) = \gamma f_I(x, r, t), \quad (3.0.3)$$

where $\gamma > 0$ denotes the recovery rate and $r_{\max} \in [0, \infty]$. The mobility radius r is restricted to $[0, r_{\max}]$ to impose restrictions on the mobility of individuals with r_{\max} denoting the maximal allowed radius. For example setting $r_{\max} = 0$ corresponds to an absolute curfew. The kernel K_2 should satisfy $K_2(x, \tilde{x}, r, \tilde{r}) = 0$ if and only if $|x - \tilde{x}| > r + \tilde{r} \iff 1 - \frac{|x - \tilde{x}|}{r + \tilde{r}} < 0$, where $|\cdot|$ denotes the absolute value in \mathbb{R} . This assumption is satisfied for example by

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$$K_2(x, \tilde{x}, r, \tilde{r}) = k \left(\frac{|x - \tilde{x}|}{r + \tilde{r}} \right) = \begin{cases} \left(1 - \frac{|x - \tilde{x}|}{r + \tilde{r}}\right)_+ & \text{if } r, \tilde{r} > 0 \text{ and } x \neq \tilde{x}, \\ 1 & \text{if } r, \tilde{r} = 0 \text{ and } x = \tilde{x}, \\ 0 & \text{if } r, \tilde{r} = 0 \text{ and } x \neq \tilde{x}. \end{cases}$$

Remark 3.0.1. Analogously to Chapter 2, we obtain the same dynamics, existence of solutions and uniqueness results for the system (3.0.1) – (3.0.3).

3.1. Traveling wave

As already mentioned above, we are interested in the existence of a *traveling wave* connecting the two disease free equilibria of (3.0.1) – (3.0.2), i.e., the equilibria $f_{I_0}(c) = 0$ and $f_{I_\infty}(c) = 0$. Note that there is no information lost if we neglect the last equation. Before we state the definition of a traveling wave, we simplify the equations by assuming that the mobility radius r is equal for all individuals and $K_2(x, \tilde{x}, r) = k \left(\frac{|x - \tilde{x}|}{2r} \right) = k \left(\frac{|x - \tilde{x}|}{\mathfrak{R}} \right)$. Thus, the simplified version is given by

$$\partial_t f_S(x, t) = -f_S(x, t) \int_{\mathbb{R}} k \left(\frac{|x - \tilde{x}|}{\mathfrak{R}} \right) f_I(\tilde{x}, t) d\tilde{x}, \quad (3.1.1)$$

$$\partial_t f_I(x, t) = f_S(x, t) \int_{\mathbb{R}} k \left(\frac{|x - \tilde{x}|}{\mathfrak{R}} \right) f_I(\tilde{x}, t) d\tilde{x} - \gamma f_I(x, t). \quad (3.1.2)$$

Definition 3.1.1. A *traveling wave* is a solution of the form $f_S = f_S(x - ct) = f_S(\xi)$ and $f_I = f_I(x - ct) = f_I(\xi)$, where \mathfrak{c} is the *speed* of the wave.

Remark 3.1.1. Note that the speed \mathfrak{c} is a positive number and later we calculate the minimal possible wave speed.

The spread of the disease is described by the wave traveling through space. The wave and time have opposite directions, that is, if time goes forward the wave travels backwards and vice versa. W.l.o.g. we suppose that the wave travels from left to right, i.e., for $\xi \rightarrow \infty$ the solutions $f_S(\xi)$ and $f_I(\xi)$ converge to the initial conditions.

3.1.1. Diffusion approximation

In order to find a traveling wave, we do a diffusion approximation in the one dimensional space variable. We start with nondimensionalizing the system (3.1.1) – (3.1.2), then we do a rescaling and finally, we use Taylor expansion to obtain a *diffusion approximation*.

3. SIR epidemiological model with mobility structure in one dimension

Nondimensionalization

We choose the following units

$$\begin{aligned} [f_S] &= [f_I] = \text{m}^{-1}, \\ [x] &= [\tilde{x}] = \text{m}, \\ [t] &= \text{s}, \end{aligned}$$

and want to find the units for k and γ in such a way that the equations (3.1.1) – (3.1.2) still hold. Therefor we write the equations in form of units. From equation (3.1.1), we obtain

$$\begin{aligned} \frac{[f_S]}{[t]} &= - [f_S] [k] [f_I] [\tilde{x}] \\ \iff \frac{1}{\text{m s}} &= \text{m}^{-1} [k] \text{m}^{-1} \text{m} \\ \implies [k] &= \text{s}^{-1}. \end{aligned}$$

To compute the unit of γ , we plug in the corresponding units in equation (3.1.2) and get

$$\begin{aligned} \frac{[f_I]}{[t]} &= [f_S] [k] [f_I] [\tilde{x}] - [\gamma] [f_I] \\ \iff \frac{1}{\text{m s}} &= \text{m}^{-1} \text{s}^{-1} \text{m}^{-1} \text{m} - [\gamma] \text{m} \\ \implies [\gamma] &= \text{s}^{-1}. \end{aligned}$$

Since we aim to state the system (3.1.1) – (3.1.2) in dimensionless form, we need the space and time variable, as well as the densities, to be dimensionless. Hence, we do a scaling with appropriate references for length and time. We choose \mathfrak{R} , coming from the kernel k , as reference length. For the reference time, we pick the disease specific constant $\frac{1}{\gamma}$ and thus, obtain

- Reference length: \mathfrak{R} with $[\mathfrak{R}] = \text{m}$,
- Reference time: $\mathfrak{T} = \frac{1}{\gamma}$ with $[\mathfrak{T}] = \text{s}$,

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and scale as follows

$$\begin{aligned}
x &= \mathfrak{R}x_s, \\
\tilde{x} &= \mathfrak{R}\tilde{x}_s, \\
t &= \mathfrak{T}t_s, \\
k\left(\frac{|x - \tilde{x}|}{\mathfrak{R}}\right) &= \frac{1}{\mathfrak{T}}k_s(|x_s - \tilde{x}_s|), \\
f_S(x, t) &= \frac{1}{\mathfrak{R}}f_{S_s}(x_s, t_s), \\
f_I(x, t) &= \frac{1}{\mathfrak{R}}f_{I_s}(x_s, t_s),
\end{aligned}$$

where $x_s, \tilde{x}_s, t_s, k_s, f_{S_s}$ and f_{I_s} denote the dimensionless versions. In order to derive the dimensionless equations, we substitute the scaled quantities in equations (3.1.1) – (3.1.2):

$$\begin{aligned}
\frac{1}{\mathfrak{T}\mathfrak{R}}\partial_{t_s}f_{S_s}(x_s, t_s) &= -\frac{1}{\mathfrak{R}}f_{S_s}(x_s, t_s)\mathfrak{R}\int_{\mathbb{R}}\frac{1}{\mathfrak{T}}k_s(|x_s - \tilde{x}_s|)\frac{1}{\mathfrak{R}}f_{I_s}(\tilde{x}_s, t_s)d\tilde{x}_s, \\
\frac{1}{\mathfrak{T}\mathfrak{R}}\partial_{t_s}f_{I_s}(x_s, t_s) &= \frac{1}{\mathfrak{R}}f_{S_s}(x_s, t_s)\mathfrak{R}\int_{\mathbb{R}}\frac{1}{\mathfrak{T}}k_s(|x_s - \tilde{x}_s|)\frac{1}{\mathfrak{R}}f_{I_s}(\tilde{x}_s, t_s)d\tilde{x}_s \\
&\quad - \frac{1}{\mathfrak{T}\mathfrak{R}}f_{I_s}(x_s, t_s).
\end{aligned}$$

In order to increase readability we skip the subscript and obtain the following dimensionless equations with dimensionless functions and variables

$$\partial_t f_S(x, t) = -f_S(x, t) \int_{\mathbb{R}^2} k(|x - \tilde{x}|) f_I(\tilde{x}, t) d\tilde{x}, \quad (3.1.3)$$

$$\partial_t f_I(x, t) = f_S(x, t) \int_{\mathbb{R}^2} k(|x - \tilde{x}|) f_I(\tilde{x}, t) d\tilde{x} - f_I(x, t). \quad (3.1.4)$$

Rescaling and Taylor expansion

For the spatial spread of diseases it is more suitable to have larger scales for the space variable. Consequently, we do a rescaling of the dimensionless space variable by ε in such a way that the result is still dimensionless

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$$\begin{aligned} x &\mapsto \frac{x}{\varepsilon}, \\ \tilde{x} &\mapsto \frac{\tilde{x}}{\varepsilon}, \end{aligned}$$

where $0 < \varepsilon \ll 1$ is dimensionless. With this rescaling equations (3.1.3) – (3.1.4) are transformed into

$$\partial_t f_S(x, t) = -f_S(x, t) \frac{1}{\varepsilon} \int_{\mathbb{R}} k\left(\frac{|x - \tilde{x}|}{\varepsilon}\right) f_I(\tilde{x}, t) d\tilde{x}, \quad (3.1.5)$$

$$\partial_t f_I(x, t) = f_S(x, t) \frac{1}{\varepsilon} \int_{\mathbb{R}} k\left(\frac{|x - \tilde{x}|}{\varepsilon}\right) f_I(\tilde{x}, t) d\tilde{x} - f_I(x, t). \quad (3.1.6)$$

Remark 3.1.2. As a consequence of the spatial rescaling, the densities also get rescaled. For the sake of brevity, however, we will denote the rescaled densities again by $f_S(x, t)$ and $f_I(x, t)$. Furthermore, without the simplification of r being equal for all individuals, this rescale would not lead to the desired form of the equations, since ε would vanish inside k .

