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„Activity Based SIR Epidemiology Model with Age Structure“

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Abstract

This work focuses on extending the well-known standard SIR-model by McKendrick and Kermack. This model describes the development of a disease by considering the tree compartments susceptible, infected and recovered, where also the abbreviation SIR comes from. The extension includes activities where the participation depends on the continuous or discrete age. It is shown that the only equilibrium is the disease-free one and a basic reproduction rate giving a threshold for the stability of that equilibrium is derived. Also, we find an implicit formula for the number of infected individuals over the course of the epidemic. Here, we show that a solution exists and is unique under certain additional assumptions. Some weak results for the maximum number of infected individuals are achieved, too. A comparison with the results of the standard model is done. The model is tested, by numerically comparing its predictions to real world data.

Zusammenfassung

Diese Arbeit konzentriert sich auf die Erweiterung des bekannten Standard-SIR-Modell von McKendrick und Kermack, welches die Entwicklung einer Krankheit durch Betrachtung der verschiedenen Gruppen von krankheitsanfälligen, infizierten und genesenen Individuen beschreibt. Die entsprechenden englischen Begriffe sind der Grund für die Abkürzung SIR. Das erweiterte Modell schließt stetiges und diskretes Alter und Aktivitäten ein, bei denen die Teilnahmerate vom Alter abhängt. Es wird gezeigt, dass das einzige Gleichgewicht jenes ohne Infizierte ist und eine Basisreproduktionszahl wird hergeleitet, die einen Schwellenwert für die Stabilität des krankheitsfreien Gleichgewichtes angibt. Weiters wird eine implizite Formel für die Anzahl an Infizierten im Laufe der Epidemie gefunden. Hier zeigen wir, dass eine Lösung existiert und unter gewissen zusätzlichen Bedingungen eindeutig ist. Man erreicht auch einige schwächere Resultate bezüglich der maximalen Anzahl an Infizierten. Die Resultate werden mit jenen des Standard-Modelles verglichen. Das erweiterte Modell wird getestet, indem dessen Vorhersagen numerisch mit realen Daten verglichen werden.

Contents

Notation

The following conventions will be used throughout the thesis:

- When something new is defined, then $:=$ means that the left hand side is defined as the right hand side. Analogously, we will use $=:$.
- The set $\{\} = \emptyset$ is the empty set, i.e., the set without elements.
- The set of natural numbers is denoted by $\mathbb{N} := \{0, 1, 2, ...\}$ and that of the integers by $\mathbb{Z} := \{0, 1, -1, 2, -2, ...\}$.
- The set of real numbers is denoted by $\mathbb{R}$, and the one of complex numbers by $\mathbb{C}$.
- For $a, b \in \mathbb{R}$ with $a \leq b$ let $[a, b] := \{x \in \mathbb{R} \,|\, a \leq x \leq b\}$ be the closed interval from a to b and $[a, \infty[:= \{x \in \mathbb{R} \,|\, x \geq a\}$ the left-closed and right-unbounded interval. Also, let $]a, \infty[:= \{x \in \mathbb{R}\ x > a\}$ be the right-unbounded and left-open, but left-bounded interval.
- For a compact set $\mathcal{A} \subseteq \mathbb{R}$ let $\mathcal{C}(\mathcal{A}) := \{f\colon\ \mathcal{A} \to \mathbb{R} \,|\, f \text{ continuous }\}$ be the set of continuous functions from $\mathcal{A}$ to $\mathbb{R}$. Normally, we will have $\mathcal{A} = [a, b]$ for some $a, b \in \mathbb{R}$, $a \leq b$.
- For a Lebesque set $\mathcal{A}$ let $L^2(\mathcal{A}) := \{f\colon\ \mathcal{A} \to \mathbb{R} \,|\, \int_{\mathcal{A}} |f(a)|^2 \,\mathrm{d}a < \infty\}$ be the set of square-integrable functions from $\mathcal{A} \to \mathbb{R}$.
- For an arbitrary set $\mathcal{A}$ over a topological space, denote by $\mathcal{A}^\circ$ the interior and by $\bar{\mathcal{A}}$ the closure of the set.
- For an ordered group $(\mathcal{A}, +)$ let $-\mathcal{A} := \{-x \,|\, x \in \mathcal{A}\}$.
- A subset of a real Banach space $\mathcal{A}$ is convex if for every $x, y \in \mathcal{A}$ and every $\lambda \in [0, 1]$ we have
$$\lambda x + (1 - \lambda)y \in \mathcal{A}\,.$$
- A function $f\colon\ \mathcal{V} \to \mathbb{R}$ over a real Banach space $\mathcal{V}$ is called concave, if for all $x, y \in \mathcal{V}$ and all $\lambda \in [0, 1]$ the inequality
$$f(\lambda x + (1 - \lambda)y) \geq \lambda f(x) + (1 - \lambda)f(y)$$
holds. A sufficient criterion for a twice differentiable function f to be concave is that the second derivative f'' is non-positive on $\mathcal{V}^\circ$.

Notation

- The function $\mathrm{id}\colon \mathcal{V} \to \mathcal{V}\colon \quad x \mapsto x$ is the identity function that maps elements to themselves on an arbitrary space $\mathcal{V}$.
- The natural logarithm is denoted by $\log(\cdot)$ and the exponential function by $\exp(\cdot)$.
- The indicator function of some set $\mathcal{A} \subseteq \mathcal{V}$ is defined by

$$\mathbb{1}_{\mathcal{A}}(x) \coloneqq \begin{cases} 1 & x \in \mathcal{A} \\ 0 & x \notin \mathcal{A} \end{cases}$$

  for $x \in \mathcal{V}$.
- A function $f\colon \mathcal{V} \times \mathcal{V} \to \mathcal{W}$ is called symmetric, if for all $x, y \in \mathcal{V}$ one has $f(x, y) = f(y, x)$.
- The Manhattan norm of a vector $x \in \mathbb{R}^n$ is defined by

$$\|x\|_1 \coloneqq \sum_{i=1}^{n} |x_i| \,.$$

  The Euclidean norm is given by

$$\|x\|_2^2 \coloneqq \sum_{i=1}^{n} x_i^2$$

  and the uniform norm by

$$\|x\|_\infty \coloneqq \max_{i \in \{1,2,\ldots,n\}} |x_i| \,.$$

- The uniform norm can also be defined for a function $f \in \mathcal{C}([a, b])$ by

$$\|f\|_\infty \coloneqq \max_{x \in [a,b]} |f(x)| \,.$$

  The notation is exactly the same as for a vector.

1. Introduction

The disease COVID-19 caused by the virus SARS-CoV-2, a strain of coronavirus, heavily influenced our lives in the last years. Since March 2020, the disease raged in Europe, sometimes more, sometimes less. In the beginning, governments closed schools and stopped industries, in order to stop the deadly disease to spread. However, many people died in spite of countermeasures. Since then, the virus developed and mutated. New variants spread faster, although with decreased mortality. In summer 2022, there nearly were no restrictions any more, despite the fact of a high incidence. Nevertheless, as in the last years, the restrictions may come back in winter, when the immune system of us humans is weaker (see [9]).
Since this is an excellent application of Biomathematics, the present master thesis has been written in that area of specialisation at the University of Vienna. The propagation of the virus was modeled as an extension of the well-known SIR epidemiological model, first described by A. G. McKendrick and W. O. Kermack in 1927 in [10]. This model separates the individuals in compartments, the susceptible ones, the infected ones and the recovered ones, hence the abbreviation SIR.
In the extension, individuals can participate at a number of activities where they can be infected. The participation at such events will depend on the age of an individual. Furthermore, it is assumed that the age of an individual also affects its recovery rate.
In the following, first the standard SIR epidemiological model will be introduced and important properties will be recalled. In Chapter 2, the extension is explained. In the following chapter, Chapter 3, some properties of the new model are derived. Chapter 4 gives some numerical simulations of the discretized model. Also, the discretization is done in that chapter. The last chapter, Chapter 5, summarizes the important results, compares them with the standard SIR model and gives a brief interpretation against the background of Corona virus. Finally, Appendix A gives some basic definitions and results of linear algebra, dynamical systems and functional analysis needed in the course of this thesis.
If one is interested in the Python implementation with which the diagrams in Section 1.1 and Chapter 4 have been created, please write a mail to schamela@gmail.com.

1.1. Recall: The SIR Model

The standard SIR epidemiological model without demography is a deterministic model. With the help of a system of ordinary differential equations we are able to describe the propagation of a disease by looking at the state of individuals. It assumes that there are N individuals. At every point in time, an individual is in exactly one state, also called

department:

- susceptible, meaning that the individual can get the disease by an infective one
- infected, i.e., the individual got the disease and is infectious
- recovered/removed, an individual that had the disease but is not infective anymore, hence, the individual does not drive the force of infection anymore. It can not regain the disease and will hence not reenter the susceptible department. In the following, this compartment is refered to as recovered.

We denote by $S(t) \geq 0$ the number of susceptible individuals at time $t \in [0, \infty[$, by $I(t) \geq 0$ the number of infected and by $R(t) \geq 0$ the number of recovered individuals. We assume no demography, meaning that no individual can enter or leave this system; there is no migration, birth or death (death due to epidemics is modeled by moving the corresponding individual to the recovered department). This is reasonable due to the quick spread of diseases as the corona virus. In that "short" time of disease spreading, the population number does not really change. Put into an equation, me may express the described relationship by

$$S(t) + I(t) + R(t) = N\,,$$

for all $t \in [0, \infty[$. Furthermore, we suppose that every individual can come into contact with every other one, also called homogeneous mixing assumption. Now, a susceptible individual having contact with an infected one will get infected itself. TThe amount of contact within the population we summarize in a contact rate $\beta > 0$. As there is a fraction of $\frac{I}{N}$ infected individuals and there are S susceptible individuals, the number of infected individuals will increase by $\beta S \frac{I}{N}$ in one unit of time and the number of susceptible individuals will decrease by the same amount. Also, infected individuals will recover at some rate $\gamma > 0$, meaning that the number of infected individuals decreases by γI, while this quantity is the increment for the number of recovered individuals. We get the following system of ordinary differential equations:

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\beta S \frac{I}{N}\,, \tag{1.1}$$

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta S \frac{I}{N} - \gamma I \quad \text{and} \tag{1.2}$$

$$\frac{\mathrm{d}R}{\mathrm{d}t} = \gamma I\,. \tag{1.3}$$

Furthermore, we assume that the initial conditions

$$\begin{aligned} S(0) &= S_0 > 0\,, \\ I(0) &= I_0 = N - S_0 > 0 \quad \text{and} \\ R(0) &= R_0 \coloneqq 0 \end{aligned}$$

are given.
Figure 1.1 is a graphical representation of this system with a small violation of notation (states are identified with the number of individuals in them).

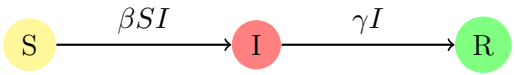

Figure 1.1.: SIR-model with corresponding rates of changes.

1.1.1. Properties of the Standard SIR Model

In the following, let us recall some important properties of the SIR model that we will use later.
First, let us modify the used differential equations to a normalized version: Often, it is easier to work with normalized sizes of the compartments, i.e.,

$$\begin{aligned} s(t) &:= \frac{S(t)}{N}\,, \\ i(t) &:= \frac{I(t)}{N} \quad \text{and} \\ r(t) &:= \frac{R(t)}{N}\,. \end{aligned}$$

Then these quantities refer to the probability of being in a certain department and

$$s(t) + i(t) + r(t) = 1\,.$$

The system of ordinary differential equations (1.1)-(1.3) becomes

$$\frac{\mathrm{d}s}{\mathrm{d}t} = -\beta si\,, \tag{1.4}$$

$$\frac{\mathrm{d}i}{\mathrm{d}t} = \beta si - \gamma i \quad \text{and} \tag{1.5}$$

$$\frac{\mathrm{d}r}{\mathrm{d}t} = \gamma i\,. \tag{1.6}$$

with initial conditions

$$\begin{aligned} s(0) &= s_0 > 0\,, \\ i(0) &= i_0 = 1 - s_0 > 0 \quad \text{and} \\ r(0) &= r_0 = 0\,. \end{aligned}$$

The following calculations are done with such normalized quantities.
In Figure 1.2 one can see a numerical simulation of this model.

Existence and Uniqueness of Solutions

With the theorem of Picard-Lindelöf, one can show that there exists a unique solution (s, i, r) for System (1.4)-(1.6).

Average Infective Period

If there are no susceptible individuals ($s_0 = 0$), then by Equation (1.4) there will be no susceptible individuals for all times $t \geq 0$. Equation (1.5) becomes

$$\frac{\mathrm{d}i}{\mathrm{d}t} = -\gamma i$$

with initial condition $i(0) = i_0$. This can be solved with the method of separation of variables in order to give

$$i(t) = i_0 \cdot \exp(-\gamma t)\,.$$

Hence, the fraction of individuals still infected after t units of time is $\exp(-\gamma t)$. Put differently, this quantity $\exp(-\gamma t)$ gives the probability of still being infected. The probability of not being infected anymore is $P(t) \coloneqq 1 - \exp(-\gamma t)$. This is the probability distribution of an exponentially distributed random variable with parameter γ which has the density

$$p(t) \coloneqq \frac{\mathrm{d}P}{\mathrm{d}t}(t) = \gamma \exp(-\gamma t)\,.$$

This means that the average time spent in the infected compartment is $\frac{1}{\gamma}$.

Equilibria

An equilibrium point is a point $(s, i, r) \in \mathcal{C}([0, \infty[)^3$ that is constant over time. In other words, the derivatives in the system of ordinary differential equations (1.4)-(1.6) are all zero.
By Equation (1.6) we need $i(t) = 0$. But this implies $\frac{\mathrm{d}s}{\mathrm{d}t} = \frac{\mathrm{d}i}{\mathrm{d}t} = 0$. Hence, all equilibria are given by $i(t) = 0$. This sort of equilibrium is also called the disease-free equilibrium.
One can show that all solutions of System (1.4)-(1.6) remain non-negative and bounded from above by 1. As $\frac{\mathrm{d}s}{\mathrm{d}t} + \frac{\mathrm{d}i}{\mathrm{d}t} = -\gamma i \leq 0$ for $i \geq 0$, the function $s + i$ is monotonically decreasing. Also, $s+i$ is bounded from below by 0. Hence, $s+i$ admits a limit as $t \to \infty$. The same holds for s, implying that also i has a limit which has to be non-negative. Hence, $\lim_{t\to\infty}(\frac{\mathrm{d}s}{\mathrm{d}t} + \frac{\mathrm{d}i}{\mathrm{d}t})(t)$ is non-positive. But if it were negative, then we would have $s + i < 0$ at some time, which cannot be. Hence, it satisfies $\lim_{t\to\infty}(\frac{\mathrm{d}s}{\mathrm{d}t} + \frac{\mathrm{d}i}{\mathrm{d}t})(t) = 0$. This shows $\lim_{t\to\infty} i(t) = \frac{1}{\gamma} \lim_{t\to\infty} \left(\frac{\mathrm{d}s}{\mathrm{d}t} + \frac{\mathrm{d}i}{\mathrm{d}t}\right)(t) = 0$. This means that the disease-free equilibrium will be achieved sooner or later and every epidemic in this model will die out. We say that the epidemic stops once $i = 0$.
One can see in Figure 1.2 that the fraction of infected individuals approaches zero.

Epidemic Threshold

We are interested in which case the number of infected individuals increases at the beginning of the epidemic. This means the question wether $\frac{\mathrm{d}i}{\mathrm{d}t}(t) > 0$ for $t = 0$. Here, beginning refers to the fact that there is only one infected individual in an otherwise

totally susceptible population.
First, Equation (1.5) can be rewritten as

$$\frac{\mathrm{d}i}{\mathrm{d}t} = i\left(\beta s - \gamma\right) = \gamma i\left(\frac{\beta s}{\gamma} - 1\right).$$

As nearly the whole population is susceptible, we can assume $s(0) \approx 1$ as $N \to \infty$. Hence, we get

$$\frac{\mathrm{d}i}{\mathrm{d}t}(0) \approx \gamma i\left(\frac{\beta}{\gamma} - 1\right).$$

As $i(0) > 0$ (the disease affects a small fraction of the population) and $\gamma > 0$ by assumption, we have $\frac{\mathrm{d}i}{\mathrm{d}t}(0) > 0$ if and only if for

$$\mathcal{R}_0 \coloneqq \frac{\beta}{\gamma} \tag{1.7}$$

we have $\mathcal{R}_0 > 1$, and $\frac{\mathrm{d}i}{\mathrm{d}t}(0) < 0$ if and only if $\mathcal{R}_0 < 1$. The quantity $\mathcal{R}_0$, defined as in (1.7), is called the basic reproduction number or basic reproduction rate and often equals the expected number of individuals one infected individual will infect during the course of its disease in an otherwise totally susceptible population. This holds also in this case, as an infected individual will infect a susceptible one at rate β, if there are only susceptible individuals to have contact with. Also, this infected individual will stay infective for $\frac{1}{\gamma}$ units of time. Hence, in total it will infect $\frac{\beta}{\gamma}$ susceptible individuals. The quantity $\mathcal{R}_0$ is an important one in epidemics as it gives a threshold for the stability of the disease-free equilibrium. In other words, it is a threshold if the epidemic will break out even if only a small fraction of individuals is infected.
This can also be seen in Figure 1.3 where shortly after a basic reproduction rate of 1 the maximum number of infected individuals starts to explode.

Maximum Number of Infected Individuals

We are interested in the maximum number of infected individuals at one time, that is, in

$$i_{\max} \coloneqq \max_{t\in[0,\infty[} i(t).$$

Considering i as an implicit function of s, one gets by the chain rule for $i \neq 0$ and using Equations (1.4) and (1.5) that

$$\frac{\mathrm{d}i}{\mathrm{d}s} = \frac{\frac{\mathrm{d}i}{\mathrm{d}t}}{\frac{\mathrm{d}s}{\mathrm{d}t}} = -1 + \frac{\gamma}{\beta s}. \tag{1.8}$$

Since i is assumed to be differentiable, we need $\frac{\mathrm{d}i}{\mathrm{d}t} = 0$ in order to have a maximum. Hence, by the chain rule, we need $\frac{\mathrm{d}i}{\mathrm{d}s} = 0$. By Equation (1.8) this is obtained at

$$-1 + \frac{\gamma}{\beta \hat{s}} = 0,$$

i.e., for

$$\hat{s} = \frac{\gamma}{\beta} = \frac{1}{\mathcal{R}_0}\,.$$

Solving the ordinary differential equation (1.8) by simple integration gives

$$i(s) = 1 - s + \frac{\gamma}{\beta}\log\left(\frac{s}{s_0}\right)$$

with initial condition $i(s_0) = i_0 = 1 - s_0$. We get

$$i_{\max} = i(\hat{s}) = 1 - \frac{1}{\mathcal{R}_0} + \frac{1}{\mathcal{R}_0}\log\left(\frac{1}{\mathcal{R}_0 s_0}\right) = 1 - \frac{1}{\mathcal{R}_0}\left(1 + \log\left(\mathcal{R}_0 s_0\right)\right)\,. \tag{1.9}$$

For $s_0 \approx 1$ we get

$$i_{\max} \approx 1 - \frac{1}{\mathcal{R}_0}\left(1 + \log\left(\mathcal{R}_0\right)\right)\,. \tag{1.10}$$

In Figure 1.2 one can see that the maximum fraction of infected individuals is quite high, as also the basic reproduction rate is much more higher than 1. However, doing the calculation of the maximum number of infected individuals with the Formula (1.9) above, one gets approximately three equal digits.

Number of Uninfected Individuals after Disease

We want to know more about $s_\infty \coloneqq \lim_{t\to\infty} s(t)$, the limiting fraction of susceptible individuals after the course of the epidemic. This limit exists as both s and $s + i$ are decreasing functions, bounded from below by 0.
Similarly as in the calculation for $i_{\max}$, we consider s as a function of r. Now, for $i \neq 0$

$$\frac{\mathrm{d}s}{\mathrm{d}r} = \frac{\frac{\mathrm{d}s}{\mathrm{d}t}}{\frac{\mathrm{d}r}{\mathrm{d}t}} = -\frac{\beta}{\gamma}\cdot s = -\mathcal{R}_0 s\,.$$

Solving with the method of separation of variables yields

$$s(r) = s_0 \cdot \exp\left(-\mathcal{R}_0 r\right)$$

due to the initial condition $s(r_0) = s(0) = s_0$. As $s_\infty = 1 - r_\infty$, where $r_\infty \coloneqq \lim_{t\to\infty} r(t)$, one can obtain s_∞ numerically by taking the limit $t \to \infty$ from the transcendent equation

$$s_\infty = s_0 \exp\left(-\mathcal{R}_0(1 - s_\infty)\right)\,. \tag{1.11}$$

This quantity satisfies $s_\infty > 0$.
One can also see this the other way round: The quantity $r_\infty = 1 - s_\infty$ denotes the fraction of individuals infected in the whole course of the epidemic. It is given by

$$r_\infty = 1 - s_0 \exp\left(-\mathcal{R}_0 \cdot r_\infty\right) \tag{1.12}$$

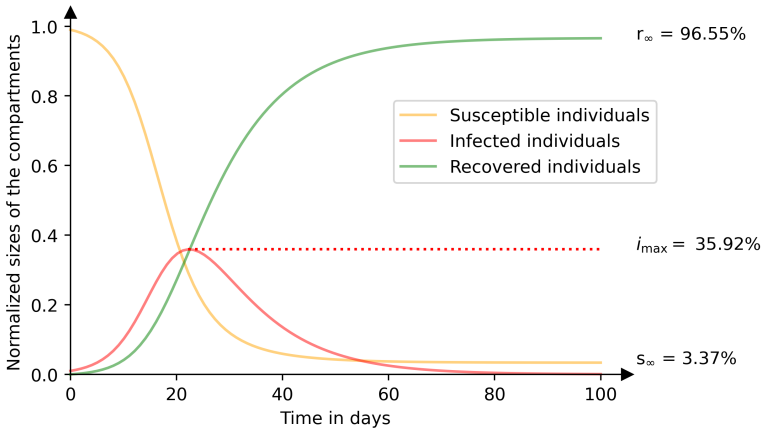

Figure 1.2.: Development over time of susceptible, infected and recovered individuals by solving the system of ordinary differential equations (1.4)-(1.6); used parameters: $s_0 = 0.99$, $i_0 = 0.01$, $r_0 = 0$, $\beta = 0.35$ and $\gamma = 0.1$, hence, $\mathcal{R}_0 = 3.5$. The outbreak is clearly visible.

and satisfies $r_\infty < 1$. Since the right-hand side is clearly smaller than 1, not the whole population will have been infected at the end of an epidemic.
For $s_0 \approx 1$, we have

$$s_\infty \approx \exp\left(\mathcal{R}_0(s_\infty - 1)\right) \quad \text{and} \tag{1.13}$$

$$r_\infty \approx 1 - \exp\left(-\mathcal{R}_0 \cdot r_\infty\right) . \tag{1.14}$$

Why does such a quantity $r_\infty \in [0, 1[$ (and, hence, $s_\infty = 1 - r_\infty$) exist and is it unique? Let $f(x) := 1 - s_0 \exp(-\mathcal{R}_0 \cdot x)$ by Equation (1.12) and $g(x) := f(x) - x$. Then $g(0) = f(0) = 1 - s_0 > 0$ and $g(1) = -s_0 \exp(-\mathcal{R}_0) < 0$. By the intermediate value theorem (see [5], Conclusion 5.2.12), there exists a point $\tilde{x} \in]0, 1[$ with $g(\tilde{x}) = 0$. In particular, $f(\tilde{x}) = \tilde{x}$ and a fixed point exists.
Now, we have $f''(x) = -s_0 \mathcal{R}_0^2 \exp(-\mathcal{R}_0 x) < 0$ which means that f is strictly concave. Assume that $\tilde{x} \neq \tilde{y}$ are two different fixed points of f. Without loss of generality, let $\tilde{x} < \tilde{y}$. Then there exists a $\lambda \in]0, 1[$ with $\tilde{x} = \lambda \cdot 0 + (1 - \lambda)\tilde{y}$, as $\tilde{x}$ lies between 0 and $\tilde{y}$. By concavity, we have

$$\tilde{x} = f(\tilde{x}) = f(\lambda \cdot 0 + (1 - \lambda)\tilde{y}) > \lambda f(0) + (1 - \lambda) f(\tilde{y}) > \lambda \cdot 0 + (1 - \lambda)\tilde{y} = \tilde{x} ,$$

which cannot be. Hence, we need $\tilde{x} = \tilde{y}$ and the fixed point is unique.
In Figure 1.2 it is clearly visible that not every individual will catch the disease even if there are only few escaping it due to the high basic reproduction rate.