Next we calculate the integral

$$\begin{aligned} \frac{1}{\varepsilon} \int_{\mathbb{R}} k\left(\frac{|x - \tilde{x}|}{\varepsilon}\right) f_I(\tilde{x}, t) d\tilde{x} &= \left| \begin{array}{l} \tilde{x} = x + \varepsilon z \\ d\tilde{x} = \varepsilon dz \end{array} \right| \\ &= \frac{\varepsilon}{\varepsilon} \int_{|z| < 1} k(|z|) f_I(x + \varepsilon z, t) dz. \end{aligned}$$

Finally, we can use Taylor expansion to approximate $f_I(x + \varepsilon z, t)$:

$$\begin{aligned} &\int_{|z| < 1} k(|z|) f_I(x + \varepsilon z, t) dz \\ &= \int_{|z| < 1} k(|z|) \left(f_I(x, t) + \varepsilon z \partial_x f_I(x, t) + \frac{\varepsilon^2}{2} z^2 \partial_x^2 f_I(x, t) \right) dz + \mathcal{O}(\varepsilon^3). \end{aligned}$$

This approximation holds formally for $\varepsilon \rightarrow 0$. We calculate the first and third integral, because the second one vanishes, as $k(|z|)$ is an even function by assumption and z is odd. This results in

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$$\begin{aligned}
f_I(x, t) \int_{|z|<1} k(|z|) dz &= 2f_I(x, t) \int_0^1 (1 - |z|)_+ dz =: \beta f_I(x, t), \\
\varepsilon \partial_x f_I(x, t) \int_{|z|<1} zk(|z|) dz &= 0, \\
\frac{\varepsilon^2}{2} \partial_x^2 f_I(x, t) \int_{|z|<1} z^2 k(|z|) dz &= \varepsilon^2 \partial_x^2 f_I(x, t) \int_0^1 z^2 (1 - |z|)_+ dz \\
&= \frac{\varepsilon^2}{6} \partial_x^2 f_I(x, t) =: \varepsilon^2 D \partial_x^2 f_I(x, t).
\end{aligned}$$

Altogether, we obtain the diffusion approximation of the system (3.1.5) – (3.1.6)

$$\partial_t f_S(x, t) = -f_S(x, t) \left(\beta f_I(x, t) + \varepsilon^2 D \partial_x^2 f_I(x, t) \right), \quad (3.1.7)$$

$$\partial_t f_I(x, t) = f_S(x, t) \left(\beta f_I(x, t) + \varepsilon^2 D \partial_x^2 f_I(x, t) \right) - f_I(x, t). \quad (3.1.8)$$

Remark 3.1.3. Note that for $\varepsilon \rightarrow 0$ the system (3.1.7) – (3.1.8) is similar to the SIR model, merely additionally depending on a spatial variable.

3.1.2. Existence of a traveling wave

In order to show the existence of a traveling wave, we substitute Definition 3.1.1 in the system (3.1.7) – (3.1.8), which yields

$$-c f'_S(\xi) = -f_S(\xi) \left(\beta f_I(\xi) + \varepsilon^2 D f''_I(\xi) \right), \quad (3.1.9)$$

$$-c f'_I(\xi) = f_S(\xi) \left(\beta f_I(\xi) + \varepsilon^2 D f''_I(\xi) \right) - f_I(\xi), \quad (3.1.10)$$

where f'_S and f'_I denote the derivatives with respect to ξ . A traveling wave exists, if the above system has a solution.

We follow the approach of [3, pp. 418-428] and recast (3.1.9) – (3.1.10) as first order system. First we divide (3.1.9) by $f_S(\xi)$ and integrate it, then we integrate the equation resulting from adding (3.1.9) and (3.1.10) w.r.t. ξ

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$$\begin{aligned} \mathfrak{c} \int_{\xi_0}^{\xi} \frac{f'_S(z)}{f_S(z)} dz &= \int_{\xi_0}^{\xi} \left(\beta f_I(z) + \varepsilon^2 D f''_I(z) \right) dz \\ \iff \mathfrak{c} \ln \left(\frac{f_S(\xi)}{f_S(\xi_0)} \right) &= \beta \int_{\xi_0}^{\xi} f_I(z) dz + \varepsilon^2 D f'_I(\xi) - \varepsilon^2 D f'_I(\xi_0), \end{aligned} \quad (3.1.11)$$

$$\begin{aligned} \mathfrak{c} \int_{\xi_0}^{\xi} (f'_I(z) + f'_S(z)) dz &= \int_{\xi_0}^{\xi} f_I(z) dz \\ \iff \mathfrak{c} (f_I(\xi) - f_I(\xi_0) + f_S(\xi) - f_S(\xi_0)) &= \int_{\xi_0}^{\xi} f_I(z) dz. \end{aligned} \quad (3.1.12)$$

Substitution of the integral in equation (3.1.11) by (3.1.12) yields

$$\varepsilon^2 D f'_I(\xi) = \varepsilon^2 D f'_I(\xi_0) + \mathfrak{c} \ln \left(\frac{f_S(\xi)}{f_S(\xi_0)} \right) - \mathfrak{c} \beta (f_I(\xi) - f_I(\xi_0) + f_S(\xi) - f_S(\xi_0)). \quad (3.1.13)$$

Next we insert (3.1.13) in (3.1.10), which gives

$$\begin{aligned} \mathfrak{c} \left(\frac{\varepsilon^2 D f'_I(\xi_0) + \mathfrak{c} \ln \left(\frac{f_S(\xi)}{f_S(\xi_0)} \right) - \mathfrak{c} \beta (f_I(\xi) - f_I(\xi_0) + f_S(\xi) - f_S(\xi_0))}{\varepsilon^2 D} \right) &= -\mathfrak{c} f'_S(\xi) + f_I(\xi) \\ \iff f'_S(\xi) &= \frac{f_I(\xi)}{\mathfrak{c}} - f'_I(\xi_0) - \frac{\mathfrak{c}}{\varepsilon^2 D} \ln \left(\frac{f_S(\xi)}{f_S(\xi_0)} \right) \\ &\quad + \frac{\mathfrak{c} \beta}{\varepsilon^2 D} (f_I(\xi) - f_I(\xi_0) + f_S(\xi) - f_S(\xi_0)). \end{aligned} \quad (3.1.14)$$

If we assume that there is a traveling wave, we expect that at position $x \in \mathbb{R}$ there are no infected individuals before the wave arrives, i.e., for $t \rightarrow -\infty$ we have $f_I(\infty) = 0$. The density of susceptible individuals at position x before the wave arrives is given by the initial condition $f_S(\infty) = f_N(\infty)$, that is, the whole population is susceptible. Also, we assume the wave starting smoothly, i.e., $f'_I(\infty) = 0$. If we set $\xi_0 = \infty$, (3.1.14) and (3.1.13) change to

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$$f'_S(\xi) = \frac{f_I(\xi)}{\mathfrak{c}} - \frac{\mathfrak{c}}{\varepsilon^2 D} \ln\left(\frac{f_S(\xi)}{f_S(\infty)}\right) + \frac{\mathfrak{c}\beta}{\varepsilon^2 D} (f_I(\xi) + f_S(\xi) - f_S(\infty)), \quad (3.1.15)$$

$$f'_I(\xi) = \frac{\mathfrak{c}}{\varepsilon^2 D} \ln\left(\frac{f_S(\xi)}{f_S(\infty)}\right) - \frac{\mathfrak{c}\beta}{\varepsilon^2 D} (f_I(\xi) + f_S(\xi) - f_S(\infty)). \quad (3.1.16)$$