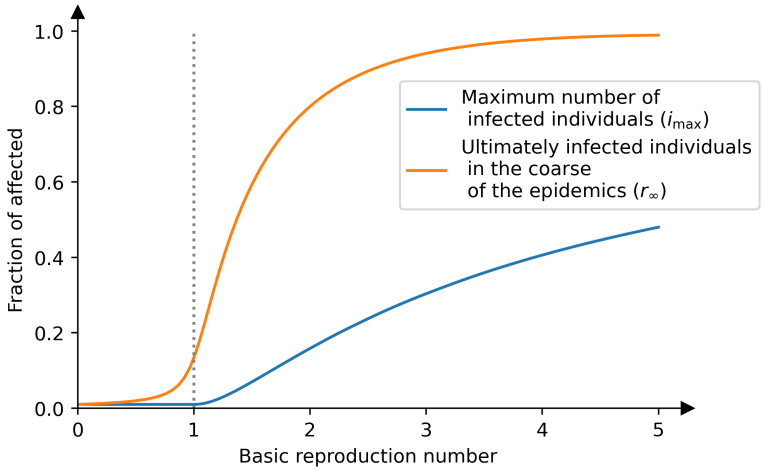

Figure 1.3.: Maximum number of infected individuals $i_{\max}$ and ultimately infected individuals r_∞ in dependency of the basic reproduction rate. As before, $s_0 = 0.99$, $i_0 = 0.01$ and $r_0 = 0$. The infection rate is $\beta = 0.35$ and the infection rate γ is chosen accordingly in order to give the stated basic reproduction rate $\mathcal{R}_0$.

2. Extended Model

In the following, an extension of the standard SIR model with activities and age structure is developed.

As in the standard SIR model, we start with a population of N individuals. That number stays constant. In other words, there is no birth, no death and no migration. An exception form individuals dead due to the epidemic where it will be explained later why. Each such individual has an age $a \in [0, \infty[$ and a state $\boldsymbol{\mathcal{C}} \in \{\boldsymbol{\mathcal{S}}, \boldsymbol{\mathcal{I}}, \boldsymbol{\mathcal{R}}\}$ (susceptible, infected, recovered, respectively). Over time, the age does not change, while the state does under certain rules. This is reasonable as we assume the disease to spread much more quickly than the change in age would happen. Now, one can divide the number of susceptible, infected or recovered individuals by the number of individuals in order to get the probability of being susceptible , infected or recovered . Violating the notation from before, we will reuse the functions S, I, R, s, i and r, but still in a similar sense.
In the following, let $t \in [0, \infty[$ be a point in time. Then let $X(t)$ be a random variable describing a random individual. This individual has a constant age Y and a state $Z(t)$. Since these two quantities are also random variables, $X(t)$ can be written as

$$X(t) = (Y, Z(t)) \,.$$

As stated before, let

$$\begin{aligned} S(t) &:= \mathbb{P}(Z(t) = \boldsymbol{\mathcal{S}}) \,, \\ I(t) &:= \mathbb{P}(Z(t) = \boldsymbol{\mathcal{I}}) \quad \text{and} \\ R(t) &:= \mathbb{P}(Z(t) = \boldsymbol{\mathcal{R}}) \,. \end{aligned}$$

Then

$$S(t) + I(t) + R(t) = 1 \,,$$

as every individual has to be in exactly one state.
In the following, we will consider the limit $N \to \infty$, if not stated otherwise. We assume that in this limit, there exists a density p describing the age of a random individual, that is,

$$\int_{a_1}^{a_2} p(a) \, \mathrm{d}a = \mathbb{P}(Y \in [a_1, a_2]) \,, \tag{2.1}$$

where $a_1, a_2 \in [0, \infty[$ are some given ages. For the rest of this thesis, p is assumed to be continuous and of compact support, i.e., $\overline{\{a \in [0, \infty[\,|\, p(a) \neq 0\}}$ is compact. This is no serious restriction, as p vanishes at infinity anyway in order for the integral to exist. Hence, there exists an $A \in]0, \infty[$ such that $\int_0^A p(a) \, \mathrm{d}a = 1$. Let us choose such an A.

Without loss of generality, one can now only look at $a \in [0, A]$.
Furthermore, we assume that there exist densities s, i and r which satisfy

$$\begin{aligned}\int_0^\infty s(a,t)\,\mathrm{d}a =& S(t)\,,\\ \int_0^\infty i(a,t)\,\mathrm{d}a =& I(t) \quad \text{and}\\ \int_0^\infty r(a,t)\,\mathrm{d}a =& R(t)\,.\end{aligned}$$

As s, i and r are densities, they satisfy $s(a,t) \geq 0$, $i(a,t) \geq 0$ and $r(a,t) \geq 0$ for all $a \in [0, A]$ and $t \in [0, \infty[$.
Furthermore, reasonable assumptions are that s, i and r are continuous functions as these quantities do not change instantaneously in real life.
Next, we want to show that the densities s, i and r add up to the density p. The conditional probability

$$\mathbb{P}(Y \in [a_1, a_2] \,|\, Z(t) = \boldsymbol{\mathcal{S}})$$

equals, by the definition of the conditional probability to

$$\mathbb{P}(Y \in [a_1, a_2] \,|\, Z(t) = \boldsymbol{\mathcal{S}}) = \frac{\mathbb{P}(Y \in [a_1, a_2])}{\mathbb{P}(Z(t) = \boldsymbol{\mathcal{S}})} = \int_{a_1}^{a_2} s(a,t)\,\mathrm{d}a \cdot \frac{1}{S(t)}\,,$$

and the analogue for $\mathbb{P}(Y \in [a_1, a_2] \,|\, Z(t) = \boldsymbol{\mathcal{I}})$ and $\mathbb{P}(Y \in [a_1, a_2] \,|\, Z(t) = \boldsymbol{\mathcal{R}})$. By the law of total probability, this implies

$$\begin{aligned}\mathbb{P}(Y \in [a_1, a_2]) =& \mathbb{P}(Y \in [a_1, a_2] \,|\, Z(t) = \boldsymbol{\mathcal{S}}) \cdot \mathbb{P}(Z(t) = \boldsymbol{\mathcal{S}})\\ &+ \mathbb{P}(Y \in [a_1, a_2] \,|\, Z(t) = \boldsymbol{\mathcal{I}}) \cdot \mathbb{P}(Z(t) = \boldsymbol{\mathcal{I}})\\ &+ \mathbb{P}(Y \in [a_1, a_2] \,|\, Z(t) = \boldsymbol{\mathcal{R}}) \cdot \mathbb{P}(Z(t) = \boldsymbol{\mathcal{R}})\\ =& \int_{a_1}^{a_2} s(a,t)\,\mathrm{d}a \cdot \frac{1}{S(t)} \cdot S(t) +\\ &+ \int_{a_1}^{a_2} i(a,t)\,\mathrm{d}a \cdot \frac{1}{I(t)} \cdot I(t)\\ &+ \int_{a_1}^{a_2} r(a,t)\,\mathrm{d}a \cdot \frac{1}{R(t)} \cdot R(t)\\ =& \int_{a_1}^{a_2} s(a,t)\,\mathrm{d}a + \int_{a_1}^{a_2} i(a,t)\,\mathrm{d}a + \int_{a_1}^{a_2} r(a,t)\,\mathrm{d}a\\ =& \int_{a_1}^{a_2} (s(a,t) + i(a,t) + r(a,t))\,\mathrm{d}a\,.\end{aligned}$$

Since $a_1, a_2 \in [0, \infty[$ are arbitrary and s, i, r and p are assumed to be continuous, we get by Equation (2.1) that

$$p(a) = s(a,t) + i(a,t) + r(a,t)\,,$$

for arbitrary $t \in [0, \infty[$. In particular, we have $p(a) = s(a,0) + i(a,0) + r(a,0)$, which is already clear by the models construction. Also, as $\int_A^\infty p(a)\,\mathrm{d}a = 0$, we have

$$s(a,t) = i(a,t) = r(a,t) = 0\,,$$

for all $a > A$ and all $t \in [0, \infty[$. This implies that the integrals in the definition of s, i and r can be cut at A.

Now, we want to search for a density of $X(t)$, where $t \in [0, \infty[$. Let

$$\Omega(t) := \{(a, \boldsymbol{\mathcal{C}}) \,|\, a \in [0, A], \boldsymbol{\mathcal{C}}(t) \in \{\boldsymbol{\mathcal{S}}, \boldsymbol{\mathcal{I}}, \boldsymbol{\mathcal{R}}\}\}$$

be the set of all possible combinations of age and state of an individual at one fixed time instance $t \in [0, \infty[$. For a set $\mathcal{A}(t) \subseteq \Omega(t)$ of individuals, define the Dirac-measures

$$\delta^t_{\boldsymbol{\mathcal{S}}} := \begin{cases} 1 & \boldsymbol{\mathcal{S}}(t) \in p_2(\mathcal{A}) \\ 0 & \boldsymbol{\mathcal{S}}(t) \notin p_2(\mathcal{A}) \end{cases},$$
$$\delta^t_{\boldsymbol{\mathcal{I}}} := \begin{cases} 1 & \boldsymbol{\mathcal{I}}(t) \in p_2(\mathcal{A}) \\ 0 & \boldsymbol{\mathcal{I}}(t) \notin p_2(\mathcal{A}) \end{cases} \quad \text{and}$$
$$\delta^t_{\boldsymbol{\mathcal{R}}} := \begin{cases} 1 & \boldsymbol{\mathcal{R}}(t) \in p_2(\mathcal{A}) \\ 0 & \boldsymbol{\mathcal{R}}(t) \notin p_2(\mathcal{A}) \end{cases}.$$

Here, $p_2(x) = x_2$ for some element $x = (x_1, x_2)$ denotes the projection onto the second entry and $p_2(\mathcal{B})$ denotes the set $\{p_2(x) \,|\, x \in \mathcal{B}\}$. Also, define the measure

$$\delta^t := \delta^t_{\boldsymbol{\mathcal{S}}} + \delta^t_{\boldsymbol{\mathcal{I}}} + \delta^t_{\boldsymbol{\mathcal{R}}}\,.$$

Then

$$f(a, \boldsymbol{\mathcal{C}}(t)) := \begin{cases} s(a,t) & \boldsymbol{\mathcal{C}}(t) = \boldsymbol{\mathcal{S}} \\ i(a,t) & \boldsymbol{\mathcal{C}}(t) = \boldsymbol{\mathcal{I}} \\ r(a,t) & \boldsymbol{\mathcal{C}}(t) = \boldsymbol{\mathcal{R}} \end{cases}$$

is a density for $X(t) = (Y, Z(t))$ with measure δ^t: For some $\mathcal{A}(t) \subseteq \Omega(t)$, we have

$$\begin{aligned}
\int_{\mathcal{A}(t)} f(a, \boldsymbol{\mathcal{C}}(t))\,\mathrm{d}\delta =& \int_{\mathcal{A}(t)} f(a, \boldsymbol{\mathcal{C}}(t))\,\mathrm{d}\delta_{\boldsymbol{\mathcal{S}}}(a, \boldsymbol{\mathcal{C}}(t)) + \\
&+ \int_{\mathcal{A}(t)} f(a, \boldsymbol{\mathcal{C}}(t))\,\mathrm{d}\delta_{\boldsymbol{\mathcal{I}}}(a, \boldsymbol{\mathcal{C}}(t)) \\
&+ \int_{\mathcal{A}(t)} f(a, \boldsymbol{\mathcal{C}}(t))\,\mathrm{d}\delta_{\boldsymbol{\mathcal{R}}}(a, \boldsymbol{\mathcal{C}}(t)) \\
=& f(a, \boldsymbol{\mathcal{S}}) \mathbb{1}_{\{\boldsymbol{\mathcal{S}} \in p_2(\mathcal{A}(t))\}} + f(a, \boldsymbol{\mathcal{I}}) \mathbb{1}_{\{\boldsymbol{\mathcal{I}} \in p_2(\mathcal{A}(t))\}} + f(a, \boldsymbol{\mathcal{R}}) \mathbb{1}_{\{\boldsymbol{\mathcal{R}} \in p_2(\mathcal{A}(t))\}} \\
=& s(a,t) \mathbb{1}_{\{\boldsymbol{\mathcal{S}} \in p_2(\mathcal{A}(t))\}} + i(a,t) \mathbb{1}_{\{\boldsymbol{\mathcal{I}} \in p_2(\mathcal{A}(t))\}} + r(a,t) \mathbb{1}_{\{\boldsymbol{\mathcal{R}} \in p_2(\mathcal{A}(t))\}} \\
=& \mathbb{P}(\mathcal{A}(t))\,.
\end{aligned}$$

2.1. Expected Age

As p, s, i, r are densities, we can calculate the expected age in the whole population, among susceptible, infected and recovered individuals. First, the expected age in the whole population equals to

$$\bar{a} \coloneqq \mathbb{E}[Y] = \int_0^A a \cdot p(a) \, \mathrm{d}a \, .$$

Now, the expected age of the susceptible individuals at some fixed time $t \in [0, \infty[$ is

$$\begin{aligned}
\bar{a}_{\boldsymbol{\mathcal{S}}}(t) \coloneqq & \mathbb{E}[Y \mid Z(t) = \boldsymbol{\mathcal{S}}] = \frac{1}{\mathbb{P}(Z(t) = \boldsymbol{\mathcal{S}})} \cdot \mathbb{E}[\mathbb{1}_{\{Z(t)=\boldsymbol{\mathcal{S}}\}} \cdot X] \\
= & \frac{1}{S(t)} \cdot \int_{\Omega(t)} a \cdot \mathbb{1}_{\{p_2(a,\boldsymbol{\mathcal{C}}(t))=\boldsymbol{\mathcal{S}}\}} f(a, \boldsymbol{\mathcal{C}}(t)) \, \mathrm{d}\delta(a, \boldsymbol{\mathcal{C}}(t)) \\
= & \frac{1}{S(t)} \cdot \int_{\Omega(t)} a \cdot \mathbb{1}_{\{\boldsymbol{\mathcal{C}}(t)=\boldsymbol{\mathcal{S}}\}} f(a, \boldsymbol{\mathcal{C}}(t)) \, \mathrm{d}\delta(a, \boldsymbol{\mathcal{C}}(t)) \\
= & \frac{1}{S(t)} \int_0^A a \cdot s(a,t) \, \mathrm{d}a \, .
\end{aligned}$$

Analogously, we get

$$\begin{aligned}
\bar{a}_{\boldsymbol{\mathcal{I}}}(t) \coloneqq & \mathbb{E}[Y \mid Z(t) = \boldsymbol{\mathcal{I}}] = \frac{1}{I(t)} \int_0^A a \cdot i(a,t) \, \mathrm{d}a \quad \text{and} \\
\bar{a}_{\boldsymbol{\mathcal{R}}}(t) \coloneqq & \mathbb{E}[Y \mid Z(t) = \boldsymbol{\mathcal{R}}] = \frac{1}{R(t)} \int_0^A a \cdot r(a,t) \, \mathrm{d}a \, .
\end{aligned}$$

Hence, the expected age in the whole population can also be rewritten as

$$\begin{aligned}
\bar{a} = & \mathbb{E}[Y] = \int_0^A a \cdot p(a) \, \mathrm{d}a \\
= & \int_0^A a \cdot (s(a,t) + i(a,t) + r(a,t)) \, \mathrm{d}a \\
= & \int_0^A a \cdot s(a,t) \, \mathrm{d}a + \int_0^A a \cdot i(a,t) \, \mathrm{d}a + \int_0^A a \cdot r(a,t) \, \mathrm{d}a \\
= & S(t)\mathbb{E}[Y \mid Z(t) = \boldsymbol{\mathcal{S}}] + I(t)\mathbb{E}[Y \mid Z(t) = \boldsymbol{\mathcal{I}}] + R(t)\mathbb{E}[Y \mid Z(t) = \boldsymbol{\mathcal{R}}] \\
= & \sum_{\boldsymbol{\mathcal{C}} \in \{\boldsymbol{\mathcal{S}}, \boldsymbol{\mathcal{I}}, \boldsymbol{\mathcal{R}}\}} \mathbb{P}(Z(t) = \boldsymbol{\mathcal{C}}) \mathbb{E}[Y \mid Z(t) = \boldsymbol{\mathcal{C}}) \, .
\end{aligned}$$

2.2. Digression: Estimation of the Age Density

The age of an individual is recorded via the date and time of its birth. However, in most official data sets of the population, only the year of birth is given. As in the

analysis according to the extended model we need the density, this discrete data may not be suitable to work with. Nevertheless, there exist techniques in order to estimate continuous (probability) densities out of discrete data. The following part originates from Wikipedia [16], including Figure 2.1.
A simple way would be to extend the discrete probability density function to a piecewise constant probability function. In other words, draw a histogram and take that as density. The disadvantage of this method is that the arising density is not continuous and only piecewise differentiable with derivative everywhere zero.
Another technique, the most used one, is the so-called kernel density estimation. Here, kernels are added, centered about each data point. All these kernels are summed up and normalized to give the kernel density estimation. This procedure gives a smooth density.

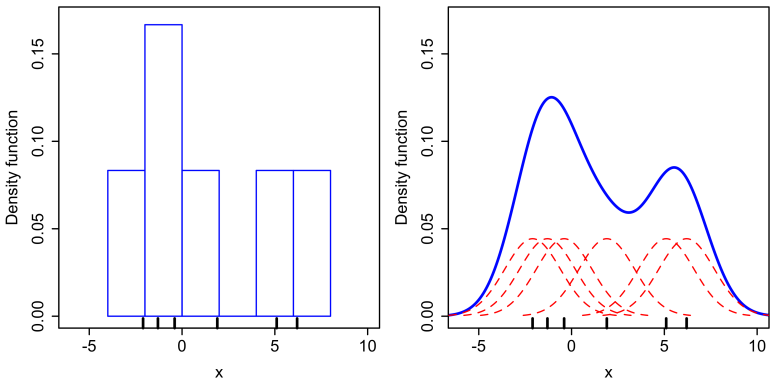

Figure 2.1.: Comparison between histogram and kernel density estimation.

The kernel density estimator for a kernel function k is given by

$$\tilde{f}_n\colon \mathbb{R} \to [0,\infty[\colon \quad t \mapsto \frac{1}{nh}\sum_{j=1}^{n} k\left(\frac{t-a_j}{h}\right)$$

where $a_1, a_2, ..., a_n$ are the n given data points and h is the so-called bandwidth and corresponds to the width of the support of the used kernels. The width h is chosen such that $h(n) = \frac{c}{n^\alpha}$ for some $0 < \alpha < \frac{1}{2}$ and $c > 0$ as then the sequence of kernel density estimators $\tilde{f}_n$ converges with probability 1 to the real density function f as $n \to \infty$.
Some possible kernels are:

$$k_G\colon \mathbb{R} \to \mathbb{R}\colon \quad t \mapsto \frac{1}{\sqrt{2\pi}} \exp\left(-\frac{1}{2}t^2\right) \qquad \text{(Gauss kernel)}$$

$$k_C\colon \mathbb{R} \to \mathbb{R}\colon \quad t \mapsto \frac{1}{\pi(1+t^2)} \qquad \text{(Cauchy kernel)}$$

$$k_P\colon \mathbb{R} \to \mathbb{R}\colon \quad t \mapsto \frac{1}{2}\exp(-|\,t\,|) \qquad \text{(Picard kernel)}$$

$$k_E\colon \mathbb{R} \to \mathbb{R}\colon \quad t \mapsto \frac{3}{4}(1-t^2)\mathbb{1}_{[-1,1]}(t)\,. \qquad \text{(Epanechnikov kernel)}$$

Here, the Epanechnikov kernel is the one that minimizes the quadratic deviation.

3. Analysis

Until now, we focussed on one time instance $t \in [0, \infty[$. We are now interested in the way the state of an individual changes over time.

3.1. Dynamics

In the extended model, we assume $K \in \mathbb{N}$ different activities $\mathcal{A}_1, \mathcal{A}_2, ..., \mathcal{A}_K$. Let $k \in \{1, 2, ..., K\}$ be fixed. Each individual of age $a \in [0, A]$ participates at activity $\mathcal{A}_k$ at a continuous rate $\pi_k(a) \geq 0$, in the following also called participation rate. Also, in order for π_k to be a valid function for this model, it is assumed that there is at least one $a \in [0, A]$ with $\pi_k(a) > 0$. The infection rate may depend on the activity $\mathcal{A}_k$, for example, it is higher in nightclubs and lower in hospitals, and is denoted by β_k. The recovery rate of an individual depends on its age $a \in [0, A]$ and will be written as $\gamma(a)$. Also, γ is assumed to be continuous. We assume both $\beta_k > 0$ and $\gamma(a) > 0$ for all $a \in [0, A]$.
First, what is the infection rate between an infected individual of age $\tilde{a} \in [0, A]$ and a susceptible one of age $a \in [0, A]$? The infected individual will be at activity $\mathcal{A}_k$, at rate $\pi_k(\tilde{a})$, while the susceptible individual will be there at rate $\pi_k(a)$. They will have contact there at rate β_k. Hence, the rate of infection at activity $\mathcal{A}_k$ equals to $\beta_k \pi_k(a)\pi_k(a)$. Now, as this holds for all activities, the total infection rate sums up to

$$\sum_{k=1}^{K} \beta_k \pi_k(a)\pi_k(\tilde{a}) =: \beta(a, \tilde{a})\,. \tag{3.1}$$

This quantity $\beta(a, \tilde{a})$ is called the infection rate between age a and age $\tilde{a}$. Clearly, β is continuous and $\beta(a, \tilde{a}) = \beta(\tilde{a}, a)$ for all $a, \tilde{a} \in [0, A]$, that is, β is symmetric.
In a more general setting, the infection rate between two ages may be defined differently, not depending on activities. Still, it may make sense to be symmetric. However, β is assumed to be positive, that is, $\beta(a, \tilde{a}) > 0$ for all $a, \tilde{a} \in [0, A]$.
Now, similarly as in the standard SIR epidemiology model, a susceptible individual of age a will be infected at rate $\beta(a, \tilde{a})$ by an infected individual of age $\tilde{a}$. As there is a density of $i(\tilde{a}, t)$ of infected individuals at time $t \in [0, \infty[$, a susceptible individual of age a will be infected by any infected individual of arbitrary age at rate

$$\int_0^A \beta(a, \tilde{a}) i(\tilde{a}, t)\, \mathrm{d}\tilde{a}\,.$$

As there is a density of $s(a, t)$ individuals of age a at time t, the density s has a change rate of

$$\frac{\partial s}{\partial t}(a, t) = -s(a, t) \cdot \int_0^A \beta(a, \tilde{a}) i(\tilde{a}, t)\, \mathrm{d}\tilde{a}\,.$$

An infected individual of age a will recover at rate $\gamma(a)$. Since there is a density of $i(a,t)$ infected individuals of age a at time t, we get

$$\frac{\partial r}{\partial t}(a,t) = \gamma(a) i(a,t)\,.$$

For the infected individuals, this means

$$\frac{\partial i}{\partial t}(a,t) = s(a,t) \cdot \int_0^A \beta(a,\tilde{a}) i(\tilde{a},t)\,\mathrm{d}\tilde{a} - \gamma(a) i(a,t)\,.$$

In summary, we get the following system of differential equations:

$$\frac{\partial s}{\partial t}(a,t) = -\, s(a,t) \cdot \int_0^A \beta(a,\tilde{a}) i(\tilde{a},t)\,\mathrm{d}\tilde{a}\,, \tag{3.2}$$

$$\frac{\partial i}{\partial t}(a,t) = s(a,t) \cdot \int_0^A \beta(a,\tilde{a}) i(\tilde{a},t)\,\mathrm{d}\tilde{a} - \gamma(a) i(a,t) \quad \text{and} \tag{3.3}$$

$$\frac{\partial r}{\partial t}(a,t) = \gamma(a) i(a,t)\,. \tag{3.4}$$

At a first glance, this system may look like a system of partial differential equations. However, no partial derivatives with respect to the variable a occur. Also, the derivative of (s,i,r) with respect to t includes an integral over the function itself. Hence, in reality, this is a system of integro-differential equations. As there are uncountably many $a \in [0,A]$, this system is, in particular, infinite-dimensional. A system of finite dimension will be derived in Section 4.
Since the Equations (3.2)-(3.4) add up to 0, it suffices to work with two of the three formulas.
Furthermore, we assume that the quantities

$$s_0(a) := s(a,t_0) \geq 0\,, \tag{3.5}$$

$$i_0(a) := i(a,t_0) \geq 0 \quad \text{and} \tag{3.6}$$

$$r_0(a) := r(a,t_0) := 0\,. \tag{3.7}$$

are given for all $a \in [0,A]$ and some $t_0 \in [0,\infty[$. If not stated otherwise, we will assume $t_0 = 0$. The last assumption (3.7) makes sense, as we can exclude already recovered individuals of our calculations by simply adjusting p. Also, we have the age distribution given by

$$p(a) = s_0(a) + i_0(a) > 0\,. \tag{3.8}$$

3.2. Properties of Solutions

It is one thing to define a system of integro-differential equations, the other is to show that it is well-posed. In the following, it is shown that there exists exactly one solution for the system of integro-differential equations (3.2)-(3.4) and some special properties of it are noted.

3.2.1. Invariance of Certain Properties

In this section, we will show that all solutions of System (3.2)-(3.4) with initial conditions (3.5)-(3.7) and (3.8) remain non-negative and satisfy $s(a,t)+i(a,t)+r(a,t)=p(a)$ for all $t \in [0,\infty[$ and all $a \in [0,A]$. For now, let $a \in [0,A]$ be fixed.
The isoclines, i.e., the sets of all points, where the time derivative is zero, are given by

- s- isocline for $\frac{\partial s}{\partial t}=0$:
$$\mathcal{I}_{\boldsymbol{\mathcal{S}},a} = \{t \in [0,A] \,|\, s(a,t)=0\} \cup \{t \in [0,\infty[\,|\,\forall \tilde{a} \in [0,A] : i(\tilde{a},t)=0\}$$
- i- isocline for $\frac{\partial i}{\partial t}=0$:
$$\mathcal{I}_{\boldsymbol{\mathcal{I}},a} = \left\{ t \in [0,\infty[\;\middle|\; \gamma(a)i(a,t) = s(a,t)\int_0^A \beta(a,\tilde{a})i(\tilde{a},t)\,\mathrm{d}\tilde{a} \right\}$$
- r- isocline for $\frac{\partial r}{\partial t}=0$:
$$\mathcal{I}_{\boldsymbol{\mathcal{R}},a} = \{t \in [0,\infty[\,|\,i(a,t)=0\}\,.$$

As the right-hand side of Equations (3.2)-(3.4) is continuous, the sign of a partial derivative does not change until the corresponding isocline is crossed. Hence, we are particularly interested in the case where an isoclise is crossed.
If $s(a,\tilde{t})=0$ for some $\tilde{t} \in [0,\infty[$, then also $\frac{\partial s}{\partial t}(a,\tilde{t})=0$ and the higher derivatives vanish, too. Hence, the solution for $s(a,\cdot)$ stays constant by Taylor expansion. Without loss of generality, assume $\tilde{t}=0$. In this case, Equation (3.3) gives
$$\frac{\partial i}{\partial t}(a,t) = -\gamma(a)i(a,t)\,,$$
where the solution
$$i(a,t) = i_0(a)\cdot\exp(-\gamma(a)t)$$
may be obtained by separation of variables.
This tends to 0 as $t \to \infty$, but stays non-negative. Additionally, this shows that the density of infected individuals at age $a \in [0,A]$ decreases exponentially with parameter $\gamma(a)$ if there is no inflow from the susceptible department.
If $s(a,t)>0$, then $\frac{\partial s}{\partial t}(a,t) \leq 0$, hence, it decreases. This means that $s(a,\cdot)$ is bounded from above by $s_0(a)$. However, as shown above, it can not go below 0, as when reaching 0, it then stays constant.
If $i(a,\cdot) \geq 0$, then by Equation (3.4) we have $\frac{\partial r}{\partial t} \geq 0$, hence, $r(a,\cdot)$ increases. In particular, $r(a,\cdot)$ stays non-negative and is bounded from below by 0. If $i(a,\tilde{t})=0$ for some $\tilde{t} \in [0,\infty[$, then also $i(a,t)=0$ for all $t \geq \tilde{t}$. As $i_0(a) \geq 0$, this implies that we can not have $i(a,t)<0$ for all $t \in [0,\infty[$. In other words, also $i(a,\cdot)$ is bounded from below by 0. By adding Equations (3.2)-(3.4), one gets that $s(a,\cdot)+i(a,\cdot)+r(a,\cdot)$ is constant. By Equation (3.8), we get $s(a,t)+i(a,t)+r(a,t)=p(a)$ for all $t \in [0,\infty[$ and $s(a,\cdot) \geq 0$, $i(a,\cdot) \geq 0$ and $r(a,\cdot) \geq 0$ we have that also $i(a,\cdot)$ and $r(a,\cdot)$ are bounded from above by $p(a)$. This completes the proof of positive invariance of the set $s(a,t), i(a,t), r(a,t) \geq 0$, $s(a,t)+i(a,t)+r(a,t)=p(a)$ under the system of integro-differential equations (3.2)-(3.4).

3.2.2. Existence and Uniqueness

With the help of the theorem of Picard-Lindelöf, it is possible for us to show that the system of integro-differential equations (3.2) -(3.4) with the corresponding initial conditions admits exactly one solution (s, i, r). The statement and a proof of this theorem can be found in [6], Theorem D.2.2.6.

Theorem 3.2.1 (Picard-Lindelöf)**.** *Let $\mathcal{V}$ be a real Banach space, $\mathcal{A} \subseteq \mathbb{R} \times \mathcal{V}$ an open set and $\mathcal{T}\colon \mathcal{A} \to \mathcal{V}$ continuous and locally Lipschitz continuous in the second variable. Furthermore, let $(t_0, y_0) \in \mathcal{A}$. Consider the differential equation*

$$y' = \mathcal{T}(t, y)\,.$$

Then a solution to this differential equation has the following properties:

- *Uniqueness: If $\varphi_1\colon \mathcal{I}_1 \to \mathcal{V}$ and $\varphi_2\colon \mathcal{I}_2 \to \mathcal{V}$ are solutions of the differential equation $y' = \mathcal{T}(t, y)$ with initial value (t_0, y_0) (i.e., we require $\varphi(t_0) = y_0$ for a solution φ), then*
$$\varphi_1|_{\mathcal{I}_1 \cap \mathcal{I}_2} = \varphi_2|_{\mathcal{I}_1 \cap \mathcal{I}_2}\,.$$
- *Existence: There exist $\varepsilon > 0$ and an open set $\mathcal{O} \subseteq \mathcal{V}$ with $y_0 \in \mathcal{O}$ with the following properties. We have $]t_0 - \varepsilon, t_0 + \varepsilon[\times \mathcal{O} \subseteq \mathcal{A}$ and for every $t_1 \in]t_0 - \varepsilon, t_0 + \varepsilon[$ and every $y_1 \in \mathcal{O}$ the differential equation $y' = \mathcal{T}(t, y)$ has a solution*
$$\varphi\colon\,]t_1 - \varepsilon, t_1 + \varepsilon[\to \mathcal{V}$$
for the initial value (t_1, y_1).
In particular, there exists a solution $\varphi\colon\,]t_0 - \varepsilon, t_0 + \varepsilon[\to \mathcal{V}$ for the initial value (t_0, y_0).

The proof also includes an explicit construction of a sequence converging to the solution. This construction is based on the Banach fixed point theorem.

In order to apply the theorem of Picard-Lindelöf, consider the space

$$\mathcal{C}([0, A]) \coloneqq \{f\colon\, [0, A] \to \mathbb{R} \mid f \text{ continuous}\}$$

of continuous functions from $[0, A]$ to $\mathbb{R}$ equipped with the norm

$$\|f\|_\infty \coloneqq \max_{a \in [0,A]} |f(a)|$$

for $f \in \mathcal{C}([0, A])$. This quantity exists as a function $f \in \mathcal{C}([0, A])$ is continuous on a compact domain and, hence, attains its minimum and maximum (see also [5], Theorem 5.2.16). In particular, all $f \in \mathcal{C}([0, A])$ are bounded. The induced metric is

$$d_\infty(f, g) = \|f - g\|_\infty$$

for $f, g \in \mathcal{C}([0, A])$. It is well known that $\mathcal{C}([0, A])$ is a Banach space over $\mathbb{R}$ with infinite dimension. One can find a proof of this in [5], Example 8.3.9. Hence, also $\mathcal{C}([0, A])^3$ is a real Banach space, equipped with the norm

$$\|(f, g, h)\| \coloneqq \max\{\|f\|_\infty, \|g\|_\infty, \|h\|_\infty\}$$

for $(f, g, h) \in \mathcal{V}$.
Let

$$\begin{aligned} \mathcal{T}\colon\ [0, \infty[\times\mathcal{C}([0, A])^3 &\to \mathcal{C}([0, A])^3 \\ (t, (f, g, h)) &\mapsto \begin{pmatrix} \mathcal{T}_1(t, (f, g, h)) \\ \mathcal{T}_2(t, (f, g, h)) \\ \mathcal{T}_3(t, (f, g, h)) \end{pmatrix}, \end{aligned}$$

where

$$\begin{aligned} \mathcal{T}_1 :\ & [0, \infty[\times\mathcal{C}([0, A])^3 \to \mathcal{C}([0, A]) : \\ & (t, (f, g, h)) \mapsto \left[a \mapsto -f(a) \int_0^A \beta(a, \tilde{a}) g(\tilde{a}) \, \mathrm{d}\tilde{a}\right], \\ \mathcal{T}_2 :\ & [0, \infty[\times\mathcal{C}([0, A])^3 \to \mathcal{C}([0, A]) : \\ & (t, (f, g, h)) \mapsto \left[a \mapsto f(a) \int_0^A \beta(a, \tilde{a}) g(\tilde{a}) \, \mathrm{d}\tilde{a} - \gamma(a) g(a)\right] \quad \text{and} \\ \mathcal{T}_3 :\ & [0, \infty[\times\mathcal{C}([0, A])^3 \to \mathcal{C}([0, A]) : \\ & (t, (f, g, h)) \mapsto [a \mapsto \gamma(a) g(a)] . \end{aligned}$$

One easily sees that $\mathcal{T}_2 = -(\mathcal{T}_1 + \mathcal{T}_3)$.
Furthermore, let $\mathcal{A} \coloneqq]-1, \infty[\times\mathcal{K}$, where

$$\mathcal{K} \coloneqq \{f \in \mathcal{C}([0, A])^3 \mid \mathrm{Im}(f) \subseteq [0, 1]^3\} \subseteq \mathcal{C}([0, A])^3 .$$

The goal is to apply the theorem of Picard-Lindelöf to the set $\mathcal{A}$ and the function $\mathcal{T}|_{\mathcal{A}}$. The function $\mathcal{T}$ does not depend on t. Hence, in order to show continuity and local Lipschitz continuity in the second variable of $\mathcal{T}|_{\mathcal{A}}$, it suffices to show Lipschitz continuity. Let $(f_1, g_1, h_1), (f_2, g_2, h_2) \in \mathcal{K}$ and $t \in [0, \infty[$. Now, bylooking at the first component of $\mathcal{T}|_{\mathcal{A}}$, one gets for $a \in [0, A]$ that

$$\begin{aligned} & |\mathcal{T}_1(t, (f_1, g_1, h_1)) - \mathcal{T}_1(t, (f_2, g_2, h_2))| \\ = & \left| -f_1(a) \int_0^A \beta(a, \tilde{a}) g_1(\tilde{a}) \, \mathrm{d}\tilde{a} - \left(-f_2(a) \int_0^A \beta(a, \tilde{a}) g_2(\tilde{a}) \, \mathrm{d}\tilde{a}\right)\right| \\ \leq & \left| -f_1(a) \int_0^A \beta(a, \tilde{a}) g_1(\tilde{a}) \, \mathrm{d}\tilde{a} + f_1(a) \int_0^A \beta(a, \tilde{a}) g_2(\tilde{a}) \, \mathrm{d}\tilde{a}\right| \\ & + \left| -f_1(a) \int_0^A \beta(a, \tilde{a}) g_2(\tilde{a}) \, \mathrm{d}\tilde{a} + f_2(a) \int_0^A \beta(a, \tilde{a}) g_2(\tilde{a}) \, \mathrm{d}\tilde{a}\right| \end{aligned}$$

$$
\begin{aligned}
&\leq |f_1(a)| \cdot \left| \int_0^A \beta(a,\tilde{a})(g_1(\tilde{a}) - g_2)(\tilde{a}) \, \mathrm{d}\tilde{a} \right| \\
&\quad + |f_1(a) - f_2(a)| \cdot \left| \int_0^A \beta(a,\tilde{a}) \, \mathrm{d}\tilde{a} \right| \|g_2\|_\infty \\
&\leq \left\| \int_0^A \beta(\cdot,\tilde{a}) \, \mathrm{d}\tilde{a} \right\|_\infty \|g_1 - g_2\|_\infty + \|f_1 - f_2\|_\infty \left\| \int_0^A \beta(\cdot,\tilde{a}) \, \mathrm{d}\tilde{a} \right\|_\infty \\
&= \left\| \int_0^A \beta(\cdot,\tilde{a}) \, \mathrm{d}\tilde{a} \right\|_\infty (\|g_1 - g_2\|_\infty + \|f_1 - f_2\|_\infty) \\
&\leq 2 \cdot \left\| \int_0^A \beta(\cdot,\tilde{a}) \, \mathrm{d}\tilde{a} \right\|_\infty \cdot \|(f_1,g_1,h_1) - (f_2,g_2,h_2)\| \, .
\end{aligned}
$$

The third component of $\mathcal{T}|_{\mathcal{A}}$ can be estimated for $a \in [0,A]$ by

$$
\begin{aligned}
|\mathcal{T}_3(t,(f_1,g_1,h_1)) - \mathcal{T}_3(t,(f_2,g_2,h_2))| &= |\gamma(a)g_1(a) - \gamma(a)g_2(a)| \\
&= \gamma(a) \cdot |g_1(a) - g_2(a)| \\
&\leq \|\gamma\|_\infty \cdot \|g_1 - g_2\|_\infty \\
&\leq \|\gamma\|_\infty \|(f_1,g_1,h_1) - (f_2,g_2,h_2)\| \, .
\end{aligned}
$$

Since the first and the third component of $\mathcal{T}|_{\mathcal{A}}$ were estimated, also the second one can easily be estimated by

$$
\begin{aligned}
&|\mathcal{T}_2(t,(f_1,g_1,h_1)) - \mathcal{T}_2(t,(f_2,g_2,h_2))| \\
=&| - (\mathcal{T}_1(t,(f_1,g_1,h_1)) + \mathcal{T}_3(t,(f_1,g_1,h_1)) + (\mathcal{T}_1(t,(f_2,g_2,h_2)) + \mathcal{T}_3(t,(f_2,g_2,h_2)))| \\
\leq &|\mathcal{T}_1(t,(f_1,g_1,h_1)) - \mathcal{T}_1(t,(f_2,g_2,h_2))| + |\mathcal{T}_3(t,(f_1,g_1,h_1)) - \mathcal{T}_3(t,(f_2,g_2,h_2))| \\
\leq &\left(2 \cdot \left\| \int_0^A \beta(\cdot,\tilde{a}) \, \mathrm{d}\tilde{a} \right\|_\infty + \|\gamma\|_\infty \right) \|(f_1,g_1,h_1) - (f_2,g_2,h_2)\| \, .
\end{aligned}
$$

In summary, we get

$$
\begin{aligned}
\|\mathcal{T}\,(t,(f_1,g_1,h_1)) - (t,(f_2,g_2,h_2))\| \leq &\left(2 \cdot \left\| \int_0^A \beta(\cdot,\tilde{a}) \, \mathrm{d}\tilde{a} \right\|_\infty + \|\gamma\|_\infty \right) \\
&\cdot \|(f_1,g_1,h_1) - (f_2,g_2,h_2)\| \, .
\end{aligned}
$$

Hence, $\mathcal{T}|_{\mathcal{A}}$ is Lipschitz continuous in the second variable with Lipschitz constant

$$
2 \cdot \left\| \int_0^A \beta(\cdot,\tilde{a}) \, \mathrm{d}\tilde{a} \right\|_\infty + \|\gamma\|_\infty \, .
$$

By the theorem of Picard-Lindelöf, there exists a unique continuous function (s,i,r) on some time interval $]t_0 - \varepsilon, t_0 + \varepsilon[$ around some $t_0 \in [0,\infty[$ and satisfying the system of integro-differential equations (3.2)-(3.4).

In Section 3.2.1 we have shown that a solution (s, i, r) of the System (3.2)-(3.4) with initial conditions (3.5)-(3.8) satisfies

$$\begin{aligned} s(a,t) \geq& 0\,, \\ i(a,t) \geq& 0\,, \\ r(a,t) \geq& 0 \quad \text{and} \\ s(a,t) + i(a,t) + r(a,t) =& p(a) \leq 1. \end{aligned}$$

In other words, also a local solution for some time interval stays bounded and non-negative.
Now, assume that the maximum existence interval of the solution is bounded from above. Then there are two cases. In the first one, the interval is closed on the right side. Using the right end-point as a new initial condition, we can extend the solution by some $\varepsilon > 0$. Hence, the interval could not have been maximal. In the other case, the interval is open on the right side. As the solution is bounded, it can be extended to the closure of this interval. Hence, also in this case, the existence interval could not have been maximal. As these are the only possibilities for the maximum existence interval to be bounded from above, this can not be the case. Hence, we get a solution on the whole interval $[0, \infty[$.

3.2.3. Remark on Smoothness

One can show that $\mathcal{T}$ is not only Lipschitz-continuous, but also smooth, i.e., infinitely differentiable. Hence, also a solution (s, i, r) of the system of integro-differential equations (3.2)-(3.4) is smooth with respect to time t, for all $t \in [0, \infty[$ (see [6], Conclusion D.4.1.7).
However, one does not know anything about differentiability with respect to the age a. Nevertheless, if all π_k, s_0 and i_0 are m-times continuously differentiable for some $m \in \mathbb{N}$, then $\mathcal{T}$ is m-times continuously differentiable. But this implies that a solution (s, i, r) is $(m+1)$-times continuously differentiable (see [6], Theorem D.4.1.6). In particular, if π_k, s_0 and i_0 are smooth for all $k \in \{1, 2, ..., K\}$, then also a solution (s, i, r) is smooth.
Nonetheless, in order to have an existing fraction of lastly infected individuals, we will assume that s_0, i_0, π_k are continuously differentiable with respect to a. In this case, also s, i and r are continuously differentiable with respect to a.