This system can be simplified by introducing new functions $X(\xi) = \frac{f_S(\xi)}{f_S(\infty)}$ and $Y(\xi) = \frac{f_I(\xi)}{f_S(\infty)}$. They take values between 0 and 1, since they are normalized by the total population density. Therefore, equations (3.1.15) and (3.1.16) become

$$\begin{aligned} f_S(\infty)X'(\xi) &= \frac{f_S(\infty)Y(\xi)}{\mathfrak{c}} - \frac{\mathfrak{c}}{\varepsilon^2 D} \ln(X(\xi)) \\ &\quad + \frac{\mathfrak{c}\beta}{\varepsilon^2 D} (f_S(\infty)Y(\xi) + f_S(\infty)X(\xi) - f_S(\infty)) \\ \Leftrightarrow \frac{\varepsilon^2 D f_S(\infty)}{\mathfrak{c}} X'(\xi) &= -\ln(X(\xi)) + \beta f_S(\infty)X(\xi) - \beta f_S(\infty) \\ &\quad + \left(\beta f_S(\infty) + \frac{\varepsilon^2 D f_S(\infty)}{\mathfrak{c}^2} \right) Y(\xi), \end{aligned} \quad (3.1.17)$$

$$\begin{aligned} f_S(\infty)Y'(\xi) &= \frac{\mathfrak{c}}{\varepsilon^2 D} \ln(X(\xi)) - \frac{\mathfrak{c}\beta}{\varepsilon^2 D} (f_S(\infty)Y(\xi) + f_S(\infty)X(\xi) - f_S(\infty)) \\ \Leftrightarrow \frac{\varepsilon^2 D f_S(\infty)}{\mathfrak{c}} Y'(\xi) &= \ln(X(\xi)) - \beta f_S(\infty)X(\xi) + \beta f_S(\infty) - \beta f_S(\infty)Y(\xi). \end{aligned} \quad (3.1.18)$$

Once the wave passed a particular position the density of infected individuals should be zero and the density of susceptible individuals should have reached some steady level. Recall that we already showed with inequality (2.1.2) that at the end of the spread of the disease there are still some susceptible individuals left, that is, the density after the spread is not zero. The end of the wave is determined by $t \rightarrow \infty$ and thus, $Y(-\infty) = 0$ and $X'(-\infty) = 0$. Insertion in (3.1.17) yields

$$\begin{aligned} \ln(X(-\infty)) &= \beta f_S(\infty)X(-\infty) - \beta f_S(\infty) \\ \Leftrightarrow X(-\infty) &= e^{\beta f_S(\infty)(X(-\infty)-1)}, \end{aligned} \quad (3.1.19)$$

which has for $\beta f_S(\infty) \leq 1$ only one solution given by $X(-\infty) = 1$. Hence, there is no spread of the disease, that is, there is no epidemic. Thus, for an epidemic to occur it is necessary that

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$$\beta f_S(\infty) > 1 \iff f_S(\infty) > \frac{1}{\beta} \quad (3.1.20)$$

holds and 3.1.19 has a solution with $X(-\infty) < 1$. The inequality (3.1.20) gives a threshold for the initial density of susceptible, i.e., if initially there are too little susceptible individuals there will not be a traveling wave.

Speed of the traveling wave

The next question is, if there is some minimal speed of the traveling wave in case it exists, i.e., (3.1.20) holds. Therefore, we have a look at the phase plane for X and Y under the assumption of (3.1.20). The system (3.1.17) – (3.1.18) has two disease free equilibria $(X(-\infty), 0)$ and $(1, 0)$. We rewrite equations (3.1.17) and (3.1.18) by

$$X'(\xi) = -\frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty)} \ln(X(\xi)) + \frac{\mathfrak{c}\beta}{\varepsilon^2 D} X(\xi) - \frac{\mathfrak{c}\beta}{\varepsilon^2 D} + \left(\frac{\mathfrak{c}\beta}{\varepsilon^2 D} + \frac{1}{\mathfrak{c}} \right) Y(\xi) =: u, \quad (3.1.21)$$

$$Y'(\xi) = \frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty)} \ln(X(\xi)) - \frac{\mathfrak{c}\beta}{\varepsilon^2 D} X(\xi) + \frac{\mathfrak{c}\beta}{\varepsilon^2 D} - \frac{\mathfrak{c}\beta}{\varepsilon^2 D} Y(\xi) =: v. \quad (3.1.22)$$

Our goal is to linearize system (3.1.21) – (3.1.22) at the equilibrium points. We start with the equilibrium $(1, 0)$ and linearize by $X(\xi) = 1 + \mu$ and $Y(\xi) = 0 + \nu$. Therefore, we calculate the Jacobian matrix evaluated at the equilibrium

$$\mathcal{J}_{u,v}(1, 0) = \begin{pmatrix} \frac{du}{dX}(1, 0) & \frac{du}{dY}(1, 0) \\ \frac{dv}{dX}(1, 0) & \frac{dv}{dY}(1, 0) \end{pmatrix} = \begin{pmatrix} \frac{\mathfrak{c}\beta}{\varepsilon^2 D} - \frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty)} & \frac{\mathfrak{c}\beta}{\varepsilon^2 D} + \frac{1}{\mathfrak{c}} \\ \frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty)} - \frac{\mathfrak{c}\beta}{\varepsilon^2 D} & -\frac{\mathfrak{c}\beta}{\varepsilon^2 D} \end{pmatrix}.$$

Thus, the linearization is given by

$$\mu' = \left(\frac{\mathfrak{c}\beta}{\varepsilon^2 D} - \frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty)} \right) \mu + \left(\frac{\mathfrak{c}\beta}{\varepsilon^2 D} + \frac{1}{\mathfrak{c}} \right) \nu, \quad (3.1.23)$$

$$\nu' = \left(\frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty)} - \frac{\mathfrak{c}\beta}{\varepsilon^2 D} \right) \mu - \frac{\mathfrak{c}\beta}{\varepsilon^2 D} \nu. \quad (3.1.24)$$

Now we can proceed in two different ways. Either we calculate the eigenvalues of the Jacobian by solving $\det(\mathcal{J}_{u,v}(1, 0) - \lambda I) = 0$, where I denotes the identity matrix. Or we solve the system (3.1.23) – (3.1.24) by using the ansatz $\mu = m e^{\lambda \xi}$ and $\nu = n e^{\lambda \xi}$ with

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$m, n \neq 0$. Following the first approach, we get

$$\begin{aligned} \det(\mathcal{J}_{u,v}(1,0) - \lambda I) &= \det \begin{pmatrix} \frac{\mathfrak{c}\beta}{\varepsilon^2 D} - \frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty)} - \lambda & \frac{\mathfrak{c}\beta}{\varepsilon^2 D} + \frac{1}{\mathfrak{c}} \\ \frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty)} - \frac{\mathfrak{c}\beta}{\varepsilon^2 D} & -\frac{\mathfrak{c}\beta}{\varepsilon^2 D} - \lambda \end{pmatrix} \\ &= \left(\frac{\mathfrak{c}\beta}{\varepsilon^2 D} - \frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty)} - \lambda \right) \left(-\frac{\mathfrak{c}\beta}{\varepsilon^2 D} - \lambda \right) \\ &\quad - \left(\frac{\mathfrak{c}\beta}{\varepsilon^2 D} + \frac{1}{\mathfrak{c}} \right) \left(\frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty)} - \frac{\mathfrak{c}\beta}{\varepsilon^2 D} \right) = 0 \\ \iff \lambda^2 + \frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty)} \lambda + \frac{1}{\varepsilon^2 D f_S(\infty)} (\beta f_S(\infty) - 1) &= 0 \\ \implies \lambda_{1,2} = \frac{-\mathfrak{c} \pm \sqrt{\mathfrak{c}^2 - 4\varepsilon^2 D f_S(\infty) (\beta f_S(\infty) - 1)}}{2\varepsilon^2 D f_S(\infty)}. \end{aligned}$$

Since we already know that $\beta f_S(\infty) > 1$ holds and we do not want oscillations to occur, we need the term in the square root to be positive. This is only the case if

$$\mathfrak{c} \geq \mathfrak{c}_{\min} = 2\varepsilon \sqrt{D f_S(\infty) (\beta f_S(\infty) - 1)} \quad (3.1.25)$$

holds. If $\mathfrak{c} \geq \mathfrak{c}_{\min}$, both eigenvalues are negative, the equilibrium $(1, 0)$ is asymptotically stable and (3.1.25) gives the minimal wave speed. An analogous minimal wave speed is found in [7, eq. (3.6)]. Note that by the stable manifold Theorem A.2.2, the properties of the dynamics near hyperbolic equilibria are shared by the nonlinear problem and its linearization. Hence, (3.1.25) also gives us a condition for the existence of a traveling wave of the original system.