3.3. Equilibria

An equilibrium is a solution of the integro-differential equations (3.2)-(3.4) that does not change over time. Hence, an equilibrium has to satisfy that all the partial derivatives with respect to the time are zero. By Equation (3.4), we need for all $t \in [0, \infty[$ and $a \in [0, A]$ that

$$\frac{\partial r}{\partial t}(a,t) = \gamma(a) i(a,t) = 0\,.$$

Therefore,

$$i(a,t) = 0\,.$$

By Equations (3.2) and (3.3), this already implies

$$\frac{\partial s}{\partial t}(a,t) = \frac{\partial i}{\partial t}(a,t) = 0\,.$$

Hence, we need $i(a,t) = 0$ for all ages $a \in [0,A]$ and all times $t \in [0,\infty[$ in order to have an equilibrium. In particular, $i_0(a) = i(a,0) = 0$ for all ages $a \in [0,A]$. But this initial condition already implies $i(a,t) = 0$ for all $t \in [0,\infty[$. Then we have $s_0(a) = p(a)$, $S(0) = 1$ and $I(0) = 0$. The equilibrium of (3.2)-(3.4) is, hence, given by $(p,0,0)$.
This type of equilibrium is typical for SIR epidemiological models and called the disease-free equilibrium. In other models, there may also exist other equilibria.
In the following section, the stability of this disease-free equilibrium is analyzed. In other words, we take upon the question what will happen if there are small perturbations? Will the disease break out or will it fade away? In the section after, Section 3.5, it is shown that lastly every epidemic will reach the disease-free equilibrium. In other words, every disease will die out. Also, the number of susceptibles at the end of the epidemic will be analyzed.

3.4. Basic Reproduction Rate

The basic reproduction rate or basic reproduction number should be a threshold for the epidemic to break out or to decrease. In other words, it is a threshold which separates increasing initial infections from decreasing ones. The basic reproduction number should be defined in such a way that the threshold is at exactly 1. Such a parameter may not necessarily be unique, already in simple models. Often, the reproduction rate is defined as the number of secondary cases one infected individual produces in a totally susceptible population. In the extended model, it may be the case that for some ages the infections increase at the beginning and in others decrease. Hence, it may be necessary to define such a threshold for every age. However, we also have an overall probability of being infected, namely I. We restrict on a single reproduction rate giving a threshold for that function I. Calculations of such a basic reproduction rate are not easy in the general case. In the following, we restrict on the case $K = 1$, in which we can calculate an indicator of the basic reproduction rate we are looking for. In Section 3.4.2, it was possible to derive a basic reproduction number in the general setting with the help of the Krein-Rutman theorem. The basic reproduction number will not be given explicitly. However, we can bound it from above in order to give a condition when the epidemic will decrease. In Section 4.1.1 a basic reproduction rate in the discrete setting is derived via two different approaches. These give an analogous threshold.
For now, we assume $K = 1$, that is, we have

$$\beta(a,\tilde{a}) = \beta_1 \pi_1(a)\pi_1(\tilde{a})\,.$$

Then Equation (3.3) becomes

$$\frac{\partial i}{\partial t}(a,t) = s(a,t)\beta_1\pi_1(a) \cdot \int_0^A \pi_1(\tilde{a}) i(\tilde{a},t)\,\mathrm{d}\tilde{a} - \gamma(a) i(a,t)\,.$$

Following [7], we can rewrite this as

$$\frac{\pi_1(a)}{\gamma(a)} \cdot \frac{\partial i}{\partial t}(a,t) = s(a,t) \cdot \frac{\beta_1 \pi_1^2(a)}{\gamma(a)} \int_0^A \pi_1(\tilde{a}) i(\tilde{a},t)\,\mathrm{d}\tilde{a} - \pi_1(a) i(a,t)\,.$$

Integration of this in the variable a from 0 to A gives

$$\begin{aligned}
\int_0^A \frac{\pi_1(a)}{\gamma(a)} \cdot \frac{\partial i}{\partial t}(a,t)\,\mathrm{d}a &= \int_0^A \left(s(a,t) \cdot \frac{\beta_1 \pi_1^2(a)}{\gamma(a)} \int_0^A \pi_1(\tilde{a}) i(\tilde{a},t)\,\mathrm{d}\tilde{a} - \pi_1(a) i(a,t) \right) \mathrm{d}a \\
&= \left(\int_0^A s(a,t) \cdot \frac{\beta_1 \pi_1^2(a)}{\gamma(a)}\,\mathrm{d}a \right) \left(\int_0^A \pi_1(\tilde{a}) i(\tilde{a},t)\,\mathrm{d}\tilde{a} \right) - \int_0^A \pi_1(a) i(a,t)\,\mathrm{d}a \\
&= \left(\int_0^A s(a,t) \cdot \frac{\beta_1 \pi_1^2(a)}{\gamma(a)}\,\mathrm{d}a - 1 \right) \int_0^A \pi_1(a) i(a,t)\,\mathrm{d}a \\
&= \left(\int_0^A s(a,t) \cdot \frac{\beta(a,a)}{\gamma(a)}\,\mathrm{d}a - 1 \right) \int_0^A \pi_1(a) i(a,t)\,\mathrm{d}a\,.
\end{aligned}$$

Define

$$\varphi(t) \coloneqq \int_0^A \frac{\pi_1(a)}{\gamma(a)} i(a,t)\,\mathrm{d}a\,.$$

For constant $\frac{\pi_1}{\gamma}$, the fact that φ is monotonically increasing at the initial moment is equivalent to the statement that the total number of infected individuals $I = \int_0^A i(a,\cdot)\,\mathrm{d}a$ is monotonically increasing at the beginning. For general $\frac{\pi_1}{\gamma}$ this may not be the case. So, if we find a quantity χ such that $\frac{\mathrm{d}\varphi}{\mathrm{d}t}(0) > 0$ if and only if $\chi > 1$ then this is only an indicator for a basic reproduction rate and not necessarily a basic reproduction number itself.
Now, at the beginning of the epidemic, there will be nearly no infected individuals and the population will consist of nearly only susceptible individuals, that is, $i_0(a) \approx 0$ and $s_0(a) \approx p(a)$ for all $a \in [0, \infty[$. As we are interested wether the number of infected individuals increases at the beginning, we can use these approximations and get

$$\frac{\mathrm{d}\varphi}{\mathrm{d}t}(0) = \int_0^A \frac{\pi_1(a)}{\gamma(a)} \cdot \frac{\partial i}{\partial t}(a,0)\,\mathrm{d}a \approx \left(\int_0^A p(a) \cdot \frac{\beta(a,a)}{\gamma(a)}\,\mathrm{d}a - 1 \right) \int_0^A \pi_1(a) i(a,0)\,\mathrm{d}a\,.$$

Since the recovery rate π_1 is positive and i is nonnegative, continuous and positive for some $a \in [0, A]$, the second integral is positive. Hence, this quantity is positive if and only if for

$$\chi \coloneqq \int_0^A p(a) \cdot \frac{\beta(a,a)}{\gamma(a)}\,\mathrm{d}a \tag{3.9}$$

we have $\chi > 1$ and negative if $\chi < 1$. Such χ can also be defined for general K. This indicator only is an interim result. In the following, after some small digression, we will be able to derive a basic reproduction rate in the general setting. Also, in Section 4.1.1 we will see two different approaches for deriving a basic reproduction rate in the discrete setting. However, both approaches give the same threshold and the analogous one of the one calculated in Section 3.4.2.

3.4.1. Digression: Separable Infection Rate between Ages

The above calculation does not only work in the case $K = 1$, but also in the much more general case that the function β is separable, i.e., if there exist functions

$$\alpha_1, \alpha_2 : [0, A] \to [0, A]$$

such that

$$\beta(a, \tilde{a}) = \alpha_1(a) \cdot \alpha_2(\tilde{a}) .$$

As β is symmetric, these functions can be chosen such that $\alpha_1 = \alpha_2$. The basic reproduction rate $\mathcal{R}_0$ is then the same as in Equation (3.9).
One simple case is that the participation rates π_k ($k \in \{1, 2, ..., K\}$) are separable in the following way: There exist functions $\mu : \{1, 2, ..., K\} \to [0, \infty[$ and $\nu : [0, A] \to [0, \infty[$ such that for $k \in \{1, 2, ..., K\}$ and $a \in [0, A]$ we have

$$\pi_k(a) = \mu(k) \cdot \nu(a) .$$

In this case we have

$$\begin{aligned}\beta(a, \tilde{a}) =& \sum_{k=1}^{K} \beta_k \pi_k(a) \pi_k(\tilde{a}) = \sum_{k=1}^{K} \beta_k \mu(k) \nu(a) \mu(k) \nu(\tilde{a}) \\ =& \nu(a) \cdot \nu(\tilde{a}) \cdot \sum_{k=1}^{K} \beta_k (\mu(k))^2 .\end{aligned}$$

However, as in our setting it is not quite realistic that different ages behave the same way in each activity (up to a factor), we will not delve further into this topic.

3.4.2. General Approach

In the following, a basic reproduction rate in the general setting is derived. The system of integro-differential equations (3.2)-(3.4) can also be written in terms of linear operators. We do not assume the reader to be familiar with this theory, and therefore present it in Appendix A.3.
Define the operators $\mathcal{G}\colon \mathcal{C}([0, A]) \to \mathcal{C}([0, A])$ and $\mathcal{F}\colon \mathcal{C}([0, A]) \to \mathcal{C}([0, A])$ by

$$\begin{aligned}\mathcal{G}(f)(a) \coloneqq& \gamma(a) f(a) \quad \text{and} \\ \mathcal{F}(f)(a) \coloneqq& p(a) \int_0^A \beta(a, \tilde{a}) f(\tilde{a}) \, \mathrm{d}\tilde{a}\end{aligned}$$

for $f \in \mathcal{C}([0, A])$ and $a \in [0, A]$. As well-known, $\mathcal{C}([0, A])$ equipped with the norm $\| \cdot \|_\infty$ is a real Banach space of infinite dimension, see also [5], Example 8.3.9.
These operators are linear, as for $f, g \in \mathcal{C}([0, A])$ and $\lambda \in \mathbb{R}$ we have

$$\begin{aligned}\mathcal{G}(\lambda f + g)(a) =& \gamma(a)(\lambda f + g)(a) \\ =& \lambda \gamma(a) f(a) + \gamma(a) g(a) \\ =& (\lambda \mathcal{G}(f) + \mathcal{G}(g))(a)\end{aligned}$$

and

$$\begin{aligned}\mathcal{F}(\lambda f+g)(a) =& p(a)\int_0^A \beta(a,\tilde{a})(\lambda f+g)(\tilde{a})\,\mathrm{d}\tilde{a}\\ =& \lambda p(a)\int_0^A \beta(a,\tilde{a})f(\tilde{a})\,\mathrm{d}\tilde{a}+p(a)\int_0^A \beta(a,\tilde{a})g(\tilde{a})\,\mathrm{d}\tilde{a}\\ =& (\lambda\mathcal{F}(f)+\mathcal{F}(g))(a)\,.\end{aligned}$$

The operator $\mathcal{G}$ is clearly invertible with its inverse being

$$\mathcal{G}^{-1}\colon\ \mathcal{C}([0,A])\to\mathcal{C}([0,A])\colon\quad f\mapsto\left[a\mapsto\frac{1}{\gamma(a)}f(a)\right].$$

All three operators are bounded, as for $f\in\mathcal{C}([0,A])$ and $a\in[0,A]$ we have

$$|\mathcal{G}(f)(a)|=|\gamma(a)f(a)|\le\|\gamma\|_\infty||f\|_\infty\,,$$

hence,

$$\|\mathcal{G}(f)\|_\infty\le\|\gamma\|_\infty\|f\|_\infty\,.$$

The same holds for $\mathcal{G}^{-1}$ with the constant $\left\|\frac{1}{\gamma}\right\|_\infty$. Also,

$$\begin{aligned}|\mathcal{F}(f)(a)| =& \left|p(a)\int_0^A \beta(a,\tilde{a})f(\tilde{a})\,\mathrm{d}\tilde{a}\right|\\ \le& \int_0^A |\beta(a,\tilde{a})|\cdot\|f\|_\infty\,\mathrm{d}\tilde{a}\\ \le& \int_0^A \|\beta(\cdot,\tilde{a})|\,\mathrm{d}\tilde{a}\cdot\|f\|_\infty\,,\end{aligned}$$

implying

$$\|\mathcal{F}(f)\|_\infty\le\int_0^A|\beta(\cdot,\tilde{a})|\,\mathrm{d}\tilde{a}\cdot\|f\|_\infty\,.$$

By Theorem A.3.3, the operators $\mathcal{F}$ and $\mathcal{G}$ are also Lipschitz continuous and, in particular, continuous.
Linearizing the integro-differential equations (3.2)-(3.4) around the disease-free equilibrium $(p,0,0)$, one gets

$$\begin{aligned}\frac{\partial s}{\partial t}(a,t) \approx& p(a)\int_0^A \beta(a,\tilde{a})i(\tilde{a},t)\,\mathrm{d}\tilde{a}=-\mathcal{F}(i)(a,t)\,,\\ \frac{\partial i}{\partial t}(a,t) \approx& p(a)\int_0^A \beta(a,\tilde{a})i(\tilde{a},t)\,\mathrm{d}\tilde{a}-\gamma(a)i(a,t)=(\mathcal{F}-\mathcal{G})(i)(a,t)\quad\text{and}\\ \frac{\partial r}{\partial t}(a,t) \approx& \gamma(a)i(a,t)=\mathcal{G}(i)(a,t)\,,\end{aligned}$$

where the operators $\mathcal{F}$ and $\mathcal{G}$ are assumed to operate only on the variable a. For Equation (3.3), one sees this by considering the function $\mathcal{T}_2$ from Section 3.2.2 and some functions $\tilde{f}, \tilde{g}, \tilde{h} \in \mathcal{C}([0, A])$ which satisfy $\|\tilde{f}\|_\infty, \|\tilde{g}\|_\infty, \|\tilde{h}\|_\infty \in \mathcal{O}(\varepsilon)$, for some $\varepsilon > 0$. Then for $t \in [0, \infty[$ and $a \in [0, A]$ we have

$$\begin{aligned}
&\mathcal{T}_2(t, (p, 0, 0) + (\tilde{f}, \tilde{g}, \tilde{h}))(a) \\
&\qquad = (p(a) + \tilde{f}(a)) \int_0^A \beta(a, \tilde{a}) \tilde{g}(\tilde{a}) \, \mathrm{d}\tilde{a} - \gamma(a) \tilde{g}(a) \\
&\qquad = p(a) \int_0^A \beta(a, \tilde{a}) \tilde{g}(\tilde{a}) \, \mathrm{d}\tilde{a} + \tilde{f}(a) \int_0^A \beta(a, \tilde{a}) \tilde{g}(\tilde{a}) \, \mathrm{d}\tilde{a} - \gamma(a) \tilde{g}(a) \\
&\qquad \approx p(a) \int_0^A \beta(a, \tilde{a}) \tilde{g}(\tilde{a}) \, \mathrm{d}\tilde{a} - \gamma(a) \tilde{g}(a) \,,
\end{aligned}$$

when ignoring terms of order $\mathcal{O}(\varepsilon^2)$. In a similar manner, one linearizes Equations (3.2) and (3.4).

For hyperbolic equilibria, it is known by the Theorem by Hartman-Grobman (see Theorem A.2.3) that local behavior around them is determined by the linearized system. Hence, such an equilibrium is stable if the real part of all eigenvalues of the linearized operator is negative. However, the disease-free equilibrium (p, a, a) is not hyperbolic as the linearized equation for s and r does not depend on s and r, respectively, and hence, there are eigenvalues with value zero. If we have a solution for the linearized equation of $i(a, \cdot)$ which decreases exponentially for all $a \in [0, A]$, then $s(a, \cdot)$ and $r(a, \cdot)$ near the equilibrium can be calculated by integration and the limit for $t \to \infty$ of $s(a, t)$ and $r(a, t)$ exists.

Despite the fact that the equilibrium is not hyperbolic, we analyze the spectral values of the linearized system. If all of them have negative real part, then we get so-called spectral stablity. This does not yet imply stability, as Example 9.1.1 of [2] shows. However, in the case of the extended model, this seems to be the case, even if no proof could have been found.
We will see that the largest absolute value of the spectral values is already an eigenvalue and hence, real and non-negative. To prove this, we need the following theorem:

Theorem 3.4.1 (Krein-Rutman, generalized version)**.** *Let $\mathcal{V}$ be a real Banach space and $\mathcal{P}$ a solid cone in $\mathcal{V}$. Let $\mathcal{F}$ be a bounded linear operator from $\mathcal{V}$ to $\mathcal{V}$, which additionally is strongly positive on $\mathcal{P}$ and satisfies $\varrho_e(\mathcal{F}) < \varrho(\mathcal{F})$. Then*

- *$\varrho(\mathcal{F})$ is a simple eigenvalue of $\mathcal{F}$ with an eigenfunction $f \in \mathcal{P}^\circ$ and*
- *$|\mu| < \varrho(\mathcal{F})$ for all $\mu \in \operatorname{spec}(\mathcal{F}) \backslash \{\varrho(\mathcal{F})\}$.*

Proof. See [17], Theorem 1.3, or [12], Theorem 7.9. ■

The set $\mathcal{P} \coloneqq \{f : \mathcal{C}([0, A]) \to \mathbb{R} \,|\, \operatorname{im}(f) \subseteq [0, \infty[\}$ is a solid cone as the following points demonstrate.

- For $f, g \in \mathcal{P}$, $\lambda \in [0,1]$ and $a \in [0,A]$ we have

$$(\lambda f + (1-\lambda)g)(a) = \lambda f(a) + (1-\lambda)g(a) \geq \lambda \cdot 0 + (1-\lambda)\cdot 0 = 0\,,$$

  i.e., $\operatorname{im}(\lambda f + (1-\lambda)g) \subseteq [0,\infty[$.

- For $t \geq 0$, $f \in \mathcal{P}$ and $a \in [0,A]$ we have

$$t \cdot f(a) \geq 0\,,$$

  that is, $tf \in \mathcal{P}$ showing $t\mathcal{P} \subseteq \mathcal{P}$.

- Clearly, $\mathcal{P} \cap (-\mathcal{P}) = \{0\}$ holds.

- For $\varepsilon > 0$, we have that the function $f\colon [0,A] \to \mathbb{R}\colon a \mapsto \varepsilon$ lies in $\mathcal{P}$. For $g \in \mathcal{P}$ with $\|f-g\|_\infty < \frac{\varepsilon}{2}$ we have for every $a \in [0,A]$ that

$$\varepsilon - g(a) = f(a) - g(a) \leq \|f(a) - g(a)\| \leq \|f-g\|_\infty < \frac{\varepsilon}{2}\,,$$

  which implies $g(a) > \frac{\varepsilon}{2} > 0$. Hence, g lies in $\mathcal{P}$ too and $\mathcal{P}^\circ$ is not empty. We get $\mathcal{P}^\circ = \{f : \mathcal{C}([0,A]) \to \mathbb{R} \,|\, \operatorname{im}(f) \subseteq]0,\infty[\}$.

Let $\Gamma \coloneqq \|\gamma\|_\infty = \max_{a\in[0,A]} \gamma(a)$ and $\hat{\Gamma} \coloneqq \min_{a\in[0,A]} \gamma(a)$. Since $\mathcal{F}$ and $\mathcal{G}$ are continuous and bounded, so is $\mathcal{F} - \mathcal{G} + \Gamma \cdot \mathrm{id}$.
Now, for $f \in \mathcal{P}$, $f \neq 0$ and $a \in [0,A]$ we have

$$\begin{aligned}(\mathcal{F} - \mathcal{G} + \Gamma\cdot\mathrm{id})(f)(a) =& \mathcal{F}(f)(a) - \mathcal{G}(f)(a) + \Gamma f(a)\\ \geq& \mathcal{F}(f)(a) - \Gamma f(a) + \Gamma f(a) = \mathcal{F}(f)(a)\\ =& p(a)\int_0^A \beta(a,\tilde{a}) f(\tilde{a})\,\mathrm{d}\tilde{a} > 0\,.\end{aligned}$$

Hence, $(\mathcal{F} - \mathcal{G} + \Gamma\cdot\mathrm{id})(f) \in \mathcal{P}^\circ$. This shows that $\mathcal{F} - \mathcal{G} + \Gamma\cdot\mathrm{id}$ is strongly positive on $\mathcal{P}$. The same holds for $\mathcal{F}\circ\mathcal{G}^{-1}$.
The operator

$$\mathcal{H}\colon\ \mathcal{C}([0,A]) \to \mathcal{C}([0,A])\colon \quad f \mapsto \left(a \mapsto \int_0^A \beta(a,\tilde{a}) f(\tilde{a})\,\mathrm{d}\tilde{a}\right)$$

is a Hilbert-Schmidt integral operator as β is continuous. Also, it is non-negative and self-adjoint, since β is symmetric. Hence,

$$\operatorname{tr}(\mathcal{H}) = \int_0^A \beta(a,a)\,\mathrm{d}a < \infty\,,$$

by Mercer's theorem and $\mathcal{H}$ is trace class. Now, define the linear operator

$$\tilde{\mathcal{H}}\colon\ \mathcal{C}([0,A]) \to \mathcal{C}([0,A])\colon \quad f \mapsto [a \mapsto p(a) f(a)]\ ,$$

which is bounded in its norm by 1. Then $\mathcal{F} = \tilde{\mathcal{H}} \circ \mathcal{H}$. As a composition of a trace class operator with a bounded linear one, $\mathcal{F}$ is also trace class. The same argument holds for $\mathcal{F} \circ \mathcal{G}^{-1}$. As trace class operators, they are, in particular, compact. Since the essential spectrum is invariant under compact perturbations we have

$$\operatorname{spec}_e(\mathcal{F}) = \operatorname{spec}_e(\mathcal{F} - \mathcal{F}) = \operatorname{spec}_e(0) = \{0\}\,,$$

hence,

$$\varrho_e(\mathcal{F}) = 0\,.$$

Analogously, we see that

$$\varrho_e(\mathcal{F} \circ \mathcal{G}^{-1}) = 0\,.$$

Now, if $\operatorname{spec}(\mathcal{F}) = \{0\}$, then $\mathcal{F} = 0$, which does not hold. Hence, $\varrho(\mathcal{F}) > 0 = \varrho_e(\mathcal{F})$ and we can apply the theorem by Krein-Rutman for $\mathcal{F}$. The same holds for $\mathcal{F} \circ \mathcal{G}^{-1}$. Hence, $\varrho(\mathcal{F})$ and $\varrho(\mathcal{F} \circ \mathcal{G}^{-1})$ are simple eigenvalues of the corresponding operator.