In order to linearize the system (3.1.21) – (3.1.22) at the equilibrium $(X(-\infty), 0)$ by $X(\xi) = X(-\infty) + \mu$ and $Y(\xi) = 0 + \nu$ we compute the Jacobian as above by

$$\mathcal{J}_{u,v}(X(-\infty), 0) = \begin{pmatrix} \frac{\mathfrak{c}\beta}{\varepsilon^2 D} - \frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty) X(-\infty)} & \frac{\mathfrak{c}\beta}{\varepsilon^2 D} + \frac{1}{\mathfrak{c}} \\ \frac{\mathfrak{c}}{\varepsilon^2 D f_S(\infty) X(-\infty)} - \frac{\mathfrak{c}\beta}{\varepsilon^2 D} & -\frac{\mathfrak{c}\beta}{\varepsilon^2 D} \end{pmatrix}.$$

Therefore, the linearization at this equilibrium is

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$$\begin{aligned}\mu' &= \left(\frac{\mathbf{c}\beta}{\varepsilon^2 D} - \frac{\mathbf{c}}{\varepsilon^2 D f_S(\infty) X(-\infty)} \right) \mu + \left(\frac{\mathbf{c}\beta}{\varepsilon^2 D} + \frac{1}{\mathbf{c}} \right) \nu, \\ \nu' &= \left(\frac{\mathbf{c}}{\varepsilon^2 D f_S(\infty) X(-\infty)} - \frac{\mathbf{c}\beta}{\varepsilon^2 D} \right) \mu - \frac{\mathbf{c}\beta}{\varepsilon^2 D} \nu.\end{aligned}$$

Solving $\det(\mathcal{J}_{u,v}(X(-\infty), 0) - \lambda I) = 0$ yields

$$\lambda_{1,2} = \frac{-\mathbf{c} \pm \sqrt{\mathbf{c}^2 - 4\varepsilon^2 D f_S(\infty) X(-\infty) (\beta f_S(\infty) X(-\infty) - 1)}}{2\varepsilon^2 D f_S(\infty) X(-\infty)}.$$

Note that $\beta f_S(\infty) X(-\infty) < 1$, so that the term in the square root is always positive and we obtain a negative and a positive eigenvalue. Therefore, the equilibrium $(X(-\infty), 0)$ is a saddle point. The eigenvectors of the saddle point are determined by

$$\begin{aligned}\mathcal{J}_{u,v}(X(-\infty), 0) \begin{pmatrix} \mu \\ \nu \end{pmatrix} &= \lambda_{1,2} \begin{pmatrix} \mu \\ \nu \end{pmatrix} \\ \Leftrightarrow \mathcal{J}_{u,v}(X(-\infty), 0) \begin{pmatrix} \mu \\ \nu \end{pmatrix} - \lambda_{1,2} \begin{pmatrix} \mu \\ \nu \end{pmatrix} &= 0.\end{aligned}$$

From the first line, we obtain two equations, which correspond to the lines intersecting the saddle point,

$$\left(\frac{\mathbf{c}\beta}{\varepsilon^2 D} - \frac{\mathbf{c}}{\varepsilon^2 D f_S(\infty) X(-\infty)} - \lambda_{1,2} \right) \mu + \left(\frac{\mathbf{c}\beta}{\varepsilon^2 D} + \frac{1}{\mathbf{c}} \right) \nu = 0. \quad (3.1.26)$$

The equation with λ_1 corresponds to the line which leaves the saddle point. The other converges to the saddle point. Thus, there is one trajectory from the equilibrium $(X(-\infty), 0)$ entering the first quadrant with increasing $X(\xi)$. We are left to show that this trajectory ends up at the second equilibrium $(1, 0)$, i.e., that there is a heteroclinic orbit connecting the two disease free equilibria. In order to do so, we will use the Poincare-Bendixson Theorem, [3, p. 137],

Theorem 3.1.1 (Poincare-Bendixson). *If there is a bounded region D in the (x, y) -plane*

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such that any solution of the system

$$\begin{aligned}\dot{x} &= f(x, y), \\ \dot{y} &= g(x, y),\end{aligned}$$

that starts in D remains in D , then D contains either a stable steady state or a limit cycle.

Therefore, we need to find a bounded region, such that any solution starting inside this region will stay there. At $Y = 0$ we have $Y' > 0$ and $X' < 0$, hence, there is no trajectory leaving the first quadrant crossing $Y = 0$. At $X = X(-\infty)$, $X' > 0$ and $Y' < 0$, thus, no trajectory can cross the line $X = X(-\infty)$ from right to left. Next we consider the line

$$\left(\frac{1}{2} - \beta f_S(\infty)\right) (X - 1) = \left(\beta f_S(\infty) + \frac{\varepsilon^2 Df_S(\infty)}{\mathfrak{c}^2}\right) Y. \quad (3.1.27)$$

This equation is obtained in the same way as (3.1.26), but we linearize at the other equilibria, i.e., replacing $X(-\infty)$ by 1 and assuming that \mathfrak{c} is minimal:

$$\begin{aligned}& \frac{c}{\varepsilon^2 Df_S(\infty)} \left(1 - \beta f_S(\infty) - \frac{1}{2} \pm \frac{1}{2} \sqrt{1 - \frac{4\varepsilon^2 Df_S(\infty) (\beta f_S(\infty) - 1)}{\mathfrak{c}^2}}\right) \mu \\ &= \frac{c}{\varepsilon^2 Df_S(\infty)} \left(\beta f_S(\infty) + \frac{\varepsilon^2 Df_S(\infty)}{\mathfrak{c}^2}\right) \nu \\ & \stackrel{\substack{\mathfrak{c} \text{ minimal} \\ \mu=X-1, \nu=Y}}{\implies} \left(\frac{1}{2} - \beta f_S(\infty)\right) (X - 1) = \left(\beta f_S(\infty) + \frac{\varepsilon^2 Df_S(\infty)}{\mathfrak{c}^2}\right) Y.\end{aligned}$$

On the line given by (3.1.27), we can estimate X' and Y' in (3.1.17) and (3.1.18) by using $\ln X \leq X - 1$ for $X > 0$. A proof of this inequality is done in Section A.2. This yields the estimation

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$$\begin{aligned}
\frac{\varepsilon^2 Df_S(\infty)}{\mathfrak{c}} X' &\geq -(X-1) + \beta f_S(\infty)(X-1) + \left(\frac{1}{2} - \beta f_S(\infty)\right)(X-1) \\
&= -\frac{1}{2}(X-1), \\
\frac{\varepsilon^2 Df_S(\infty)}{\mathfrak{c}} Y' &\leq (X-1) - \beta f_S(\infty)(X-1) - \beta f_S(\infty) \frac{\left(\frac{1}{2} - \beta f_S(\infty)\right)(X-1)}{\left(\beta f_S(\infty) + \frac{\varepsilon^2 Df_S(\infty)}{\mathfrak{c}^2}\right)} \\
&= \frac{\left(\frac{1}{2}\beta f_S(\infty) + \frac{\varepsilon^2 Df_S(\infty)}{\mathfrak{c}^2} - \frac{\varepsilon^2 D\beta f_S^2(\infty)}{\mathfrak{c}^2}\right)(X-1)}{\left(\beta f_S(\infty) + \frac{\varepsilon^2 Df_S(\infty)}{\mathfrak{c}^2}\right)},
\end{aligned}$$

and therefore,

$$\frac{dY}{dX} \leq \frac{\frac{2\varepsilon^2 Df_S(\infty)}{\mathfrak{c}^2} (\beta f_S(\infty) - 1) - \beta f_S(\infty)}{\left(\beta f_S(\infty) + \frac{\varepsilon^2 Df_S(\infty)}{\mathfrak{c}^2}\right)} \underset{\text{minimal}}{\mathfrak{c}} \frac{\frac{1}{2} - \beta f_S(\infty)}{\left(\beta f_S(\infty) + \frac{\varepsilon^2 Df_S(\infty)}{\mathfrak{c}^2}\right)}.$$

Since $\beta f_S(\infty) > 1$, $\frac{dY}{dX} \leq 0$ holds and there can not be a trajectory crossing the line (3.1.27) from below to above. The bounded region, which we need to apply the Poincare-Bendixson Theorem, is given by $Y = 0$, $X = X(-\infty)$ and (3.1.27). There can not be a solution, which starts inside this triangle and ends outside of it. Thus, the trajectory leaving $(X(-\infty), 0)$ must go either to a limit cycle or the other equilibrium. We can exclude that there exists a limit cycle, because there is no other equilibrium inside the bounded region, which would be necessary. Therefore, we are left with the only other possibility: The unique trajectory starting in $(X(-\infty), 0)$ ends at $(1, 0)$ is a heteroclinic orbit.

Summarizing our observation yields the following conclusions:

- There can not be a traveling wave, i.e., no spread of the disease, if the density of susceptible individuals is too low. This condition is captured in equation (3.1.20).
- There is no wave with speed less than \mathfrak{c}_{\min} , defined in (3.1.25). But there can be a wave with higher speed. This does not change the fact that there is a trajectory from $(X(-\infty), 0)$ to $(1, 0)$, only the shape of it changes.

4. SIR epidemiological model with mobility structure in two dimensions

Since individuals do not move only in one dimension, but in a two dimensional space, we set $x \in \mathbb{R}^2$. Analogous to (3.0.1) – (3.0.3), we obtain the following SIR model with mobility structure in two dimensions

$$\partial_t f_S(x, r, t) = -f_S(x, r, t) \int_0^{r_{\max}} \int_{\mathbb{R}^2} K_2(x, \tilde{x}, r, \tilde{r}) f_I(\tilde{x}, \tilde{r}, t) d\tilde{x} d\tilde{r}, \quad (4.0.1)$$

$$\partial_t f_I(x, r, t) = f_S(x, r, t) \int_0^{r_{\max}} \int_{\mathbb{R}^2} K_2(x, \tilde{x}, r, \tilde{r}) f_I(\tilde{x}, \tilde{r}, t) d\tilde{x} d\tilde{r} - \gamma f_I(x, r, t), \quad (4.0.2)$$

$$\partial_t f_R(x, r, t) = \gamma f_I(x, r, t). \quad (4.0.3)$$

The initial conditions and assumptions on r made in Chapter 3 still hold. The mobility kernel in two dimensions should, again analogously to Chapter 3, satisfy $K_2(x, \tilde{x}, r, \tilde{r}) = 0$ if and only if $B_r(x) \cap B_{\tilde{r}}(\tilde{x}) = \emptyset \iff |x - \tilde{x}| > r + \tilde{r} \iff 1 - \frac{|x - \tilde{x}|}{r + \tilde{r}} < 0$, where $|\cdot|$ denotes the euclidean norm in \mathbb{R}^2 . As in Chapter 3 already suggested, this assumption is satisfied for example by the function

$$K_2(x, \tilde{x}, r, \tilde{r}) = k \left(\frac{|x - \tilde{x}|}{r + \tilde{r}} \right) = \begin{cases} \left(1 - \frac{|x - \tilde{x}|}{r + \tilde{r}}\right)_+ & \text{if } r, \tilde{r} > 0 \text{ and } x \neq \tilde{x}, \\ 1 & \text{if } r, \tilde{r} = 0 \text{ and } x = \tilde{x}, \\ 0 & \text{if } r, \tilde{r} = 0 \text{ and } x \neq \tilde{x}. \end{cases}$$

4.1. Traveling wave

In two dimensions we need to choose a direction of the traveling wave, cf. Definition 3.1.1. Since the kernel K_2 is rotation invariant, we can choose any direction in \mathbb{R}^2 , w.l.o.g. we choose x_1 and thus, we get

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$$f_S = f_S(x_1 - ct) = f_S(\xi) \quad \text{and} \quad f_I = f_I(x_1 - ct) = f_I(\xi). \quad (4.1.1)$$

Assuming, like in the one dimensional case, that the mobility radius r is equal for all individuals and consequently, $K_2(x, \tilde{x}, r, \tilde{r}) = k\left(\frac{|x - \tilde{x}|}{2r}\right) = k\left(\frac{|x - \tilde{x}|}{\mathfrak{R}}\right)$. Hence, equations (4.0.1) – (4.0.2) simplify to

$$\partial_t f_S(x, t) = -f_S(x, t) \int_{\mathbb{R}^2} k\left(\frac{|x - \tilde{x}|}{\mathfrak{R}}\right) f_I(\tilde{x}, t) d\tilde{x}, \quad (4.1.2)$$

$$\partial_t f_I(x, t) = f_S(x, t) \int_{\mathbb{R}^2} k\left(\frac{|x - \tilde{x}|}{\mathfrak{R}}\right) f_I(\tilde{x}, t) d\tilde{x} - \gamma f_I(x, t). \quad (4.1.3)$$

The diffusion approximation works with a two dimensional space variable as well. We just need to make some adaptations.

The units for the densities f_S and f_I , as well as for the space variables $x = (x_1, x_2)$ and $\tilde{x} = (\tilde{x}_1, \tilde{x}_2)$, in the nondimensionalization process change to

$$\begin{aligned} [f_S] &= [f_I] = \text{m}^{-2}, \\ [x_1] &= [x_2] = [\tilde{x}_1] = [\tilde{x}_2] = \text{m}. \end{aligned}$$

Thus, the dimensionless equations of (4.1.2) – (4.1.3) with dimensionless functions and variables are

$$\begin{aligned} \partial_t f_S(x, t) &= -f_S(x, t) \int_{\mathbb{R}^2} k(|x - \tilde{x}|) f_I(\tilde{x}, t) d\tilde{x}, \\ \partial_t f_I(x, t) &= f_S(x, t) \int_{\mathbb{R}^2} k(|x - \tilde{x}|) f_I(\tilde{x}, t) d\tilde{x} - f_I(x, t). \end{aligned}$$

The rescaling

$$\begin{aligned} x &\mapsto \frac{x}{\varepsilon}, \\ \tilde{x} &\mapsto \frac{\tilde{x}}{\varepsilon}, \end{aligned}$$

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with $0 < \varepsilon \ll 1$ dimensionless, yields

$$\partial_t f_S(x, t) = -f_S(x, t) \frac{1}{\varepsilon^2} \int_{\mathbb{R}^2} k\left(\frac{|x - \tilde{x}|}{\varepsilon}\right) f_I(\tilde{x}, t) d\tilde{x}, \quad (4.1.4)$$

$$\partial_t f_I(x, t) = f_S(x, t) \frac{1}{\varepsilon^2} \int_{\mathbb{R}^2} k\left(\frac{|x - \tilde{x}|}{\varepsilon}\right) f_I(\tilde{x}, t) d\tilde{x} - f_I(x, t). \quad (4.1.5)$$

Calculating the integral justifies the application of the Taylor expansion

$$\begin{aligned} \frac{1}{\varepsilon^2} \int_{\mathbb{R}^2} k\left(\frac{|x - \tilde{x}|}{\varepsilon}\right) f_I(\tilde{x}, t) d\tilde{x} &= \left| \begin{array}{l} \tilde{x} = x + \varepsilon z \\ d\tilde{x} = \varepsilon^2 dz \end{array} \right| \\ &= \frac{\varepsilon^2}{\varepsilon^2} \int_{|z| < 1} k(|z|) f_I(x + \varepsilon z, t) dz \\ &= \int_{|z| < 1} k(|z|) (f_I(x, t) + \varepsilon z \cdot \nabla_x f_I(x, t) \\ &\quad + \frac{\varepsilon^2}{2} z^\top \nabla_x^2 f(x, t) z) dz + \mathcal{O}(\varepsilon^3), \end{aligned}$$

where \cdot denotes the inner product, ∇_x denotes the gradient w.r.t. x and ∇_x^2 is the Hessian w.r.t. x . We calculate the three integrals, starting with the first one

$$\begin{aligned} f_I(x, t) \int_{|z| < 1} k(|z|) dz &= \left| \begin{array}{l} z = (r \cos(\varphi), r \sin(\varphi)) \\ dz = r dr d\varphi \end{array} \right| \\ &= f_I(x, t) \int_0^{2\pi} \int_0^1 (1-r) r dr d\varphi = \frac{\pi}{3} f_I(x, t) =: \beta f_I(x, t), \end{aligned}$$

where we used the transformation to polar coordinates. The second integral vanishes, because $k(|z|)$ is an even function by assumption and z is odd, that is

$$\varepsilon \nabla_x f_I(x, t) \cdot \int_{|z| < 1} z k(|z|) dz = 0.$$

For the calculation of the last integral we set $z = (z_1, z_2)$ and use again polar coordinates:

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$$\begin{aligned}
& \frac{\varepsilon^2}{2} \int_{|z|<1} z^\top \nabla_x^2 f_I(x, t) z k(|z|) dz \\
&= \frac{\varepsilon^2}{2} \sum_{i,j=1}^2 \frac{\partial^2 f_I(x, t)}{\partial x_i \partial x_j} \int_{|z|<1} z_i z_j k(|z|) dz \\
&= \frac{\varepsilon^2}{2} \left(\frac{\partial^2 f_I(x, t)}{\partial x_1^2} \int_{|z|<1} z_1^2 k(|z|) dz + 2 \frac{\partial^2 f_I(x, t)}{\partial x_1 \partial x_2} \int_{|z|<1} z_1 z_2 k(|z|) dz \right. \\
&\quad \left. + \frac{\partial^2 f_I(x, t)}{\partial x_2^2} \int_{|z|<1} z_2^2 k(|z|) dz \right) \\
&= \left| \begin{array}{l} z = (r \cos(\varphi), r \sin(\varphi)) \\ dz = r dr d\varphi \end{array} \right| \\
&= \frac{\varepsilon^2}{2} \Delta_x f_I(x, t) \int_0^{2\pi} \int_0^1 (1-r) r^3 dr d\varphi \\
&= \varepsilon^2 \pi \left(\frac{1}{4} - \frac{1}{5} \right) \Delta_x f_I(x, t) =: \varepsilon^2 D \Delta_x f_I(x, t).
\end{aligned}$$

Altogether, we obtain the diffusion approximation of the system (4.1.4) – (4.1.5)

$$\begin{aligned}
\partial_t f_S(x, t) &= -f_S(x, t) \left(\beta f_I(x, t) + \varepsilon^2 D \Delta_x f_I(x, t) \right), \\
\partial_t f_I(x, t) &= f_S(x, t) \left(\beta f_I(x, t) + \varepsilon^2 D \Delta_x f_I(x, t) \right) - f_I(x, t).
\end{aligned}$$

Inserting (4.1.1) in the above equations yields

$$-\mathbf{c} f'_S(\xi) = -f_S(\xi) \left(\beta f_I(\xi) + \varepsilon^2 D f''_I(\xi) \right), \quad (4.1.6)$$

$$-\mathbf{c} f'_I(\xi) = f_S(\xi) \left(\beta f_I(\xi) + \varepsilon^2 D f''_I(\xi) \right) - f_I(\xi), \quad (4.1.7)$$

where f'_S and f'_I denote the derivatives w.r.t. ξ . Since the system (4.1.6) – (4.1.7) is exactly the same as (3.1.9) – (3.1.10), we obtain the same results as in Section 3.1.2.