As already stated, the essential spectrum does not change under compact perturbations. This means that

$$\operatorname{spec}_e(\mathcal{F} - \mathcal{G} + \Gamma \cdot \mathrm{id}) = \operatorname{spec}_e(\Gamma \cdot \mathrm{id} - \mathcal{G})\,.$$

Since the essential spectrum is a subset of the spectrum, we have

$$\operatorname{spec}_e(\Gamma \cdot \mathrm{id} - \mathcal{G}) \subseteq \operatorname{spec}(\Gamma \cdot \mathrm{id} - \mathcal{G}) \subseteq \{\lambda \in \mathbb{C} \,|\, |\lambda| \leq \|\Gamma \cdot \mathrm{id} - \mathcal{G}\|\}\,.$$

We estimate the operator norm by considering $f \in \mathcal{C}([0, A])$ and $a \in [0, A]$ and get

$$|(\Gamma \cdot \mathrm{id} - \mathcal{G})(f)(a)| = |\Gamma f(a) - \gamma(a) f(a)| = (\Gamma - \gamma(a))|f(a)| \leq (\Gamma - \hat{\Gamma})\|f\|_\infty.$$

We get

$$\operatorname{spec}_e(\mathcal{F} - \mathcal{G} + \Gamma \cdot \mathrm{id}) = \operatorname{spec}_e(\Gamma \cdot \mathrm{id} - \mathcal{G}) \subseteq \{\lambda \in \mathbb{C} \,|\, |\lambda| \leq \Gamma - \hat{\Gamma}\}\,,$$

and in particular,

$$\varrho_e(\mathcal{F} - \mathcal{G} + \Gamma \cdot \mathrm{id}) \leq \Gamma - \hat{\Gamma}\,.$$

We know that the spectrum is bounded by the operator norm, i.e.,

$$\varrho(\mathcal{F} - \mathcal{G} + \Gamma \cdot \mathrm{id}) \leq \|\mathcal{F} - \mathcal{G} + \Gamma \cdot \mathrm{id}\| \leq \left\| \int_0^A \beta(\cdot, \tilde{a})\, \mathrm{d}\tilde{a} \right\| + (\Gamma - \hat{\Gamma})\,.$$

The second inequality is easily shown. Now, under the assumption $\varrho(\mathcal{F} - \mathcal{G} + \Gamma \cdot \mathrm{id}) > \Gamma - \hat{\Gamma}$, which, between others, is the case for constant γ, we clearly have

$$\varrho_e(\mathcal{F} - \mathcal{G} + \Gamma \cdot \mathrm{id}) < \varrho(\mathcal{F} - \mathcal{G} + \Gamma \cdot \mathrm{id})$$

and one can apply the theorem by Krein-Rutman. This means that $\varrho(\mathcal{F}-\mathcal{G}+\Gamma\cdot\mathrm{id})$ is a simple eigenvalue of $\mathcal{F}-\mathcal{G}+\Gamma\cdot\mathrm{id}$. Note that all other spectral values have real part smaller than $\varrho(\mathcal{F}-\mathcal{G}+\Gamma\cdot\mathrm{id})$. Let $\hat{f}\in P^\circ$ be a corresponding eigenfunction. Then

$$\begin{aligned}(\mathcal{F}-\mathcal{G})(\hat{f}) =&(\mathcal{F}-\mathcal{G}+\Gamma\cdot\mathrm{id})(\hat{f})-(\Gamma\cdot\mathrm{id})(\hat{f})\\ =&\varrho(\mathcal{F}-\mathcal{G}+\Gamma\cdot\mathrm{id})\hat{f}-\Gamma\hat{f}\\ =&(\varrho(\mathcal{F}-\mathcal{G}+\Gamma\cdot\mathrm{id})-\Gamma)\hat{f}\,.\end{aligned}$$

This means that

$$\hat{\lambda}\coloneqq\varrho(\mathcal{F}-\mathcal{G}+\Gamma\cdot\mathrm{id})-\Gamma\leq\left\|\int_0^A\beta(\cdot,\tilde{a})\,\mathrm{d}\tilde{a}\right\|-\hat{\Gamma}$$

is the unique eigenvalue of $\mathcal{F}-\mathcal{G}$ with largest absolute value and its corresponding eigenfunction is $\hat{f}$. Since $\mathcal{F}-\mathcal{G}$ is bounded, the spectrum of the adjoint operator $\mathcal{F}^*-\mathcal{G}^*=(\mathcal{F}-\mathcal{G})^*$ is the same as of the original one where $\mathcal{G}$ is selfadjoint ($\mathcal{G}^*=\mathcal{G}$) and the adjoint of $\mathcal{F}$ is given by

$$\mathcal{F}^*(f)(a)=\int_0^A p(\tilde{a})\beta(\tilde{a},a)f(\tilde{a})\,\mathrm{d}\tilde{a}$$

for $f\in\mathcal{C}([0,A])$ and $a\in[0,A]$. By the Krein-Rutman theorem, there exists an eigenfunction $\tilde{f}\in P^\circ$, corresponding to the eigenvalue $\hat{\lambda}$ for the adjoint operator.
Let $\hat{g}\in\mathcal{P}^\circ$ be an eigenfunction corresponding to $\varrho(\mathcal{F}\circ\mathcal{G}^{-1})$ by the theorem of Krein-Rutman. Then for $\tilde{g}\coloneqq\mathcal{G}^{-1}(\hat{g})$ we have

$$\mathcal{F}(\tilde{g})=(\mathcal{F}\circ\mathcal{G}^{-1})(\hat{g})=\varrho(\mathcal{F}\circ\mathcal{G}^{-1})(\hat{g})=\varrho(\mathcal{F}\circ\mathcal{G}^{-1})\mathcal{G}(\tilde{g})\,.$$

The scalar product on $\mathcal{C}([0,A])$ is defined by $\langle f,g\rangle\coloneqq\int_0^A f(a)g(a)\,\mathrm{d}a$ for $f,g\in\mathcal{C}([0,A])$. Remember in this setting that $\mathcal{C}([0,A])\subseteq L^2([0,A])$. Now, we can calculate

$$\begin{aligned}\hat{\lambda}\langle\tilde{f},\tilde{g}\rangle =&\langle\lambda\tilde{f},\tilde{g}\rangle\\ =&\langle(\mathcal{F}-\mathcal{G})^*(\tilde{f}),\tilde{g}\rangle\\ =&\langle\tilde{f},(\mathcal{F}-\mathcal{G})(\tilde{g})\rangle\\ =&\langle\tilde{f},\mathcal{F}(\tilde{g})-\mathcal{G}(\tilde{g})\rangle\\ =&\langle\tilde{f},\varrho(\mathcal{F}\circ\mathcal{G}^{-1})(\mathcal{G}(\tilde{g}))-\mathcal{G}(\tilde{g})\rangle\\ =&\langle\tilde{f},(\varrho(\mathcal{F}\circ\mathcal{G}^{-1})-1)\mathcal{G}(\tilde{g})\rangle\\ =&(\varrho(\mathcal{F}\circ\mathcal{G}^{-1})-1)\langle\tilde{f},\mathcal{G}(\tilde{g})\rangle\,.\end{aligned}$$

As both $\tilde{f}$, $\tilde{g}$ are positive (that is, lie in $\mathcal{P}^\circ$) and $\mathcal{G}$ is a strongly positive operator, $\langle\tilde{f},\tilde{g}\rangle>0$ and $\langle\tilde{f},\mathcal{G}(\tilde{g})\rangle>0$. Hence, the sign of $\hat{\lambda}$ is determined by $\varrho(\mathcal{F}\circ\mathcal{G}^{-1})-1$. In other words, if $\varrho(\mathcal{F}\circ\mathcal{G}^{-1})<1$, then all spectral values have negative real part. Hence, the definition of the basic reproduction rate

$$\mathcal{R}_0\coloneqq\varrho(\mathcal{F}\circ\mathcal{G}^{-1})\tag{3.10}$$

makes sense, at least, if spectral stability implied stability.

In the following, we will bound the basic reproduction rate from above via two different approaches.
Since $\mathcal{F} \circ \mathcal{G}^{-1}$ is trace class, by Theorem 3.1 of [1] and Definition (3.9)

$$\operatorname{tr}(\mathcal{F} \circ \mathcal{G}^{-1}) = \int_0^A \frac{p(a)}{\gamma(a)} \beta(a,a)\, \mathrm{d}a = \chi\,.$$

As a trace class operator, it is, in particular, compact. The spectrum of such operators is at most countable by the Riesz's Theorem. Hence, the number of eigenvalues as a subset of the spectrum is at most countable. Let $\lambda_0, \lambda_1, \lambda_2, ...$ be the list of the eigenvalues of $\mathcal{F} \circ \mathcal{G}^{-1}$, listed in order of nonincreasing absolute value and repeated according to algebraic multiplicity. By Lidskii's Theorem, we get

$$\operatorname{tr}(\mathcal{F} \circ \mathcal{G}^{-1}) = \sum_{n \in \mathbb{N}} \lambda_n\,.$$

Similarly as in Section 4.1.1, one can show that $\mathcal{F} \circ \mathcal{G}^{-1}$ with β as in Equation (3.1) only has non-negative eigenvalues. This is done via writing $\mathcal{F} \circ \mathcal{G}^{-1}$ as a product of two Hilbert-Schmidt operators which always is possible for trace class operators. By a version of the Jacobson Lemma (see Theorem A.1.4 for the discrete version), the spectrum of Hilbert-Schmidt operators in reversed order is the same as in original order. This reversed order then gives a positive semi-definit operator which has to have only non-negative eigenvalues. However, doing this rigorously would extent beyond the scope of this thesis. As all eigenvalues are non-negative, we have

$$\mathcal{R}_0 = \varrho(\mathcal{F} \circ \mathcal{G}^{-1}) \leq \sum_{n \in \mathbb{N}} \lambda_n = \operatorname{tr}(\mathcal{F} \circ \mathcal{G}^{-1}) = \chi\,. \tag{3.11}$$

Hence, if $\chi < 1$, there will be no outbreak.
We can do some further calculations:

$$\begin{aligned}\chi - 1 &= \int_0^A p(a) \frac{\beta(a,a,)}{\gamma(a)}\, \mathrm{d}a - \int_0^A p(a)\, \mathrm{d}a \\ &= \int_0^A p(a) \left(\frac{\beta(a,a)}{\gamma(a)} - 1 \right) \mathrm{d}a\,.\end{aligned}$$

Loosely speaking, if $\chi < 1$, then $\frac{\beta(a,a)}{\gamma(a)} < 1$ for "more" values $a \in [0, A]$ than $\frac{\beta(a,a)}{\gamma(a)} \geq 1$. In other words, $\frac{\beta}{\gamma}$ has to be sufficiently small in order that the disease does not break out.
Remember that $\mathcal{R}_0 < 1$ only means that I decreases. However, there may still exist ages $a \in [0, A]$ where $i(a, \cdot)$ increases at the beginning. Also, we can not make a statement if $\chi > 1$. In that case, $\mathcal{R}_0 > 1$ may hold, but also $\mathcal{R}_0 < 1$. Hence, the disease can either increase or decrease.

As as eigenvalue of $\mathcal{F} \circ \mathcal{G}^{-1}$, the spectral radius satisfies

$$\varrho(\mathcal{F} \circ \mathcal{G}^{-1}) \leq \|\mathcal{F} \circ \mathcal{G}^{-1}\|.$$

The operator norm is estimated by considering $f \in \mathcal{C}([0, A])$ and $a \in [0, A]$ which gives

$$\begin{aligned} \left|(\mathcal{F} \circ \mathcal{G}^{-1})(f)(a)\right| &= \left| p(a) \int_0^A \beta(a, \tilde{a}) \frac{1}{\gamma(\tilde{a})} f(\tilde{a}) \, \mathrm{d}\tilde{a} \right| \\ &\leq \left(p(a) \int_0^A \beta(a, \tilde{a}) \frac{1}{\gamma(\tilde{a})} \, \mathrm{d}\tilde{a} \right) \|f\|_\infty \,, \end{aligned}$$

and hence,

$$\varrho(\mathcal{F} \circ \mathcal{G}^{-1}) \leq \|\mathcal{F} \circ \mathcal{G}^{-1}\| \leq \max_{a \in [0,1]} \int_0^A p(a) \frac{\beta(a, \tilde{a})}{\gamma(\tilde{a})} \, \mathrm{d}\tilde{a} \,. \tag{3.12}$$

3.5. Long-term Behavior

We are interested what happens in the long-run of the epidemic. As it will be shown, the disease will die out for sure. However, not every individual will get ill. In other words, there will be susceptible individuals even if the disease raged through the population.

In Section 3.2.1 it is shown that the system of integro-differential equations (3.2)-(3.4) fulfills the properties $s(a,t)+i(a,t)+r(a,t) = p(a)$, $s(a,t), i(a,t), r(a,t) \geq 0$ for all times $t \geq \tilde{t}$ if they are satisfied for one $\tilde{t} \in [0, \infty[$.
Now, it is time to prove that every disease following the extended model will die out: As before, let $a \in [0, \infty[$ be fixed. We have

$$\frac{\partial(s+i)}{\partial t}(a,t) = -\gamma(a) i(a,t).$$

This quantity is negative, assuming $i(a,\cdot) > 0$. In other words, $s(a,\cdot) + i(a,\cdot)$ is strictly monotonically decreasing whenever $i(a,\cdot)$ is positive. But $s(a,\cdot)+i(a,\cdot)$ is bounded from below by 0. As the function $(s+i)(a,\cdot)$ is strictly monotonically decreasing and bounded from below, there exists a limit. Also, $s(a,\cdot)$ is strictly monotonically decreasing for $i(a,\cdot) > 0$ as shown above and bounded from below by 0, and hence, converges. Call the limit $s_\infty(a)$. This means that also $i(a,\cdot)$ and $r(a,\cdot)$ converge. Since $i(a,t) \geq 0$ for all $t \in [0, \infty[$, also the limit of $i(a,\cdot)$ is non-negative and $\frac{\partial(s+i)}{\partial t}(a,t) = -\gamma(a) i(a,t)$ has a non-positive limit. Now, if $\lim_{t\to\infty} \frac{\partial(s+i)}{\partial t}(a,t) < 0$, then from some $\tilde{t} > 0$ onwards we have $(s+i)(a,t) < 0$ for all $t \geq \tilde{t}$. As $s+i$ is non-negative by construction, this can not be. Hence,

$$\lim_{t\to\infty} \frac{\partial(s+i)}{\partial t}(a,t) = 0 \,.$$

We get,

$$i_\infty(a) \coloneqq \lim_{t\to\infty} i(a,t) = -\frac{1}{\gamma(a)} \lim_{t\to\infty} \frac{\partial(s+i)}{\partial t}(a,t) = 0 \,. \tag{3.13}$$

Since this holds for all ages a, we get by dominated convergence ($0 \leq i(a,t) \leq p(a)$ which integrates to 1)

$$\lim_{t\to\infty} I(t) = \lim_{t\to\infty} \int_0^A i(a,t)\,\mathrm{d}a = \int_0^A \lim_{t\to\infty} i(a,t)\,\mathrm{d}a = \int_0^A 0\,\mathrm{d}a = 0\,.$$

This means that a disease following Equations (3.2)-(3.4) will eventually die out.

We are interested in the total number of infected individuals in the course of the epidemic. This can be described by the number of recovered individuals when the disease has died out. Again, we follow the steps in [7] to calculate this quantity.
By integrating Equation (3.4) in the variable t from 0 to $T \in [0,\infty[$ we get

$$r(a,T) - r(a,0) = \int_0^T \frac{\partial r}{\partial t}(a,t)\,\mathrm{d}t = \int_0^T \gamma(a) i(a,t)\,\mathrm{d}t = \gamma(a)\int_0^T i(a,t)\,\mathrm{d}t\,.$$

As $r(a,0) = 0$ by assumption, we have

$$r(a,T) = \gamma(a)\int_0^T i(a,t)\,\mathrm{d}t\,. \tag{3.14}$$

Defining $r_\infty(a) \coloneqq \lim_{T\to\infty} r(a,T)$, this implies

$$r_\infty(a) = \gamma(a)\int_0^\infty i(a,t)\,\mathrm{d}t\,, \tag{3.15}$$

by letting $T \to \infty$.
Now, adding Equations (3.2) and (3.3) and integrating the result in t from 0 to $T \in [0,\infty[$, we get

$$s(a,T) + i(a,T) - (s(a,0) + i(a,0)) = \int_0^T \frac{\partial(s+i)}{\partial t}(a,t)\,\mathrm{d}t = -\gamma(a)\int_0^T i(a,t)\,\mathrm{d}t\,.$$

Letting $T \to \infty$ and defining $s_\infty(a) \coloneqq \lim_{T\to\infty} s(a,T)$, this gives

$$s_\infty(a) + i_\infty(a) - (s(a,0) + i(a,0)) = -\gamma(a)\int_0^\infty i(a,t)\,\mathrm{d}t\,.$$

Since $i_\infty(a) = 0$ by Equation (3.13) and inserting the initial conditions, we get

$$s_\infty(a) - (s_0(a) + i_0(a)) = -\gamma(a)\int_0^\infty i(a,t)\,\mathrm{d}t\,.$$

Combining this with Equation (3.15), we have

$$s_\infty(a) - (s_0(a) + i_0(a)) = -r_\infty(a)\,. \tag{3.16}$$

Now, by Equation (3.2), we have

$$\frac{1}{s(a,t)} \cdot \frac{\partial s}{\partial t}(a,t) = -\int_0^A \beta(a,\tilde{a}) i(\tilde{a},t)\,\mathrm{d}\tilde{a}\,.$$

Solving this with the method of separation of variables, we get by integration from 0 to T that

$$\log\left(\frac{s(a,T)}{s(a,0)}\right) = \log(s(a,T)) - \log(s(a,0)) = -\int_0^T \int_0^A \beta(a,\tilde{a}) i(\tilde{a},t)\,\mathrm{d}\tilde{a}\,\mathrm{d}t\,.$$

Rearrangement and using the initial condition (3.5) yields

$$\begin{aligned} s(a,T) &= \exp\left(-\int_0^A \beta(a,\tilde{a})\left(\int_0^T i(\tilde{a},t)\,\mathrm{d}t\right)\mathrm{d}\tilde{a}\right)\cdot s_0(a) \\ &= \exp\left(-\int_0^A \beta(a,\tilde{a})\left(\frac{r(\tilde{a},T)}{\gamma(\tilde{a})}\right)\mathrm{d}\tilde{a}\right)\cdot s_0(a)\,, \end{aligned}$$

where in the last step Equation (3.14) has been used. Letting $T \to \infty$, this becomes

$$s_\infty(a) = \exp\left(-\int_0^A \beta(a,\tilde{a})\cdot\frac{r_\infty(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right)\cdot s_0(a)\,.$$

By Equation (3.16), this equals

$$s_0(a) + i_0(a) - r_\infty(a) = \exp\left(-\int_0^A \beta(a,\tilde{a})\cdot\frac{r_\infty(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right)\cdot s_0(a)\,,$$

and hence,

$$r_\infty(a) = \left(1 - \exp\left(-\int_0^A \beta(a,\tilde{a})\frac{r_\infty(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right)\right)\cdot s_0(a) + i_0(a)\,. \tag{3.17}$$

As $s_0(a) + i_0(a) = p(a)$, one can rewrite this also as

$$r_\infty(a) = p(a) - \exp\left(-\int_0^A \beta(a,\tilde{a})\frac{r_\infty(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right)\cdot s_0(a)\,. \tag{3.18}$$

Equations (3.17) and (3.18) also give an implicit equation for the final size

$$R_\infty \coloneqq \int_0^A r_\infty(a)\,\mathrm{d}a$$

of the epidemic.

Under the assumption of existence, we can already estimate the number of once infected individuals at the end of the epidemic as

$$1 - \exp\left(-\int_0^A \beta(a,\tilde{a})\frac{r_\infty(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right) > 0\,.$$

We have $r_\infty(a) \geq i_0(a)$ by Equation (3.17). This implies

$$R_\infty = \int_0^A r_\infty(a)\,\mathrm{d}a \geq \int_0^A i_0(a)\,\mathrm{d}a = I(0)\,.$$

Furthermore, by Equation (3.18)

$$r_\infty(a) < s_0(a) + i_0(a) = p(a)\,,$$

hence,

$$R_\infty = \int_0^A r_\infty(a)\,\mathrm{d}a < \int_0^A p(a)\,\mathrm{d}a = 1\,.$$

In terms of the disease, this means that not every individual in the population will get infected.

Looking at this the other way round, the number of susceptible individuals at the end of the epidemic

$$S_\infty \coloneqq \lim_{t\to\infty} \int_0^A s(a,t)\,\mathrm{d}a = 1 - R_\infty$$

is strictly positive and at most the number of susceptible individuals in the first run. While the latter is clear by construction of the model, the first is not trivial at all.

In the following, it is proven that such a function r_∞ satisfying Equation (3.17) or Equation (3.18) exists and it is analyzed for uniqueness.

3.5.1. Existence

The following theorem is used in order to prove the existence of a function r_∞ satisfying Equation (3.17) under some additional assumptions. First, we state the original statement from [14].

Theorem 3.5.1 (Schauder fixed-point theorem)**.** *Let $\tilde{\mathcal{K}}$ be a non-empty, convex and closed subset of a Banach space $\mathcal{V}$ and $\tilde{\mathcal{T}}\colon \tilde{\mathcal{K}} \to \tilde{\mathcal{K}}$ a continuous mapping from $\tilde{\mathcal{K}}$ into itself. Furthermore, let $\tilde{\mathcal{T}}(\tilde{\mathcal{K}}) \subseteq \tilde{\mathcal{K}}$ be compact. Then there exists a fixed point.*

Let $\tilde{\mathcal{K}} \coloneqq \{f \in \mathcal{C}([0,A]) \,|\, \mathrm{Im}(f) \subseteq [0,1]\} \subseteq \mathcal{C}([0,A])$, that is, it consists of all continuous, nonnegative functions starting in $[0,A]$ and with image in $[0,1]$. As explained already in Section 3.2.2, $\mathcal{C}([0,A])$ is a real Banach space. The set $\tilde{\mathcal{K}}$ is non-empty and bounded as every $f \in \tilde{\mathcal{K}}$ satisfies $\|f\|_\infty \leq 1$. To see that $\tilde{\mathcal{K}}$ is also closed, let $f_n \in \tilde{\mathcal{K}}$ for $n \in \mathbb{N}$ with limit $g \in \mathcal{C}([0,A])$ as $n \to \infty$. This means that the limit

$$\lim_{n\to\infty} f_n(a) = g(a)$$

is uniform. Suppose $\|g\|_\infty > 1$. Let $\delta \coloneqq \|g\|_\infty - 1 > 0$. Since g is the limit of $(f_n)_{n\in\mathbb{N}}$, there exists an $N \in \mathbb{N}$ such that $\|f_n - g\|_\infty < \frac{\delta}{2}$ for all $n \geq N$. Then

$$\|g\|_\infty = \|g - f_n + f_n\|_\infty \leq \|g - f_n\|_\infty + \|f_n\|_\infty \leq \frac{\delta}{2} + 1 < \delta + 1\,,$$

which can not be the case as $\|g\|_\infty = \delta + 1$. Hence, $\|g\|_\infty \leq 1$ and $\tilde{\mathcal{K}}$ is closed. But $\tilde{\mathcal{K}}$ is not compact, as $f_n(a) \coloneqq a^n$ has no continuous limit as $n \to \infty$.

It is easy to see that $\tilde{\mathcal{K}}$ is also convex: Let $f, g \in \tilde{\mathcal{K}}$ and $\lambda \in \mathbb{R}$. Then

$$\lambda f(a) + (1-\lambda)g(a) \leq \lambda \cdot 1 + (1-\lambda) \cdot 1 = 1$$

and

$$\lambda f(a) + (1-\lambda)g(a) \geq \lambda \cdot 0 + (1-\lambda) \cdot 0 = 0\,.$$

Hence, $\operatorname{im}(\lambda f + (1-\lambda)g) \in [0,1]$ and $\lambda f + (1-\lambda)g \in \tilde{\mathcal{K}}$.

Now, consider the operator

$$\tilde{\mathcal{T}}\colon\ \tilde{\mathcal{K}} \to \mathcal{C}([0,A])\colon \qquad f \mapsto \left[a \mapsto \left(1 - \exp\left(-\int_0^A \beta(a,\tilde{a})\frac{f(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right)\right) \cdot s_0(a) + i_0(a)\right].$$

This operator satisfies

$$\tilde{\mathcal{T}}(f)(a) = \left(1 - \exp\left(-\int_0^A \beta(a,\tilde{a})\frac{f(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right)\right) \cdot s_0(a) + i_0(a) \geq i_0(a) \geq 0$$

for all $f \in \tilde{K}$ and $a \in [0,A]$. We have by Equation (3.18) that

$$\begin{aligned}
\|\tilde{\mathcal{T}}(f)\|_\infty &= \max_{a\in[0,A]} |\tilde{\mathcal{T}}(f)(a)| \\
&= \max_{a\in[0,A]} \left(p(a) - \exp\left(-\int_0^A \beta(a,\tilde{a})\frac{f(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right) \cdot s_0(a)\right) \\
&\leq \max_{a\in[0,A]} p(a) \leq 1\,.
\end{aligned}$$

Hence, $\tilde{\mathcal{T}}(f) \in \tilde{\mathcal{K}}$ and $\operatorname{im}(\tilde{\mathcal{T}}) \subseteq \tilde{\mathcal{K}}$.
The operator $\tilde{\mathcal{T}}$ is Lipschitz-continuous with Lipschitz constant

$$L \coloneqq \max_{a\in[0,A]} \int_0^A \frac{p(a)}{\gamma(\tilde{a})}\beta(a,\tilde{a})\,\mathrm{d}\tilde{a}\,, \tag{3.19}$$

and hence, in particular, continuous. The maximum exists as β is continuous (see also [5], Proposition 5.2.16). To show Lipschitz-continuity, let $f, g \in \tilde{\mathcal{K}}$. For some arbitrary $a \in [0,1]$, we calculate

$$\begin{aligned}
&|\tilde{\mathcal{T}}(f)(a) - \tilde{\mathcal{T}}(g)(a)| \\
&\quad= \left|\left[\left(1 - \exp\left(-\int_0^A \beta(a,\tilde{a})\frac{f(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right)\right) \cdot s_0(a) + i_0(a)\right]\right. \\
&\qquad\left. - \left[\left(1 - \exp\left(-\int_0^A \beta(a,\tilde{a})\frac{g(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right)\right) \cdot s_0(a) + i_0(a)\right]\right| \\
&\quad= \left|\exp\left(-\int_0^A \beta(a,\tilde{a})\frac{g(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right) - \exp\left(-\int_0^A \beta(a,\tilde{a})\frac{f(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right)\right| \cdot s_0(a)\,.
\end{aligned}$$

Let $\xi_a \coloneqq -\int_0^A \beta(a,\tilde{a})\frac{f(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}$ and $\zeta_a \coloneqq -\int_0^A \beta(a,\tilde{a})\frac{g(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}$. Assume $\xi_a \neq \zeta_a$. Otherwise, $|\tilde{\mathcal{T}}(f)(a) - \tilde{\mathcal{T}}(g)(a)| = 0$.
By the mean value theorem, there exists an $\eta_a \in]\min\{\zeta_a,\xi_a\}, \max\{\zeta_a,\xi_a\}[$ such that

$$|\exp(\xi_a) - \exp(\zeta_a)| = \exp(\eta_a)\cdot|\xi_a - \zeta_a|\,.$$

As $\xi_a \leq 0$ and $\zeta_a \leq 0$, we have $\eta_a < 0$ and $\exp(\eta_a) < 1$. We denote this quantity by $\kappa_a \coloneqq \exp(\eta_a)$. We get

$$\begin{aligned}|\tilde{\mathcal{T}}(f)(a) - \tilde{\mathcal{T}}(g)(a)| =& \kappa_a \cdot \left| -\int_0^A \beta(a,\tilde{a})\frac{f(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a} - \left(-\int_0^A \beta(a,\tilde{a})\frac{g(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right)\right| \cdot s_0(a)\\ =& \kappa_a \cdot \left| -\int_0^A \frac{\beta(a,\tilde{a})}{\gamma(\tilde{a})}(f(\tilde{a}) - g(\tilde{a}))\,\mathrm{d}\tilde{a}\right| \cdot s_0(a)\,.\end{aligned}$$

Now, we can apply the mean value theorem for integrals which gives us a value $y_a \in [0,A]$ depending on a such that

$$|\tilde{\mathcal{T}}(f)(a) - \tilde{\mathcal{T}}(g)(a)| = \kappa_a\,|f(y_a) - g(y_a)| \int_0^A s_0(a)\frac{\beta(a,\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\,.$$

Clearly, if we regard the maximum over all $a \in [0,A]$, we then have

$$\begin{aligned}\|\tilde{\mathcal{T}}(f) - \tilde{\mathcal{T}}(g)\|_\infty \leq& \max_{a\in[0,A]} \kappa_a \cdot \max_{a\in[0,A]} \int_0^A s_0(a)\frac{\beta(a,\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a} \cdot \max_{y\in[0,A]} |f(y) - g(y)|\\ \leq& \kappa \cdot \max_{a\in[0,A]} \int_0^A p(a)\frac{\beta(a,\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a} \cdot \|f-g\|_\infty\\ <& L\cdot\|f-g\|_\infty\end{aligned}$$

where $\kappa \coloneqq \max_{a\in[0,A]} \kappa_a < 1$ and L is defined as above in Equation (3.19).

In order to show that $\mathrm{im}(\tilde{\mathcal{T}})$ is contained in a compact subset of $\tilde{\mathcal{K}}$ we formulate an intermediate result, which may be found in [6], Theorem D.1.3.3. The required definition is found in Definition D.1.3.1 of the same source.

Definition 3.5.2 (Equicontinuity)**.** Let $(\mathcal{V},d)$ and $(\mathcal{W},\tilde{d})$ be metric spaces, $\emptyset \neq \mathcal{A} \subseteq \mathcal{V}$ and $(g_n\colon \mathcal{A}\to\mathcal{W})_{n\in\mathbb{N}}$ a family of functions. Let $a \in \mathcal{A}$ and $\varepsilon > 0$. Assume there exists a $\delta > 0$ such that for every $n \in \mathbb{N}$ and all $\tilde{a} \in \mathcal{A}$ we have that $d(a,\tilde{a}) < \delta$ implies $\tilde{d}(g_n(a), g_n(\tilde{a}) < \varepsilon$. Then the family $(g_n)_{n\in\mathbb{N}}$ is called **(uniformly) equicontinuous**.

Theorem 3.5.3 (Arzelà-Ascoli)**.** *Let $(\mathcal{V},d)$ and $(\mathcal{W},\tilde{d})$ be metric spaces, $\emptyset \neq \mathcal{A} \subseteq \mathcal{V}$ a compact set and $(g_n\colon \mathcal{A}\to\mathcal{W})_{n\in\mathbb{N}}$ an equicontinuous sequence of functions. Furthermore, let $\mathcal{B} \subseteq \mathcal{W}$ be compact and let $g_n(\mathcal{A}) \subseteq \mathcal{B}$ for all $n \in \mathbb{N}$. Then the sequence $(g_n)_{n\in\mathbb{N}}$ has a subsequence which converges uniformly.*

Consider $(\mathcal{V},d) \coloneqq (\mathcal{W},\tilde{d}) \coloneqq (\mathbb{R},|\cdot|)$, $\mathcal{A} \coloneqq [0,A]$ and $\mathcal{B} \coloneqq [0,1]$. If $(g_n \coloneqq \tilde{\mathcal{T}}(f_n))_{n\in\mathbb{N}}$ is a sequence in $\mathrm{im}(\tilde{\mathcal{T}})$, then $g_n([0,A]) \subseteq [0,1]$ as $\|g_n\|_\infty \leq 1$ and $g_n \geq 0$ for all $n \in \mathbb{N}$.

Assume additionally that s_0, i_0 and π_k (for all $k \in \{1, 2, ...K\}$) are continuously differentiable. Also, remember that π_k in the definition of β (see Equation (3.1)) is defined on a compact domain for all $k \in \{1, 2, ..., K\}$. Hence, there exist $B_1 > 0$, $B_2 > 0$ and $\tilde{b}_k > 0$ such that

$$\begin{aligned} \|s_0'\|_\infty \leq & B_1 \,, \\ \|i_0'\|_\infty \leq & B_2 \quad \text{and} \\ \|\pi_k'\|_\infty \leq & \tilde{b}_k \end{aligned}$$

for all $k \in \{1, 2, ..., K\}$. Then for $a, \tilde{a} \in [0, A]$ and $B_3 \coloneqq \sum_{k=1}^{K} \beta_k \tilde{b}_k \|\pi_k\|_\infty$ we have

$$\begin{aligned} \left| \frac{\partial \beta}{\partial a}(a, \tilde{a}) \right| &= \left| \sum_{k=1}^{K} \beta_k \pi_k'(a) \pi_k(\tilde{a}) \right| \\ &\leq \sum_{k=1}^{K} \beta_k \tilde{b}_k \|\pi_k\|_\infty = B_3 \,. \end{aligned}$$

For general $\beta \colon \mathcal{C}([0, A]) \times \mathcal{C}([0, A]) \to [0, \infty[$, just assume that β is continuously differentiable in the first variable as then there exists a $B_3 > 0$ with $\left\| \frac{\partial \beta}{\partial a} \right\|_\infty \leq B_3$.
We get for $g_n = \tilde{\mathcal{T}}(f_n) \in \tilde{\mathcal{K}}$ and arbitrary $a \in [0, A]$ that

$$\begin{aligned} |g_n'(a)| = & \left| \left(1 - \exp\left(- \int_0^A \beta(a, \tilde{a}) \frac{f_n(\tilde{a})}{\gamma(\tilde{a})} \, \mathrm{d}\tilde{a} \right) \right) \cdot s_0'(a) - \right. \\ & \left. - \exp\left(- \int_0^A \beta(a, \tilde{a}) \frac{f_n(\tilde{a})}{\gamma(\tilde{a})} \, \mathrm{d}\tilde{a} \right) \cdot \left(- \int_0^A \frac{\partial \beta}{\partial a}(a, \tilde{a}) \frac{f_n(\tilde{a})}{\gamma(\tilde{a})} \, \mathrm{d}\tilde{a} \right) \cdot s_0(a) + i_0'(a) \right| \\ \leq & |s_0'(a)| + \int_0^A |\beta'(a, \tilde{a})| \frac{f_n(\tilde{a})}{\gamma(\tilde{a})} \, \mathrm{d}\tilde{a} + |i_0'(a)| \\ \leq & B_1 + B_3 \int_0^A \frac{f_n(\tilde{a})}{\gamma(\tilde{a})} \, \mathrm{d}\tilde{a} + B_2 \\ \leq & B_1 + B_3 \int_0^A \frac{1}{\gamma(\tilde{a})} \, \mathrm{d}\tilde{a} + B_2 \\ \leq & B_4 \,, \end{aligned}$$

for some constant $B_4 > 0$.
Now, let $\varepsilon > 0$ and $a, \tilde{a} \in [0, A]$. Without loss of generality, $a < \tilde{a}$. Define $\delta \coloneqq \frac{\varepsilon}{B_4}$. By the mean value theorem, there exists an $\hat{a} \in [a, \tilde{a}]$ such that

$$|g_n(a) - g_n(\tilde{a})| = |g_n'(\hat{a})||a - \tilde{a}| \leq B_4 |a - \tilde{a}| \,.$$

Now, if $|a - \tilde{a}| < \delta$, then $|g_n(a) - g_n(\tilde{a})| < \varepsilon$. Hence, the sequence $(g_n)_{n \in \mathbb{N}}$ is equicontinuous.

By the theorem of Arzelà-Ascoli, each sequence in $\mathrm{im}(\tilde{\mathcal{T}})$ has a subsequence which converges uniformly. As all g_n are continuous, also the limit is continuous (see [5], Theorem 8.8.4), and hence, lies in $\mathcal{C}([0, A])$. Thus, $\mathrm{im}(\tilde{\mathcal{T}})$ is a sequentially compact subset of $\tilde{\mathcal{K}}$, that is, for every sequence there exists a convergent subsequence (see [4], Definition 10.34). But in metric spaces, sequential compactness is equivalent to compactness (see [4], Theorem 10.43). So, $\mathrm{im}(\tilde{\mathcal{T}})$ is a compact set.

All conditions of the Schauder fixed-point theorem are satisfied. This implies that there exists a continuous function $r_\infty : [0, A] \to [0, 1]$ satisfying Equation (3.17), which gives the density of recovered individuals at the end of the epidemic.

3.5.2. Uniqueness

In order to analyze uniqueness, we will use Banach fixed-point theorem which can be found, together with a proof, in [5], Theorem 8.7.7. In this case, it suffices to analyze the case in which $\tilde{\mathcal{T}}$ is a contraction, that is, when there exists a $q \in [0, 1[$ such that

$$d_\infty(\tilde{\mathcal{T}}(f), \tilde{\mathcal{T}}(g)) \leq q \cdot d_\infty(f, g)$$

for all $f, g \in \tilde{\mathcal{K}}$.

Theorem 3.5.4 (Banach Fixed Point Theorem)**.** *Let $(\mathcal{V}, d)$ be a non-empty complete metric space with a contraction mapping $\mathcal{F}\colon \mathcal{V} \to \mathcal{V}$. Then $\mathcal{F}$ admits a unique fixed-point $\tilde{x}$ in $\mathcal{V}$, i.e., $\mathcal{F}(\tilde{x}) = \tilde{x}$.*
Furthermore, $\tilde{x}$ can be found as follows: start with an arbitrary element $x_0 \in \mathcal{V}$ and iteratively define a sequence $(x_n)_{n\in\mathbb{N}}$ by $x_{n+1} = \mathcal{F}(x_n)$ for $n \in \mathbb{N}$. Then

$$\lim_{n\to\infty} x_n = \tilde{x}\,.$$

As already shown in Section 3.5.1, the function $\tilde{\mathcal{T}}$ on the metric space $\tilde{\mathcal{K}}$ is Lipschitz-continuous with Lipschitz constant $\kappa \cdot L$, where $\kappa < 1$ and

$$L = \max_{a\in[0,1]} \int_0^A p(a) \frac{\beta(a, \tilde{a})}{\gamma(\tilde{a})}\, \mathrm{d}\tilde{a}\,.$$

In order to see when $\tilde{\mathcal{T}}$ is a contraction, hence, it suffices to analyze in which case we have $L \leq 1$. If this is the case, then by Equation (3.12), the epidemic will not break out. Since the functions p, β and γ depend on the actual situation, we will not delve further into this subject.
If $L \leq 1$, one can use $r_\infty(a) = i_0(a)$ as a first approximation.

3.6. Maximum Fraction of Infected Individuals

Since the model takes multiple factors into account, it is complicated to calculate the maximum number of infected individuals. However, we can show some weak results: If

the mean age of the infected individuals $\bar{a}_{\boldsymbol{\mathcal{I}}}$ changes at the maximum number of infected individuals, then the peaks of the corresponding ages for the infected individuals are shifted and do not fall on the same time instance.
Assume there exists

$$\hat{T} \in \operatorname*{arg\,max}_{t\in[0,\infty[} I(t)$$

with $\frac{\mathrm{d}I}{\mathrm{d}t}(\hat{T}) = 0$, i.e., a maximum occurs not only at the beginning of the epidemic. Let

$$I_{\max} \coloneqq \max_{t\in[0,\infty[} I(t) = I(\hat{T})\,.$$

In the following, we pose the quite restrictive assumption that such a $\hat{T}$ is unique. One is able to show numerically for the discrete case that this assumption may not hold.
We have that S, I, R, s, i and r are continuously differentiable.
Suppose that the peaks of $i(a,\cdot)$ coincide in time, that is,

$$\tilde{t}(a) \coloneqq \operatorname*{arg\,max}_{t\in[0,\infty[} i(a,t) = \hat{t}$$

is constant. Then $\frac{\partial i}{\partial t}(a,\hat{t}(a)) = 0$ and for all $t \in [0,\infty[$ we have

$$i(a,t) \le i(a,\hat{t})\,.$$

Hence,

$$I(t) = \int_0^A i(a,t)\,\mathrm{d}a \le \int_0^A i(a,\hat{t})\,\mathrm{d}a = I(\hat{T})\,,$$

for all $t \in [0,\infty[$. Since $\hat{T}$ gives the unique maximum of I, we need

$$\hat{t} = \hat{T}\,.$$

Now,

$$\bar{a}_{\boldsymbol{\mathcal{I}}}(t) = \mathbb{E}[Y \mid Z(t) = \boldsymbol{\mathcal{I}}] = \frac{1}{I(t)}\int_0^A a\cdot i(a,t)\,\mathrm{d}a$$

and

$$\begin{aligned}\frac{\mathrm{d}\bar{a}_{\boldsymbol{\mathcal{I}}}}{\mathrm{d}t}(\hat{T}) =& \frac{\mathrm{d}}{\mathrm{d}t}\left(\frac{1}{I(t)}\int_0^A a\cdot i(a,t)\,\mathrm{d}a\right)(\hat{T})\\ =& \left(\int_0^A a\cdot\frac{\partial i}{\partial t}(a,\hat{T})\,\mathrm{d}a\cdot I(\hat{T}) - \frac{\mathrm{d}I}{\mathrm{d}t}(\hat{T})\cdot\int_0^A a\cdot i(a,\hat{T})\,\mathrm{d}a\right)\cdot\left(\frac{1}{I(t)}\right)^2 = 0\end{aligned}$$

as both $\frac{\partial i}{\partial t}(a,\hat{T}) = 0$ and $\frac{\mathrm{d}I}{\mathrm{d}t}(\hat{T}) = 0$ hold by the definition of $\hat{T}$.
Hence, the expected age in the infected compartment does not change at the point where the number of infected individuals is maximized.
This shows that if $\bar{a}_{\boldsymbol{\mathcal{I}}}$ changes, then also $\hat{t}(a)$ has to change, i.e., not stay constant.
However, it may be that the peaks are shifted and still $\frac{\mathrm{d}\bar{a}_{\boldsymbol{\mathcal{I}}}}{\mathrm{d}t}(\hat{T}) = 0$. Also, the question remains if the case $\frac{\mathrm{d}\bar{a}_{\boldsymbol{\mathcal{I}}}}{\mathrm{d}t}(\hat{T}) \neq 0$ can occur. It may be shown numerically that such scenarios are possible.

4. Discrete Model and Numerical Simulations

In this section, the extended model will be discretized and some numerical calculations as example how to apply it are done.