5. SIR epidemiological model with contact intensity and mobility structure in two dimensions

Finally, we combine the two improvements of the Chapters 2 and 4 to obtain a SIR model with kernels that measure the interaction of the individuals in two ways. It measures if contact is possible due to the position and mobility of the individuals and if the contact is intense or distanced. Hence, we obtain a SIR model with contact intensity and mobility structure in two dimensions

$$\partial_t f_S(x, r, c, t) = -f_S(x, r, c, t) \int_0^1 \int_0^{r_{\max}} \int_{\mathbb{R}^2} K_1(c, \tilde{c}) K_2(x, \tilde{x}, r, \tilde{r}) f_I(\tilde{x}, \tilde{r}, \tilde{c}, t) d\tilde{x} d\tilde{r} d\tilde{c}, \quad (5.0.1)$$

$$\begin{aligned} \partial_t f_I(x, r, c, t) = & f_S(x, r, c, t) \int_0^1 \int_0^{r_{\max}} \int_{\mathbb{R}^2} K_1(c, \tilde{c}) K_2(x, \tilde{x}, r, \tilde{r}) f_I(\tilde{x}, \tilde{r}, \tilde{c}, t) d\tilde{x} d\tilde{r} d\tilde{c} \\ & - \gamma f_I(x, r, c, t), \end{aligned} \quad (5.0.2)$$

$$\partial_t f_R(x, r, c, t) = \gamma f_I(x, r, c, t). \quad (5.0.3)$$

The initial conditions are $f_S(x, r, c, 0) = f_{S_0}(x, r, c) > 0$, $f_I(x, r, c, 0) = f_{I_0}(x, r, c) > 0$ and $f_R(x, r, c, 0) = f_{R_0}(x, r, c) = 0$ and $f_S(x, r, c, t) + f_I(x, r, c, t) + f_R(x, r, c, t) = f_N(x, r, c)$ holds for all $t \in \mathbb{R}$, $t \geq 0$. The assumptions of the kernels $K_1(c, \tilde{c})$ and $K_2(x, \tilde{x}, r, \tilde{r})$ and r are the same as in the previous chapters.

Remark 5.0.1. The dynamics, existence of solutions and uniqueness results of Chapter 2 remain valid for the system (5.0.1) – (5.0.3).

The goal is to rewrite the system (5.0.1) – (5.0.2) in the form of (3.1.9) – (3.1.10) and (4.1.6) – (4.1.7). Therefore, we follow the procedure of Subsection 3.1.1, keeping the changes already made in Section 4.1. The first step is again to simplify the model by the assumption that r is equal for all individuals, which yields

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$$\partial_t f_S(x, c, t) = -f_S(x, c, t) \int_0^1 \int_{\mathbb{R}^2} K_1(c, \tilde{c}) k\left(\frac{|x - \tilde{x}|}{\mathfrak{R}}\right) f_I(\tilde{x}, \tilde{c}, t) d\tilde{x} d\tilde{c}, \quad (5.0.4)$$

$$\partial_t f_I(x, c, t) = f_S(x, c, t) \int_0^1 \int_{\mathbb{R}^2} K_1(c, \tilde{c}) k\left(\frac{|x - \tilde{x}|}{\mathfrak{R}}\right) f_I(\tilde{x}, \tilde{c}, t) d\tilde{x} d\tilde{c} - \gamma f_I(x, c, t). \quad (5.0.5)$$

For the nondimensionalization, the only thing we need to discuss in addition is the contact intensity and the corresponding kernel. Since there is no physical unit for contact intensity, it seems natural that it is dimensionless. Also, $[k] = \text{s}^{-1}$ and $[\gamma] = \text{s}^{-1}$ remain valid. We keep the same references for length and time as in Subsection 3.1.1

1. Reference length: \mathfrak{R} with $[\mathfrak{R}] = \text{m}$,
2. Reference time: $\mathfrak{T} = \frac{1}{\gamma}$ with $[\mathfrak{T}] = \text{s}$,

and scale by

$$\begin{aligned} x &= \mathfrak{R}x_s, \\ \tilde{x} &= \mathfrak{R}\tilde{x}_s, \\ c &= c_s, \\ \tilde{c} &= \tilde{c}_s, \\ t &= \mathfrak{T}t_s, \\ K_1(c, \tilde{c}) &= K_{1_s}(c_s, \tilde{c}_s), \\ k\left(\frac{|x - \tilde{x}|}{\mathfrak{R}}\right) &= \frac{1}{\mathfrak{T}} k_s(|x_s - \tilde{x}_s|), \\ f_S(x, c, t) &= \frac{1}{\mathfrak{R}^2} f_{S_s}(x_s, c_s, t_s), \\ f_I(x, c, t) &= \frac{1}{\mathfrak{R}^2} f_{I_s}(x_s, c_s, t_s), \end{aligned}$$

where the index s denotes the dimensionless variables and functions. Substituting this scaling in (5.0.4) – (5.0.5) gives

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$$\begin{aligned}
\frac{1}{\mathfrak{I}\mathfrak{R}^2} \partial_{t_s} f_{S_s}(x_s, c_s, t_s) &= -\frac{1}{\mathfrak{R}^2} f_{S_s}(x_s, c_s, t_s) \\
&\quad \mathfrak{R}^2 \int_0^1 \int_{\mathbb{R}^2} K_{1,s}(c_s, \tilde{c}_s) \frac{1}{\mathfrak{I}} k_s(|x_s - \tilde{x}_s|) \frac{1}{\mathfrak{R}^2} f_{I_s}(\tilde{x}_s, \tilde{c}_s, t_s) d\tilde{x}_s d\tilde{c}_s, \\
\frac{1}{\mathfrak{I}\mathfrak{R}^2} \partial_{t_s} f_{S_s}(x_s, c_s, t_s) &= \frac{1}{\mathfrak{R}^2} f_{S_s}(x_s, c_s, t_s) \\
&\quad \mathfrak{R}^2 \int_0^1 \int_{\mathbb{R}^2} K_{1,s}(c_s, \tilde{c}_s) \frac{1}{\mathfrak{I}} k_s(|x_s - \tilde{x}_s|) \frac{1}{\mathfrak{R}^2} f_{I_s}(\tilde{x}_s, \tilde{c}_s, t_s) d\tilde{x}_s d\tilde{c}_s \\
&\quad - \frac{1}{\mathfrak{I}\mathfrak{R}^2} f_{I_s}(x_s, c_s, t_s).
\end{aligned}$$

We drop the index s for easier notation and obtain

$$\begin{aligned}
\partial_t f_S(x, c, t) &= -f_S(x, c, t) \int_0^1 K_1(c, \tilde{c}) \int_{\mathbb{R}^2} k(|x - \tilde{x}|) f_I(\tilde{x}, \tilde{c}, t) d\tilde{x} d\tilde{c}, \\
\partial_t f_I(x, c, t) &= f_S(x, c, t) \int_0^1 K_1(c, \tilde{c}) \int_{\mathbb{R}^2} k(|x - \tilde{x}|) f_I(\tilde{x}, \tilde{c}, t) d\tilde{x} d\tilde{c} - \gamma f_I(x, c, t).
\end{aligned}$$

Rescaling the space variable $x \in \mathbb{R}^2$ like in Subsection 3.1.1 yields

$$\begin{aligned}
\partial_t f_S(x, c, t) &= -f_S(x, c, t) \frac{1}{\varepsilon^2} \int_0^1 K_1(c, \tilde{c}) \int_{\mathbb{R}^2} k\left(\frac{|x - \tilde{x}|}{\varepsilon}\right) f_I(\tilde{x}, \tilde{c}, t) d\tilde{x} d\tilde{c}, \\
\partial_t f_I(x, c, t) &= f_S(x, c, t) \frac{1}{\varepsilon^2} \int_0^1 K_1(c, \tilde{c}) \int_{\mathbb{R}^2} k\left(\frac{|x - \tilde{x}|}{\varepsilon}\right) f_I(\tilde{x}, \tilde{c}, t) d\tilde{x} d\tilde{c} - f_I(x, c, t).
\end{aligned}$$

We can calculate the inner integral in the same way as in Section 4.1. Altogether, the system (5.0.1) – (5.0.2) transforms into

$$\begin{aligned}
\partial_t f_S(x, c, t) &= -f_S(x, c, t) \int_0^1 K_1(c, \tilde{c}) \left(\beta f_I(x, c, t) + \varepsilon^2 D \Delta_x f_I(x, t) \right) d\tilde{c}, \\
\partial_t f_I(x, c, t) &= f_S(x, c, t) \int_0^1 K_1(c, \tilde{c}) \left(\beta f_I(x, c, t) + \varepsilon^2 D \Delta_x f_I(x, t) \right) d\tilde{c} - f_I(x, c, t).
\end{aligned}$$

Remark 5.0.2. For $\varepsilon \rightarrow 0$ the above system is, as analogously in Remark 3.1.3, similar to the SIR model, additionally depending on a spatial variable and the contact intensity with the corresponding kernel K_1 .

Plugging in the Definition (4.1.1), we obtain the system

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$$\begin{aligned}
 -\mathbf{c}f'_S(\xi, c) &= -f_S(\xi, c) \int_0^1 K_1(c, \tilde{c}) \left(\beta f_I(\xi, \tilde{c}) + \varepsilon^2 Df''_I(\xi, \tilde{c}) \right) d\tilde{c}, \\
 -\mathbf{c}f'_I(\xi, c) &= f_S(\xi, c) \int_0^1 K_1(c, \tilde{c}) \left(\beta f_I(\xi, \tilde{c}) + \varepsilon^2 Df''_I(\xi, \tilde{c}) \right) d\tilde{c} - f_I(\xi, c).
 \end{aligned}$$

Unfortunately, we can not proceed as in the previous chapters to obtain existence results of a traveling wave, since the above system is too complicated for an analysis. Although, the SIR model with contact intensity and mobility structure in two dimensions is more realistic than the models presented in Chapters 2, 3 and 4, we can not use it for the mathematical discussion of the existence of a traveling wave. This problem is often noticed in mathematical modeling. Either the model is very realistic, but can hardly be mathematically investigated or it is very simple in comparison to reality, but can easily be analyzed.

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A.1. Python code

The following python codes create the plots of Figures 1.1 and 1.2, for the documentations see [11] and [9].

```
#First we import all the needed packages.
import numpy as np
from scipy.integrate import odeint
import matplotlib.pyplot as plt

#We set intial conditions for the normalized sizes of the
#compartments, define the parameters and generate hunderd
#time steps.
S0=0.99
I0=0.01
R0=0
beta=0.5
gamma=(1./10)
t=np.linspace(0, 100, 100)

#The function, defined in the followig, describes the SIR model.
def deriv(a, t, beta, gamma):
    S, I, R =a
    dSdt=-beta*S*I
    dIdt=beta*S*I-gamma*I
    dRdt=gamma*I
    return dSdt, dIdt, dRdt

a0= S0, I0, R0
S, I, R =odeint(deriv, a0, t, args=(beta, gamma)).T
```


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```
#Finally , we plot the graph with several steps , in order to
#have a nice appreance.
fig , ax =plt.subplots()

#We delete the top and right part of the by default created
#box around the plot , but we keep the bottem and the left part.
#Therefore , we obtain a coordinate system.
ax.spines[ 'top '].set_visible(False)
ax.spines[ 'right '].set_visible(False)
ax.spines[ 'bottom '].set_visible(True)
ax.spines[ 'left '].set_visible(True)

#Additionally , we want the axis to start in zero , define their
#length and plot some black arrows at the end of the axis.
ax.spines[ 'left '].set_position(('data' , 0))
ax.spines[ 'bottom '].set_position(('data' , 0))
ax.spines[ 'left '].set_bounds(0 , 1.05)
ax.spines[ 'bottom '].set_bounds(0 , 105)
ax.plot(1 , 0 , '>k' , transform=ax.get_yaxis_transform() ,
        clip_on=False)
ax.plot(0 , 1 , '^k' , transform=ax.get_xaxis_transform() ,
        clip_on=False)

#The following plots the graphs of the three compartments and
#labels the axis.
plt.plot(t , S , 'b' , alpha=0.5 , label='Susceptible ')
plt.plot(t , I , 'r' , alpha=0.5 , label='Infected ')
plt.plot(t , R , 'g' , alpha=0.5 , label='Recovered ')
plt.xlabel('Time in days')
plt.ylabel('Normalized sizes of the compartments')
plt.legend()
plt.show()



---


import numpy as np
from scipy.integrate import odeint
```

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```
import matplotlib.pyplot as plt
import math

S0=0.99
I0=0.01
R0=0
beta=0.5
gamma=(1./10)
t=np.linspace(0, 100, 100)

def deriv(a, t, beta, gamma):
    S, I, R =a
    dSdt=-beta*S*I
    dIdt=beta*S*I-gamma*I
    dRdt=gamma*I
    return dSdt, dIdt, dRdt

a0= S0, I0, R0
S, I, R =odeint(deriv, a0, t, args=(beta, gamma)).T

#Calculation of the Maximum of I(t).
Imax=-gamma/beta+gamma/beta*math.log(gamma/beta)+S0+I0
      -gamma/beta*math.log(S0)

fig, ax =plt.subplots()
ax.spines['top'].set_visible(False)
ax.spines['right'].set_visible(False)
ax.spines['bottom'].set_visible(True)
ax.spines['left'].set_visible(True)
ax.spines['left'].set_position(('data', 0))
ax.spines['bottom'].set_position(('data', 0))
ax.spines['left'].set_bounds(0, 1.05)
ax.spines['bottom'].set_bounds(0, 1.05)
ax.plot(1, 0, '>k', transform=ax.get_yaxis_transform(),
        clip_on=False)
ax.plot(0, 1, '^k', transform=ax.get_xaxis_transform(),
```

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```
clip_on=False)