4.1. Discretization

In order to make it possible to solve the system of integro-differential equations (3.2)-(3.4) numerically, it suffices to discretize the age. For this purpose, we split the interval $[0, A]$ in $J \in \mathbb{N}$ (possibly equidistant) intervals $\mathcal{I}_j \subseteq [0, A]$ which are disjoint except possibly for the endpoints. We get

$$[0, A] = \bigcup_{j=1}^{J} \mathcal{I}_j \,.$$

Then for $j \in \{1, 2, ..., J\}$, the quantity

$$\tilde{p}_j \coloneqq \int_{\mathcal{I}_j} p(a)\,\mathrm{d}a$$

gives the probability of having an age in the interval $\mathcal{I}_j \subseteq [0, A]$ for $j \in \{1, 2, ..., J\}$. In the following, we refer to such an interval $\mathcal{I}_j$ also as age group j. The quantities

$$\begin{aligned} s_j(t) &\coloneqq \int_{\mathcal{I}_j} s(a,t)\,\mathrm{d}a\,, \\ i_j(t) &\coloneqq \int_{\mathcal{I}_j} i(a,t)\,\mathrm{d}a \quad \text{and} \\ r_j(t) &\coloneqq \int_{\mathcal{I}_j} r(a,t)\,\mathrm{d}a \end{aligned}$$

give the probabilities of an individul being in a certain state and of age group j, for $j \in \{1, 2, ..., J\}$. The probabilities of an individual being susceptible, infected and recov-

ered, respectively, become

$$\tilde{S}(t) = \sum_{j=1}^{J} s_j(t)\,,$$

$$\tilde{I}(t) = \sum_{j=1}^{J} i_j(t) \quad \text{and}$$

$$\tilde{R}(t) = \sum_{j=1}^{J} r_j(t)\,.$$

In order to take into account the higher fraction of individuals of a certain age, the following quantities are defined with the help of a weighted mean.
The participation rate at a certain activity $k \in \{1, 2, ..., K\}$ for age group $j \in \{1, 2, ..., J\}$ is

$$\tilde{\pi}_k(j) = \int_{\mathcal{I}_j} p(a)\pi_k(a)\,\mathrm{d}a$$

and the infection rate between individuals of age group $j \in \{1, 2, ..., J\}$ and age group $m \in \{1, 2, ..., J\}$ becomes

$$\tilde{\beta}(j, m) = \sum_{k=1}^{K} \beta_k \tilde{\pi}_k(j)\tilde{\pi}_k(m)\,.$$

Also, the recovery rate is

$$\tilde{\gamma}_j \coloneqq \int_{\mathcal{I}_j} p(a)\gamma(a)\,\mathrm{d}a\,.$$

For later use, let $\tilde{\gamma} := (\tilde{\gamma}_1, \tilde{\gamma}_2, ..., \tilde{\gamma}_J)$.
In the end, the discretized model reads

$$\frac{\mathrm{d}s_j}{\mathrm{d}t}(t) = -\, s_j(t) \cdot \sum_{m=1}^{J} \tilde{\beta}(j, m) i_m(t)\,, \tag{4.1}$$

$$\frac{\mathrm{d}i_j}{\mathrm{d}t}(t) = s_j(t) \cdot \sum_{m=1}^{J} \tilde{\beta}(j, m) i_m(t) - \tilde{\gamma}_j i_j(t) \quad \text{and} \tag{4.2}$$

$$\frac{\mathrm{d}r_j}{\mathrm{d}t}(t) = \tilde{\gamma}_j i_j(t)\,, \tag{4.3}$$

for $j \in \{1, 2, ..., J\}$, with initial values

$$s_{j,0} = \int_{\mathcal{I}_j} s_0(a)\,\mathrm{d}a\,,$$

$$i_{j,0} = \int_{\mathcal{I}_j} i_0(a)\,\mathrm{d}a \quad \text{and}$$

$$r_{j,0} = \int_{\mathcal{I}_j} r_0(a)\,\mathrm{d}a\,.$$

Here, the assumptions

$$\begin{aligned} \gamma(a) &\approx \tilde{\gamma}_j \,, \\ \pi_k(a) &\approx \tilde{\pi}_k(j) \quad \text{and} \\ \beta(a, \tilde{a}) &\approx \tilde{\beta}(j, m) \end{aligned}$$

have been used, where $j, m \in \{1, 2, ..., J\}$ and $a \in \mathcal{I}_j, \tilde{a} \in \mathcal{I}_m$.
As in the continuous case, the only equilibrium is the disease-free one. For

$$\tilde{p} \coloneqq (\tilde{p}_1, \tilde{p}_2, ..., \tilde{p}_J)$$

it can be written as $(\tilde{p}, 0, 0)$.
By doing the analogue to calculation in Section 3.5, one gets the equation

$$r_{j,\infty} = \left(1 - \exp\left(-\sum_{m=1}^{J} \tilde{\beta}(j, m) \frac{\pi_{m,\infty}}{\tilde{\gamma}_m}\right)\right) \cdot s_{j,0} + i_{j,0} \,,$$

for $j \in \{1, 2, ..., J\}$ for the overall fraction of infected individuals. This can be solved numerically.

4.1.1. Basic Reproduction Rate

There exist various ways to calculate basic reproduction rates of discrete models. One of the most famous is the so-called next generation approach. Following personal correspondence with professor Schmeiser, the author received an approach for the discrete case employing the Perron-Frobenius theorem, which in a more general form is also applicable to the continuous case (see Section 3.4.2). However, both approaches give the same threshold for the stability of the disease-free equilibrium.

Next Generation Approach

Following the so-called next generation approach in [15], one can calculate a basic reproduction rate for the discrete setting for a general number of activities K.
We define two matrices $F, G \in \mathbb{R}^{J \times J}$ in the following. For an infected individual introduced into compartment i_m ($m \in \{1, 2, ..., J\}$) of a disease free population, let $(G_{j,m})^{-1}$ give the average length of time this individual spends in compartment j during their lifetime. The entry $F_{j,m}$ gives the rate at which an infected individual of compartment i_m produces new infections in compartment i_j, still in an otherwise disease free population. Recall that $\tilde{\gamma} := (\tilde{\gamma}_1, \tilde{\gamma}_2, ..., \tilde{\gamma}_J)$. Hence, we have

$$G = \operatorname{diag}(\tilde{\gamma})$$

and

$$F = \left(\tilde{p}_j \beta(j, m)\right)_{j,m \in \{1,2,...J\}} \,.$$

The matrix $P := FG^{-1}$ is called the next generation matrix. It gives the expected number of new infections in compartment i_j produced by an infected individual originally introduced into compartment i_m. Its largest eigenvalue in absolute values can be interpreted as a reproduction number, i.e.,

$$\tilde{\mathcal{R}}_0 := \varrho(P). \tag{4.4}$$

One can show (see Theorem 2 in [15]) that this indeed gives a threshold for the stability of the disease-free equilibrium.

Alternative Approach with Theorem by Perron

The following approach is based on an elegant method professor Schmeiser communicated to the author about how to follow that $\tilde{\mathcal{R}}_0 = \varrho(P)$ is a basic reproduction rate.
As in the next generation approach, let $G := \mathrm{diag}(\tilde{\gamma}) \in \mathbb{R}^{J\times J}$ and $F \in \mathbb{R}^{J\times J}$ defined by $F_{j,m} := \tilde{p}_j\beta(j,m)$. Then for $i(t) := (i_1(t), i_2(t), ..., i_J(t))$ we have $(G \cdot i(t))_j = \tilde{\gamma}_j i_j$ and

$$(F \cdot i(t))_j = \sum_{m=1}^{J} F_{j,m} i_m(t) = \sum_{m=1}^{J} \tilde{p}_j\beta(j,m) i_m(t) = \tilde{p_j} \sum_{m=1}^{J} \beta(j,m) i_m(t)\,.$$

Here, as in the continuous case, it suffices to look only at the linearization of Equation (4.2) around the disease-free equilibrium $(\tilde{p}, 0, 0)$. We get

$$\frac{\partial i_j}{\partial t}(t) = \tilde{p}_j \sum_{m=1}^{J} \beta(j,m) i_m(t) - \tilde{\gamma}_j i_j(t) = ((F-G)(i(t)))_j\,.$$

Hence,

$$\frac{\partial i}{\partial t}(t) = (F-G)(i(t))\,.$$

As in the continuous case, the stability of a hyperbolic equilibrium is determined by the eigenvalues of the Jacobian matrix, as is given by the Hartman-Grobman-Theorem. However, the disease-free equilibrium $(\tilde{p}, 0, 0)$ is not hyperbolic. Nevertheless, we will analyze the eigenvalues of the Jacobian matrix $F - G$ in order to gain knowledge about spectral stability. Hence, we consider the eigenvalue problem

$$(F-G)v = \lambda v\,.$$

Define $\tilde{\Gamma} := \max\{\tilde{\gamma}_1, \tilde{\gamma}_2, ..., \tilde{\gamma}_J\}$. Clearly, the matrix $F-G+\tilde{\Gamma}\cdot\mathrm{id}$ is positive, that is, every entry is positive. Hence, we can apply the theorem by Perron (see [8], Theorem 8.2.8), a specialized version of the widely known theorem by Perron-Frobenius.

Theorem 4.1.1 (Perron)**.** *Let $A \in \mathbb{R}^{n\times n}$ be positive. Then*

- $\varrho(A) > 0$
- $\varrho(A)$ *is an algebraically simple eigenvalue of* A

- *There is a unique real vector* $v \in \mathbb{R}^n$ *such that* $Av = \varrho(A)v$ *and* $v_1+v_2+...+v_n = 1$. *This vector is positive.*
- *There exists a unique real vector* $w \in \mathbb{R}^n$ *such that* $w^{\mathrm{T}}A = \varrho(A)w^{\mathrm{T}}$ *and that* $v_1w_1 + v_2w_2 + ... + v_nw_n = 1$. *This vector is positive.*
- $\lambda < \varrho(A)$ *for every* $\lambda \in \mathrm{spec}(A)\backslash\{\varrho(A)\}$.
- $(\varrho(A)^{-1}A)^n \to vw^{\mathrm{T}}$ *as* $n \to \infty$.

Hence, $\varrho(F-G+\tilde{\Gamma}\cdot\mathrm{id})$ is a simple eigenvalue of $F-G+\tilde{\Gamma}\cdot\mathrm{id}$. Let $\hat{v}$ be the corresponding, positive and normalized right eigenvector. Hence,

$$\begin{aligned}(F-G)\hat{v} =&(F-G+\tilde{\Gamma}\cdot\mathrm{id})\hat{v} - \tilde{\Gamma}\cdot\mathrm{id}\hat{v}\\ =&\varrho(F-G+\tilde{\Gamma}\cdot\mathrm{id})\hat{v} - \tilde{\Gamma}\hat{v}\\ =&(\varrho(F-G+\tilde{\Gamma}\cdot\mathrm{id}) - \Gamma)\hat{v}\end{aligned}$$

and $\tilde{\lambda} \coloneqq \varrho(F-G+\tilde{\Gamma}\cdot\mathrm{id})-\tilde{\Gamma}$ is the unique eigenvalue of $F-G$ with largest real part and corresponding eigenvector $\hat{v}$. Since the characteristic equation of $F-G$ and $(F-G)^{\mathrm{T}}$ is the same ($\det(A) = \det(A^{\mathrm{T}})$ for an arbitrary matrix A), also the eigenvalues are the same. Hence, there exists a positive vector $\tilde{v} \in \mathbb{R}^n$ by the same reasoning as above such that

$$(F-G)^{\mathrm{T}}\tilde{v} = \tilde{\lambda}\tilde{v}\,.$$

Now, also the matrix $P = FG^{-1}$ is positive and hence, its spectral radius is a positive eigenvalue. Let $\hat{w}$ be a corresponding positive eigenvector. Then

$$FG^{-1}\hat{w} = \varrho(P)\hat{w}\,.$$

Define $\tilde{w} \coloneqq G^{-1}\hat{w}$ which is positive. This implies

$$F\tilde{w} = \varrho(P)G\tilde{w}$$

and

$$\begin{aligned}\tilde{\lambda}\tilde{v}^{\mathrm{T}}\tilde{w} =&(\tilde{\lambda}\tilde{v})^{\mathrm{T}}\tilde{w}\\ =&((F-G)^{\mathrm{T}}\tilde{v})^{\mathrm{T}}\tilde{w}\\ =&\tilde{v}^{\mathrm{T}}(F-G)\tilde{w} = \tilde{v}^{\mathrm{T}}(F\tilde{w} - G\tilde{w})\\ =&\tilde{v}^{\mathrm{T}}(\varrho(P)G\tilde{w} - G\tilde{w})\\ =&\tilde{v}^{\mathrm{T}}(\varrho(P)-1)G\tilde{w}\\ =&(\varrho(P)-1)\tilde{v}^{\mathrm{T}}G\tilde{w}\\ =&(\varrho(P)-1)\tilde{v}^{\mathrm{T}}\hat{w}\,.\end{aligned}$$

As $\tilde{v}^{\mathrm{T}}\tilde{w} > 0$ and $\tilde{v}^{\mathrm{T}}\hat{w} > 0$ (remember that $\tilde{v}$, $\tilde{w}$ and $\hat{w}$ are positive), we have

$$\mathrm{sign}(\tilde{\lambda}) = \mathrm{sign}(\varrho(P)-1)\,,$$

and $\tilde{\mathcal{R}}_0 = \varrho(P)$ determines the spectral stability of the disease-free equilibrium. However, this does not yet imply stability. Nevertheless, stability has been shown via another approach in Section 4.1.1.

Estimation of the Spectral Radius

In the following, some calculations are done, in order to get an idea how one could estimate the basic reproduction rate $\tilde{\mathcal{R}}_0 = \varrho(P)$ from before.
First of all, the matrix G can easily be inverted as it is a diagonal matrix in order to get

$$G^{-1} = \operatorname{diag}\left((\tilde{\gamma}_j^{-1})_{j\in\{1,2,...,J\}}\right) .$$

Then we have

$$P_{j,m} = \tilde{p}_j \frac{\tilde{\beta}(j,m)}{\tilde{\gamma}_m}$$

for $j, m \in \{1, 2, ..., J\}$.
If there is only one age group ($J = 1$), then the matrix P simplifies to the simple number $\tilde{\chi}$ from Definition (4.5). In the case $J = 2$, it is quite easy to derive a formula for the spectral radius.
Also for $J = 3$ and $J = 4$, such a calculation would be possible as there exists an analytic formula to solve for the zeroes of the characteristic equation. However, it is much more complicated.
For the cases $J \geq 5$, analogous calculations generally are not possible anymore as there does not exist an analytic formula for the zeroes of a general polynom of degree greater than 4. This is the statement of Abel–Ruffini theorem (see [18]).

For general $\tilde{\beta}$, the spectral radius of P can not be simplified further. However, in our case and under the assumption $K \leq J$ (less activities than age groups) we can, using the definition of $\tilde{\beta}$, rewrite P as

$$\begin{aligned} P_{j,m} =& \frac{\tilde{p}_j}{\tilde{\gamma}_m} \sum_{k=1}^{K} \beta_k \tilde{\pi}_k(j) \tilde{\pi}_k(m) \\ =& \sum_{k=1}^{K} \tilde{p}_j \sqrt{\beta_k} \pi_k(j) \cdot \frac{1}{\tilde{\gamma}_m} \sqrt{\beta_k} \pi_k(m) \\ =& \sum_{k=1}^{K} M_{j,k} \cdot N_{k,m} = (M \cdot N)_{j,m} \end{aligned}$$

where $M \in \mathbb{R}^{J\times K}$ and $N \in \mathbb{R}^{K\times J}$ are defined for $j \in \{1, 2, ..., J\}$, $k \in \{1, 2, ..., K\}$ by

$$\begin{aligned} M_{j,k} =& \tilde{p}_j \sqrt{\beta_k} \pi_k(j) \quad \text{and} \\ N_{k,j} =& \frac{1}{\tilde{\gamma}_j} \sqrt{\beta_k} \pi_k(j) . \end{aligned}$$

We know that the set of all eigenvalues does not change under commutation of the matrices (see Theorem A.1.4), possibly with less or additional zeroes. Thus, the spectral radius of $P = M \cdot N$ is the same as of $Q \coloneqq N \cdot M$. Hence, we get

$$\tilde{\mathcal{R}}_0 = \varrho(P) = \varrho(Q) .$$

But Q is sometimes of smaller dimension than P, as P has dimension at most J while Q has dimension at most K. Hence, it may be easier to calculate the spectral radius of Q than the one of P.

We are able to bound the basic reproduction number from above. First, we need to calculate the trace of P and get

$$\begin{aligned}\operatorname{tr}(P) &= \sum_{j=1}^{J} P_{j,j} \\ &= \sum_{j=1}^{J} \frac{\tilde{p}_j}{\tilde{\gamma}_j} \sum_{k=1}^{K} \beta_k \tilde{\pi}_k(j) \tilde{\pi}_k(j) \\ &= \sum_{j=1}^{J} \frac{\tilde{p}_j}{\tilde{\gamma}_j} \tilde{\beta}(j,j)\,.\end{aligned}$$

Define

$$\tilde{\chi} \coloneqq \sum_{j=1}^{J} \frac{\tilde{p}_j}{\tilde{\gamma}_j} \tilde{\beta}(j,j) = \operatorname{tr}(P)\,, \tag{4.5}$$

which is the analogue definition of (3.9).
Also, we can rewrite Q as

$$\begin{aligned}Q_{k,\tilde{k}} &= \sum_{j=1}^{J} N_{k,j} M_{j,\tilde{k}} \\ &= \sum_{j=1}^{J} \frac{\tilde{p}_j}{\tilde{\gamma}_j} \sqrt{\beta_k \beta_{\tilde{k}}}\, \tilde{\pi}_k(j) \tilde{\pi}_{\tilde{k}}(j) \\ &= \sum_{j=1}^{J} \sqrt{\frac{\tilde{p}_j}{\tilde{\gamma}_j} \beta_k}\, \tilde{\pi}_k(j) \cdot \sqrt{\frac{\tilde{p}_j}{\tilde{\gamma}_j} \beta_{\tilde{k}}}\, \tilde{\pi}_{\tilde{k}}(j)\,,\end{aligned}$$

for $k, \tilde{k} \in \{1, 2, ..., K\}$.
One easily sees that Q is symmetric and positive. Defining $D \in \mathbb{R}^{J \times K}$ by

$$D_{j,k} \coloneqq \sqrt{\frac{\tilde{p}_j}{\tilde{\gamma}_j} \beta_k}\, \tilde{\pi}_k(j)$$

for $j \in \{1, 2, ..., J\}$, $k \in \{1, 2, ..., K\}$, we get

$$Q = D^{\mathrm{T}} \cdot D\,.$$

Hence, Q is positive semi-definite. But this implies also that all eigenvalues are real and non-negative (see Theorem A.1.7 for both implications). The same holds, therefore, for P.

With this, we can bound the spectral radius of P from above: The trace of a matrix equals the sum of its eigenvalues (see Theorem A.1.3). Let $\lambda_1, \lambda_2, ..., \lambda_K$ be the K eigenvalues of Q, counted with multiplicity. Since all of these are non-negative in our case, we get

$$\tilde{\mathcal{R}}_0 = \varrho(P) \leq \sum_{k=1}^{K} \lambda_k = \mathrm{tr}(P) = \tilde{\chi}\,. \tag{4.6}$$

However, if there is equality, then all other eigenvalues have to be 0. This means nothing else than that P has rank 1. But then P has to be the product of the transpose of a vector with another vector. This would be the case, for example, if $\pi_k(j) = \mu(k) \cdot \nu(j)$ for all $k \in \{1, 2, ..., K\}$ and $j \in \{1, 2, ...J\}$, which is not very realistic as explained in Section 3.4.1. Hence, normally we will get $\varrho(P) < \tilde{\chi}$. The only exception is $K = 1$, where clearly $\varrho(P) = \tilde{\chi}$.
However, if $\tilde{\chi} < 1$, then also $\tilde{\mathcal{R}}_0 < 1$ and there will be no outbreak.

We also have the lower bound

$$\varrho(P) \geq \frac{\tilde{\chi}}{K - m}\,,$$

where $m \in \mathbb{N}$ is at most the multiplicity of the possible eigenvalue 0. If this bound would not hold, then

$$\tilde{\chi} = \sum_{k=1}^{K} \lambda_k \leq (K - m) \cdot \varrho(P) < \tilde{\chi}\,,$$

which clearly cannot be the case. This bound is not sharp but may be useful for large $\tilde{\chi}$. The largest eigenvalue can, for example, be determined with the help of Theorem A.1.5

$$\varrho(P) = \max_{\substack{v \neq 0 \\ \|v\|_2 = 1}} v^{\mathrm{T}} P v\,.$$

The maximum can then be found by defining the Lagrange-function

$$f(v, \lambda) \coloneqq v^{\mathrm{T}} P v + \lambda(1 - \|v\|_2^2)$$

and differentiating with respect to each component

$$\frac{\partial f}{\partial v_{\tilde{k}}}(\lambda, v)$$

and with respect to λ, which gives

$$\frac{\partial f}{\partial \lambda}(v, \lambda) = 1 - \|v\|_2^2\,.$$

We set this equal to 0 for every component. The derivative for λ gives us the condition of a normalized vector. Hence, the calculation of the spectral radius simplifies to find the zeroes of the above functions.

age group j	age	$\tilde{\gamma}$ starting on 28^{th} April 2020	17^{th} June 2020	12^{th} February 2021
1	< 5 years	0,061	0,075	0,062
2	$5 - 14$ years	0,060	0,072	0,061
3	$15 - 24$ years	0,066	0,062	0,061
4	$25 - 34$ years	0,076	0,063	0,060
5	$35 - 44$ years	0,070	0,064	0,059
6	$45 - 54$ years	0,070	0,057	0,060
7	$55 - 614$ years	0,063	0,056	0,059
8	$65 - 74$ years	0,044	0,037	0,055
9	$75 - 84$ years	0,040	0,029	0,050
10	> 84 years	0,034	0,017	0,051

Table 4.1.: Age groups and mean daily recovery rates for three time periods of each 50 days.

4.2. Example Calculations

In this chapter, some example calculations with fictional functions $\tilde{\pi}_k$ for $k \in \{1, 2, ..., K\}$, $\tilde{\gamma}$ and fictional parameters β_k for $k \in \{1, 2, ..., K\}$ are done. These are then compared with data from Austria which can be found on `https://covid19-dashboard.ages.at/`. The used table, named "CovidFaelle_Altersgruppe.csv", is from the 3^{rd} of January, 2023. Dead individuals are shifted to the recovered compartment, as this model does not differ between these two groups. Here, the $J = 10$ age groups are given as in Table 4.1.
In order to perform a numerical simulation, we assume the parameters are given as in Table 4.2. There are given $K = 6$ activities with the corresponding infection and particitation rates.
These values do not come from any real data but are chosen through an educated guess. The reason is that for the exact age groups given in the data of the corona virus, it is hard to find these parameters. Especially, the infection rates β_k are hard to estimate and no data for these can be found. Hence, these parameters may be by no means realistic and the model might not give any valuable results. However, we will see that the model nevertheless perform quite well.
In order to allow for different basic reproduction rates, the β_k's are scaled accordingly after calculating the spectral radius of the matrix P, defined as in Section 4.1.1. With the given values as in Table 4.2, we get a spectral radius of the matrix P of 731.06.
For each time period, the recovery rates are calculated from the given data as the mean daily recovery rate

$$\frac{r(a, t+1) - r(a)}{i(a, t)}$$

over the whole period. The probabilty for having a certain age is calculated as the relative part of the population that did not recover yet, i.e., we ignore individuals which already

$\mathcal{A}_k$	school	night club	retirement home	family	friends and hobbies	office
k	1	2	3	4	5	6
β_k	2	10	4	4	3	1
$\tilde{\pi}_k(1)$	0	0	0	2	1	0
$\tilde{\pi}_k(2)$	5	1	0	4	2	0
$\tilde{\pi}_k(3)$	2	3	0	1	4	1
$\tilde{\pi}_k(4)$	0.5	2	0	2	3	1
$\tilde{\pi}_k(5)$	0	0.5	0	3	3	3
$\tilde{\pi}_k(6)$	0	0	0	2	2	2
$\tilde{\pi}_k(7)$	0	0	0.5	1	2	2
$\tilde{\pi}_k(8)$	0	0	2	0.5	1	0.5
$\tilde{\pi}_k(9)$	0	0	3	0.5	0.5	0
$\tilde{\pi}_k(10)$	0	0	5	1	0.5	0

Table 4.2.: Possible activities and their rates.

recovered from the disease at the start of each simulated period.