#We plot the dashed lines , the labeled graph of S+I and the
#SI-plane with labeled axis.
plt.plot([0, gamma/beta], [Imax, Imax], 'k', alpha=0.5,
         linestyle='--')
plt.plot([gamma/beta, gamma/beta], [0, Imax], 'k', alpha=0.5,
         linestyle='--')
plt.plot([1,0], 'k', alpha=0.5)
plt.text(0.55, 0.5, 'S+I=1', ha='center', va='bottom',
         transform=ax.transData)
plt.plot(S, I, '-', alpha=0.5)
plt.xlabel('S(t)')
plt.ylabel('I(S(t))')
plt.show()
```

A.2. Basic definitions and statements

In the following we state basic analysis definitions and the Banach fixed point Theorem, which can be found in [13, pp. 1-2, pp. 181-182]. We assume throughout the appendix that $\mathbb{K} = \mathbb{R}$ or $\mathbb{K} = \mathbb{C}$.

Definition A.2.1. Let X be a \mathbb{K} -vector space. A map $\|\cdot\| : X \rightarrow [0, \infty)$ is called *norm*, if

- (i) $\|x\| = 0 \implies x = 0$,
- (ii) $\|\lambda x\| = |\lambda| \|x\| \quad \forall \lambda \in \mathbb{K}, x \in X$,
- (iii) $\|x + y\| \leq \|x\| + \|y\| \quad \forall x, y \in X$

holds. Then $(X, \|\cdot\|)$ is called a *normed vector space*.

Definition A.2.2. Let X be a \mathbb{K} -vector space. A map $d(\cdot, \cdot) : X \times X \rightarrow [0, \infty)$ is called *metric*, if

- (i) $d(x, y) \geq 0 \quad \forall x, y \in X$,
- (ii) $d(x, y) = 0 \iff x = y \in X$,

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$$(iii) \quad d(x, y) = d(y, x) \quad \forall x, y \in X,$$

$$(iv) \quad d(x, z) \leq d(x, y) + d(y, z) \quad \forall x, y, z \in X$$

holds. Then (X, d) is called a *metric space*.

Remark A.2.1. We can easily equip the normed vector space $(X, \|\cdot\|)$ with a metric by $d(x, y) = \|x - y\| \quad \forall x, y \in X$.

Definition A.2.3. A sequence $(x_n) \in X$, $n \in \mathbb{N}$, where X is a normed vector space, is called a *Cauchy sequence*, if the following is true:

$$\forall \varepsilon > 0 \exists N \in \mathbb{N} \forall n, m \geq N \text{ such that } \|x_n - x_m\| < \varepsilon.$$

Definition A.2.4. A sequence (x_n) *converges* to $x \in X$, if

$$\forall \varepsilon > 0 \exists N \in \mathbb{N} \forall n \geq N \text{ such that } \|x_n - x\| < \varepsilon$$

holds.

Definition A.2.5. A metric space, where every Cauchy sequence is convergent, is called *complete*. A complete normed vector space is called *Banach space*.

Theorem A.2.1 (Banach fixed point Theorem). *Let (X, d) be a complete metric space and let $F : X \rightarrow X$ be a contraction, i.e., there exists a number $q < 1$ such that*

$$d(F(x), F(y)) \leq qd(x, y) \quad \text{for all } x, y \in X.$$

Then F has exactly one fixed point $F(\xi) = \xi$. Furthermore, if $x_0 \in X$ is arbitrary, then the sequence

$$x_{n+1} = F(x_n), \quad n \geq 0$$

converges to the uniquely determined fixed point ξ and the following holds:

$$d(x_n, \xi) \leq \frac{q^n}{1 - q} d(x_1, x_0).$$

The next definition can be found in [12, p. 27].

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Definition A.2.6. A function f is called *locally Lipschitz continuous*, if there exists a finite constant $L > 0$, called *Lipschitz constant*, such that

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

holds for every compact subset of the domain of f .

Next we recall some definitions and properties of dynamical systems from [10]. We consider the initial value problem (2.2.1).

Definition A.2.7. Let \mathcal{M} be a metric space (the state space or phase space) and let the set of times \mathcal{T} be either \mathbb{R} , $[0, \infty)$, \mathbb{Z} , or \mathbb{N}_0 . A *deterministic dynamical system* is a map $\mathcal{T} \times \mathcal{M} \rightarrow \mathcal{M}$, $(t, u_0) \mapsto S_t(u_0)$, satisfying

- (1) $\forall u_0 \in \mathcal{M}: S_0(u_0) = u_0$,
- (2) $\forall u_0 \in \mathcal{M}, s, t \in \mathcal{T}: S_{s+t}(u_0) = S_s(S_t(u_0))$,
- (3) $\forall t \in \mathcal{T}: u_0 \mapsto S_t(u_0)$ is continuous.

In the cases $\mathcal{T} = [0, \infty)$ and $\mathcal{T} = \mathbb{N}_0$, S_t is called a *forward dynamical system*; for $\mathcal{T} = \mathbb{Z}$ or $\mathcal{T} = \mathbb{N}_0$ it is called a *discrete dynamical system*; and for $\mathcal{T} = \mathbb{R}$ or $\mathcal{T} = [0, \infty)$ it is called a *continuous dynamical system*. For fixed $u_0 \in \mathcal{M}$, the set $\{S_t(u_0): t \in \mathcal{T}\}$ is called the *trajectory* through u_0 . The collection of all trajectories is called the *phase portrait* of the dynamical system.

Definition A.2.8. Let $S_t, t \in \mathcal{T}$, be a dynamical system on (\mathcal{M}, d) . Every $\bar{u} \in \mathcal{M}$ satisfying $S_t(\bar{u}) = \bar{u}$ for all $t \in \mathcal{T}$ is called *stationary point* or *steady state* or *equilibrium*. An equilibrium is called *stable*, if

$$\forall \varepsilon > 0 \exists \delta > 0 : d(u_0, \bar{u}) < \delta \implies d(S_t(u_0), \bar{u}) < \varepsilon \forall t > 0.$$

If \bar{u} is not stable, it is called *unstable*.

A stable equilibrium \bar{u} is called (*locally*) *asymptotically stable*, if

$$\exists \delta > 0 : d(u_0, \bar{u}) < \delta \implies \lim_{t \rightarrow \infty} S_t(u_0) = \bar{u}.$$

An asymptotically stable equilibrium \bar{u} is called *globally asymptotically stable*, if

$$\forall u_0 \in \mathcal{M} : \lim_{t \rightarrow \infty} S_t(u_0) = \bar{u}.$$

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Remark A.2.2. The equilibria of an ordinary differential equation of the form (2.2.1) are the zeros of f , i.e., $f(\bar{u}) = 0$. Steady states of the recursion $u_{k+1} = f(u_k)$ are the fixed points of f , i.e., $\bar{u} = f(\bar{u})$.

Definition A.2.9. Let $n \geq 1$ and let \bar{u} be an equilibrium of (2.2.1). Then \bar{u} is called *hyperbolic*, if $\operatorname{Re}(\lambda) \neq 0$ for all eigenvalues λ of the Jacobian of $f(\bar{u})$.

Remark A.2.3. For hyperbolic equilibria the Jacobian can be block diagonalized, i.e.,

$$\mathcal{J}_f(\bar{u}) = R\Lambda R^{-1}, \text{ with } \Lambda \begin{pmatrix} \Lambda_- & 0 \\ 0 & \Lambda_+ \end{pmatrix} \text{ and } R = (R_-, R_+), \quad (\text{A.2.1})$$

where $\Lambda_- \in \mathbb{R}^{k \times k}$, $0 \leq k \leq n$, has only eigenvalues with negative real parts and $\Lambda_+ \in \mathbb{R}^{(n-k) \times (n-k)}$ has only eigenvalues with positive real parts. The columns of $R_- \in \mathbb{R}^{n \times k}$ are generalized eigenvectors corresponding to the eigenvalues with negative real parts, and the columns of $R_+ \in \mathbb{R}^{n \times (n-k)}$ are generalized eigenvectors corresponding to the eigenvalues with positive real parts.

Theorem A.2.2 (Stable manifold Theorem). *Let $\bar{u} \in \mathbb{R}^n$ be an hyperbolic equilibrium of the dynamical system S_t generated by (2.2.1). Then there is a neighborhood $U \subset \mathbb{R}^n$ of \bar{u} , such that*

$$\mathcal{M}_s[\bar{u}] := \{u_0 \in U : S_t(u_0) \in U, t \geq 0\}$$

is a k -dimensional (referring to the diagonalization (A.2.1)) manifold in \mathbb{R}^n , called the stable manifold of \bar{u} . For all $u_0 \in \mathcal{M}_s[\bar{u}]$,

$$|S_t(u_0) - \bar{u}| \leq ce^{\lambda_- t}, \quad t \geq 0,$$

where $c \geq 0$ and $\lambda_- < 0$ is the constant $\bar{\lambda}$ for the matrix Λ_- from [10, Lemma 2]. The tangent space of $\mathcal{M}_s[\bar{u}]$ at \bar{u} is spanned by the columns of R_- from (A.2.1), i.e., by the eigenvectors corresponding to eigenvalues of $\mathcal{J}_f(\bar{u})$ with negative real parts.

Analogously, the set

$$\mathcal{M}_u[\bar{u}] := \{u_0 \in U : S_t(u_0) \in U, t \leq 0\}$$

is a $(n - k)$ -dimensional manifold in \mathbb{R}^n , called the unstable manifold of \bar{u} . For all $u_0 \in \mathcal{M}_u[\bar{u}]$,

$$|S_t(u_0) - \bar{u}| \leq ce^{\lambda_+ t}, \quad t \leq 0,$$

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where $c \geq 0$ and $-\lambda_+ < 0$ is the constant $\bar{\lambda}$ for the matrix $-\Lambda_+$. The tangent space of $\mathcal{M}_u[\bar{u}]$ at \bar{u} is spanned by the columns of R_+ .

Definition A.2.10. A *limit cycle* of (2.2.1) is a periodic solution $u_\infty(t)$ with the additional property that there exists at least one other solution $u(t)$, $t \geq 0$, and $\tau \in \mathbb{R}$ such that

$$\lim_{t \rightarrow \infty} (u(t) - u_\infty(\tau + t)) = 0.$$

Definition A.2.11. A trajectory $\{S_t(u_0) : t \in \mathbb{R}\}$ of a continuous dynamical system is called *heteroclinic orbit*, if the limits

$$u_\pm = \lim_{t \rightarrow \pm\infty} S_t(u_0)$$

exists and $u_- \neq u_+$. It is called a *homoclinic orbit*, if $u_- = u_+$.

In the following we prove the statement $\ln(X) \leq X - 1$ for $X > 0$, used in Section 3.1.2:

Let $f(X) = \ln(X) - X + 1$. The derivative is given by $f'(X) = \frac{1}{x} - 1$, which is positive for $0 < X < 1$ and negative for $X > 1$. Thus, $f(X)$ has a maximum at $X = 1$, $f(1) = \ln(1) - 1 + 1 = 0$. Consequently, for $X > 0$, we obtain $f(X) \leq 0 \implies \ln(X) - X + 1 \leq 0 \implies \ln(X) \leq X - 1$.

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