Clearly, the extended model does not model lockdowns and other restrictions which may lower the basic reproduction rate significantly. Also, the behavior of people can change significantly if the disease spreads. Hence, the model may be good only for some small time periods. The simulation has been executed for every tenth day, out of practical reasons and because the number of infected individuals does not change significantly from one day to the next, over a period of 50 days with different basic reproduction rates in steps of 0.05. The best results in comparison with the real course of the epidemic were then chosen and are displayed in Figures 4.1-4.3. Here, we display $\frac{i_j}{\tilde{p}_j}$ for each age group $j \in \{1, 2, ..., J\}$, as this quantity may be more intuitive to the reader than i_j. In other words, the fraction of infected individuals is shown, given that these are in a certain age group.
One sees that the extended model makes relatively good predictions, also regarding the different behavior of the different age groups. However, no comparisom between different numbers of activities has been done. Also, the best predictions have been chosen, others are not as good, even if no lockdown or other restriction have been imposed on the population.

If one is interested in the Python implementation producing Figures 4.1-4.3, please write a mail to schamela@gmail.com. Also, a function to calculate the analytic value of the fraction of overall infected individuals and to compare it with the numerical result is implemented. Furthermore, one can plot the mean age of the infected individuals.

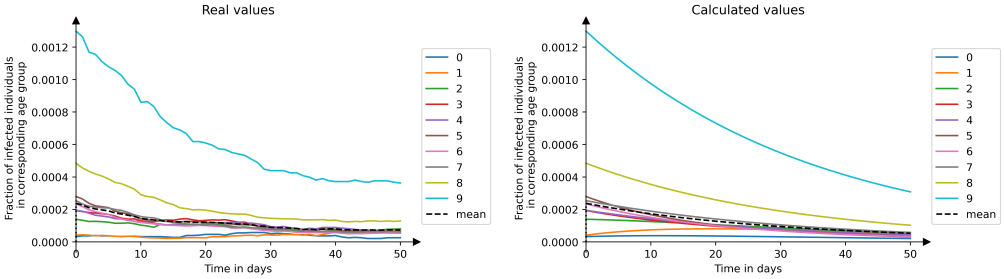

Figure 4.1.: Real and simulated course of the corona virus disease in Austria from the 28th of April, 2020, onwards, with parameters as in text. The best basic reproduction rate in the simulation is 0.55. The dotted vertical line gives the day of the maximal fraction of infected individuals over the displayed period.

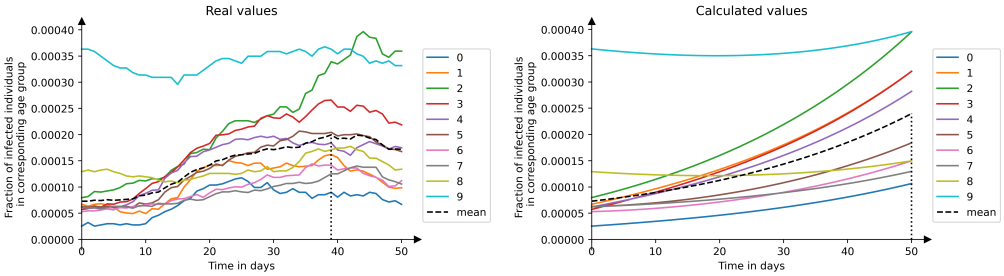

Figure 4.2.: Real and simulated course of the corona virus disease in Austria from the 17th of June, 2020, onwards, with parameters as in text. The best basic reproduction rate in the simulation is 1.45. The dotted vertical line gives the day of the maximal fraction of infected individuals over the displayed period.

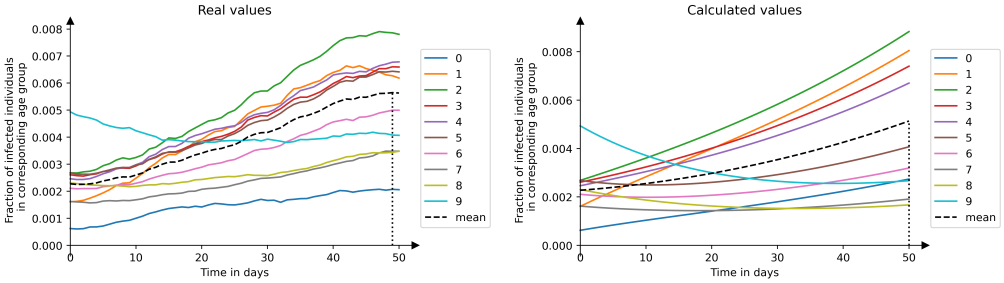

Figure 4.3.: Real and simulated course of the corona virus disease in Austria from the 12th of February, 2021, onwards, with parameters as in text. The best basic reproduction rate in the simulation is 1.35. The dotted vertical line gives the day of the maximal fraction of infected individuals over the displayed period.

5. Summary

This chapter summarizes the results of the thesis and considers possible extensions in order to mention open problems or questions arising with this work.

5.1. Comparison

For the extendend model, even if much more complicated than the standard SIR model, we were able to derive some important properties. Also, for $K = 1$ and discrete age groups with only one age group, we receive the standard SIR model. Hence, the standard SIR model can be seen as a special version of the extended model. Also, for general K and continuous age we get some similarities: the only equilibrium in both models is the disease-free one which is lastly achieved. In other words, in both models every epidemic will die out in the long-term.

The basic reproduction rate in the continuous version of the extended model is given by Equation (3.10) and equals

$$\mathcal{R}_0 = \varrho(\mathcal{F} \circ \mathcal{G}^{-1}) \leq \int_0^A \frac{p(a)}{\gamma(a)} \beta(a,a)\, \mathrm{d}a\,,$$

where

$$(\mathcal{F} \circ \mathcal{G}^{-1})(f)(a) = p(a) \int_0^A \beta(a,\tilde{a}) \frac{1}{\gamma(a)} f(\tilde{a})\, \mathrm{d}\tilde{a}\,,$$

for $f \in \mathcal{C}([0,A])$ and $a \in [0,A]$ and the inequality is given in Equation (3.11). In the discrete setting, we have by Equation (4.4) and Equation (4.6) that

$$\tilde{\mathcal{R}}_0 = \varrho(FG^{-1}) \leq \sum_{j=1}^{J} \frac{\tilde{p}_j}{\tilde{\gamma}_j} \tilde{\beta}(j,j)$$

where

$$(FG^{-1})_{j,\iota} = \tilde{p}_j \frac{\tilde{\beta}(j,\iota)}{\tilde{\gamma}_\iota}\,,$$

for $j, \iota \in \{1, 2, ..., J\}$. The basic reproduction rate of the standard model is given by Equation (1.7), i.e.,

$$\mathcal{R}_0^{\mathrm{std}} = \frac{\beta}{\gamma}\,.$$

If $\frac{\beta(\cdot,\cdot)}{\gamma} =: c$ is constant, then $c = \mathcal{R}_0$. This is due to the fact that for $a \in [0, A]$ we have that

$$c \cdot p(a) = c \cdot p(a) \cdot \int_0^A p(\tilde{a})\,\mathrm{d}\tilde{a} = p(a) \int_0^A \frac{\beta(a,\tilde{a})}{\gamma(\tilde{a})} p(\tilde{a})\,\mathrm{d}a = (\mathcal{F} \circ \mathcal{G}^{-1})(p)(a)\,,$$

i.e., p is an eigenfunction with eigenvalue c. Also, by Equation (3.11) we have

$$\mathcal{R}_0 \leq \int_0^A \frac{p(a)}{\gamma(a)} \beta(a,a)\,\mathrm{d}a = c \cdot \int_0^A p(a)\,\mathrm{d}a = c\,.$$

Hence, $c = \mathcal{R}_0$ and we get the same formula for the basic reproduction rate as with the standard model. The same calculation can be done for the discrete case.

Now, take a look at the fraction of totally infected in the course of the epidemic. In the standard model, we have by Equation (1.12) that

$$r_\infty = 1 - \exp(-\mathcal{R}_0 \cdot r_\infty) \cdot s_0$$

and that there is a unique solution, while in the extended model, by Equation (3.18), we have

$$r_\infty(a) = p(a) - \exp\left(-\int_0^A \beta(a,\tilde{a}) \frac{r_\infty(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right) \cdot s_0(a)\,,$$

for $a \in [0, A]$, with existing, but not necessarily unique solution. Integrating the second expression over all $a \in [0, A]$, we get

$$R_\infty \coloneqq \int_0^A r_\infty(a)\,\mathrm{d}a = 1 - \int_0^A \exp\left(-\int_0^A \beta(a,\tilde{a}) \frac{r_\infty(\tilde{a})}{\gamma(\tilde{a})}\,\mathrm{d}\tilde{a}\right) \cdot s_0(a)\,\mathrm{d}a\,.$$

If $\frac{\beta(\cdot,\cdot)}{\gamma} =: c$ is constant with respect to both ages, then

$$\begin{aligned} R_\infty =& 1 - \int_0^A \exp\left(-c \int_0^A r_\infty(\tilde{a})\,\mathrm{d}\tilde{a}\right) \cdot s_0(a)\,\mathrm{d}a \\ =& 1 - \exp\left(-c \cdot R_\infty\right) S_0\,. \end{aligned}$$

Hence, the formula for the fraction of totally infected in the course of the disease of the extended model gives the same as in the standard model. The same holds for the discrete version of the extended model.

Looking at the maximum fraction of infected, it is quite easy to derive a formula in the standard model, see also Equation (1.9). However, in the extended model, such a calculation is not possible any more and only some weaker results have been achieved.

5.2. Open Problems

This thesis gives some answers, but also opens up new questions: even if the extended model is quite realistic and detailed, is it of use in the real world? Many of the used parameters may be hard to estimate, like the participation rates π_k and the infection rates β_k. Also, the more parameters, the more sensitive a model is to small changes in them.
Some proofs are not done rigorously or are toally missing. For example, does the spectral stability of the extended model already imply stability? How can $\mathcal{R}_0$ be related to the Lipschitz-constant L in Equation (3.19) in order to have a unique solution of the fraction of totally infected in the course of the infection given by Equation (3.17)? What further predictions can be made about the maximum fraction of infected individuals?
In the discrete case, it may be shown numerically that a time derivative smaller than zero for some ages at the beginning of the epidemic does not necessarily mean that it stays smaller than zero for all later times. However, the question arises wether a local maximum with time derivative zero has to be unique, i.e., if once the fraction of infected individuals increases, it then only can decrease once already decreasing. Or is it even possible to have a constant maximum? At least for $\pi_k > 0$ for all $k \in \{1, 2, ..., K\}$, the former seems to be reasonable.

A. Theoretic Mathematical Results

In the following, we give some results, most of them fundamental, which may or may not be known to the reader. For this, let $m, n \in \mathbb{N}$.

A.1. Eigenvalues

In the following, we give the statements of some basic results of linear algebra. For some proofs we refere to relevant literature.
The following definitions can be found in [8], Chapter 0:

Definition A.1.1. Let $A \in \mathbb{R}^{n\times n}$ be an $n \times n$-matrix.
Then

$$\operatorname{tr}(A) \coloneqq \sum_{i=0}^{n} A_{i,i}$$

is called the **trace** of the matrix. The **determinant** is the only function $f\colon \mathbb{R}^{n\times n} \to \mathbb{R}$ that is

1. multilinear in the rows of its argument
2. alternating
3. normalized: $f(\mathrm{id}) = 1$.

It is explicitly given by

$$\det A = \sum_{\sigma\in S_n} \left(\operatorname{sign}(\sigma) \prod_{i=1}^{n} A_{i,\sigma(i)} \right)$$

where $S_n = \{\sigma\colon \{1, 2, ..., n\} \to \{1, 2, ..., n\} \,|\, \sigma \text{ bijective }\}$.
The **rank** $\operatorname{rk}(A)$ of matrix A is the maximum number of linearly independet columns (or rows) of A.
The matrix A is called **symmetric** if for all $i, j \in \{1, 2, ..., n\}$ we have

$$A_{i,j} = A_{j,i}\,.$$

Also the next definitions are from [8]:

Definition A.1.2. Let $A \in \mathbb{R}^{n\times n}$ be an $n \times n$-matrix.
A value $\lambda \in \mathbb{R}$ is called an **eigenvalue** if there exists a vector $v \in \mathbb{R}^n, v \neq 0$ such that

$$Av = \lambda v\,.$$

Such a vector v is then called an **eigenvector**. The **multiplicity** of an eigenvalue is the multiplicity as a zero of the **characteristic polynomial** $\det(\lambda I_n - A)$. The set of all eigenvalues is called **spectrum** and denoted by

$$\operatorname{spec}(A) \coloneqq \{\lambda \in \mathbb{R} \,|\, \lambda \text{ eigenvalue of } A\}\,.$$

The **spectral radius** is the biggest eigenvalue in absolute values, which we write as

$$\varrho(A) \coloneqq \max\{|\lambda| \,|\, \lambda \in \operatorname{spec}(A)\}\,.$$

Theorem A.1.3. *Let $A \in \mathbb{R}^{n\times n}$ be a symmetric $n \times n$-matrix with real eigenvalues $\lambda_1, \lambda_2, ..., \lambda_n \in \mathbb{R}$, counted with multiplicity. Then*

$$\sum_{j=1}^{n} \lambda_j = \operatorname{tr}(A)$$

and

$$\prod_{j=1}^{n} \lambda_j = \det(A)\,.$$

Proof. See [8], Chapter 1, the part below equation (1.2.4c). ■

Theorem A.1.4 (Jacobson Lemma, particular version)**.** *Let $m, n \in \mathbb{N}$. Furthermore, let A be an $m \times n$ matrix and B an $n \times m$ matrix. Without loss of generality, let $n \geq m$. Then*

$$\operatorname{spec}(BA) = \operatorname{spec}(AB) \cup \{0\}$$

if $n > m$ and

$$\operatorname{spec}(BA) = \operatorname{spec}(AB)$$

for $m = n$. In particular, $\operatorname{tr}(AB) = \operatorname{tr}(BA)$.

Proof. See [8], Theorem 1.3.22. ■

Theorem A.1.5 (Rayleigh)**.** *Let $A \in \mathbb{R}^{n\times n}$ be a symmetric matrix. Then*

$$\varrho(A) = \max_{x\neq 0} \frac{x^{\mathrm{T}} A x}{x^{\mathrm{T}} x} = \max_{\substack{x\neq 0 \\ \|x\|_2=1}} x^{\mathrm{T}} A x\,.$$

Proof. See [8], Theorem 4.2.2. ■

Remark. This theorem is also named the min-max theorem, variational theorem or Courant–Fischer–Weyl min-max principle. We only give that part of the theorem which is needed in this thesis.

The following definition and theorem are from [8], Chapter 7:

Definition A.1.6. A matrix $A \in \mathbb{R}^{n\times n}$ is called postive semi-definite, if

$$x^{\mathrm{T}} A x \geq 0$$

for all $x \in \mathbb{R}^n$.

Theorem A.1.7. *The following statements are equivalent for an arbitrary symmetric matrix $A \in \mathbb{C}^{n\times n}$:*

1. *A is positive semi-definite*
2. *all eigenvalues of A are non-negative*
3. *there exists a matrix B such that $B^T B = A$. In particular, if $\mathrm{rk}(A) = 1$, then there exists a vector $v \in \mathbb{R}^n$ with $A = x^T x$.*

Proof. See [8], Theorem 7.2.1 and Theorem 7.2.7. ■

One last definition is needed in the course of this thesis regarding linear algebra, which can be found in Chapter 8 of [8]:

Theorem A.1.8. *A matrix $A \in \mathbb{R}^{n\times n}$ is called **positive**, if for all $i, j \in \{1, 2, ..., n\}$ we have $A_{i,j} > 0$, that is, every entry is positive. Similarly, a vector $x \in \mathbb{R}^n$ is called positive, if $x_i > 0$ for all $i \in \{1, 2, ..., n\}$.*

A.2. Dynamical Systems

The following definitions and theorems refer to general dynamical systems in finite or infinite dimension. They are from my notes of the lecture "Dynamical Systems and Nonlinear Differential Equations" in summer term 2020 with professor Hendrik Bruin at the University of Vienna.

Definition A.2.1. Let $\mathcal{I} \in \{\mathbb{N}, \mathbb{Z}, [0, \infty[, \mathbb{R}\}$ and $\mathcal{V}$ be a metric space. A **dynamical system** is a map $\mathcal{I} \times \mathcal{V} \to \mathcal{V}\colon\ (t, v) \mapsto S_t(v)$ satisfying

- $S_0(v) = v$ for all $v \in \mathcal{V}$,
- $v \mapsto S_t(v)$ is continuous for all $t \in \mathcal{I}$ and
- $S_{s+t}(v) = S_s(S_t(v))$ for all $v \in \mathcal{V}$ and all $s, t \in \mathcal{I}$.

For fixed $v \in \mathcal{V}$, the function $\mathcal{I} \to \mathcal{V}\colon\ t \mapsto S_t(v)$ is called the **flow** through v.

Definition A.2.2. Let $f : \mathcal{V} \to \mathcal{V}$ be a function over a Banach space $\mathcal{V}$, real or complex. An **equilibrium (point)** or **stationary point** x^* for the differential equation

$$x'(t) = f(x(t))$$

is a solution of $f(x) = 0$. Such an equilibrium is **(Lyapunov) stable** if for all $\varepsilon > 0$ there exists $\delta > 0$ such that if $\|\varphi(0) - x^*\| < \delta$, then also $\|\varphi(t) - x^*\| < \varepsilon$ for all $t \geq 0$. It is called **asymptotically stable** if there exists $\delta > 0$ such that for all solutions φ of $x' = f(x)$ with $\|\varphi(0) - x^*\| < \delta$, $\lim_{t\to\infty} \|\varphi(t) - x^*\| = 0$ holds. The equilibrium x^* is **hyperbolic**, if the eigenvalues of the corresponding Jacobian matrix $Df(x^*)$ or the operator $Df(x^*)$, respectively, all have nonzero real part, otherwise **non-hyperbolic**. An equilibrium is called **spectral stable** if all elements of the spectrum of the linearized operator have negative real part.

Theorem A.2.3 (Hartman-Grobman)**.** *Let f be a continuously differentiable function on $\mathbb{R}^n$ and x^* be a hyperbolic equilibrium of $x' = f(x)$. Then there exists a neighbourhood U of x^* and a diffeomorphism $h\colon U \to h(U)$ such that $h(x^*) = x^*$ and the flow $\varphi^t(x)$ of $x' = f(x)$ satisfies*

$$h \circ \varphi^t(x) = x^* e^{At}(h(x)_x^*)$$

for all $x \in U$. In other words, $h \circ \varphi^t(x)$ is a solution of the linearized differential equation $x' = f(x^*) + A(x - x^*)$ with Jacobian matrix $A = Df(x^*)$.

Proof. A sketch of the proof has been given in the lecture "Dynamical Systems and Nonlinear Differential Equations". ■

Remark. The theorem by Hartman-Grobman can also be proven for infinite-dimensional Banach spaces.

A.3. Functional Analysis and Operator Theory

The following theory about linear operators is needed particularly in Section 3.4.2 in order to derive a basic reproduction rate in the continuous case. Most of it is from [2], Chapters 1, 4 and 5, if not stated otherwise.

The following important definitions are from [12], Sections 2.2 and 2.3.

Definition A.3.1. Let $\mathcal{V}$ be a real Banach space. A convex set $\mathcal{P} \subseteq \mathcal{V}$ with $t\mathcal{P} \subseteq \mathcal{P}$ for all $t \geq 0$ and $\mathcal{P} \cap (-\mathcal{P}) = \{0\}$ is called a **cone**. Such a cone is **solid** if $\mathcal{P}^\circ \neq \emptyset$. A function $f\colon \mathcal{V} \to \mathcal{V}$ is called **strongly positive on** P if $f(\mathcal{P}\backslash\{0\}) \subseteq \mathcal{P}^\circ$.

The following definition and theorem are from [5]:

Definition A.3.2. Let $(\mathcal{V}, \|\cdot\|_\mathcal{V})$ and $(\mathcal{W}, \|\cdot\|_\mathcal{W})$ be normed vector spaces over a field $\mathbb{K}$. A function $f\colon \mathcal{V} \to \mathcal{W}$ is called **($\mathbb{K}$-)linear** if for all $x, y \in \mathcal{V}$ and all $c \in \mathbb{K}$

$$f(cx + y) = cf(x) + f(y)\,.$$

A linear function f is **bounded**, if there exists a $c > 0$ with $\|f(x)\|_\mathcal{W} \leq c\|x\|_\mathcal{V}$ for every $x \in \mathcal{V}$.

Theorem A.3.3. *Let $(\mathcal{V}, \|\cdot\|_\mathcal{V})$ and $(\mathcal{W}, \|\cdot\|_\mathcal{W})$ be normed vector spaces over a field $\mathbb{K}$ and $f\colon \mathcal{V} \to \mathcal{W}$ be $\mathbb{K}$-linear. The following assertions are equivalent:*

- *The function f is Lipschitz continuous*
- *The function f is uniformly continuous*
- *The function f is continuous*
- *The function f is continuous at one point $a \in V$*
- *The function f is continuous at $x = 0$*
- *The set $\{f(x) \mid \|x\|_{\mathcal{V}} \leq 1\}$ is bounded in W*
- *The function f is bounded.*

Proof. See [5], Theorem 8.9.6. ■

Theorem A.3.4. *Let $(\mathcal{V}, \|\cdot\|_{\mathcal{V}})$ and $(\mathcal{W}, \|\cdot\|_{\mathcal{W}})$ be normed vector spaces over a field $\mathbb{K}$. The set of all $\mathbb{K}$-linear continuous functions $L(\mathcal{V}, \mathcal{W})$ is a $\mathbb{K}$-vector space. If, additionally, $\mathcal{W}$ is a Banach space, then also $L(\mathcal{V}, \mathcal{W})$ is a Banach space with respect to the **operator norm** $\|\cdot\|_{\text{op}}$, where for $f \in L(\mathcal{V}, \mathcal{W})$*

$$\begin{aligned}\|f\|_{\text{op}} \coloneqq \|f\| &\coloneqq \sup(\{\|f(x)\|_{\mathcal{W}} \mid x \in \mathcal{V} \wedge \|x\|_{\mathcal{V}} = 1\}) \\ &= \inf(\{c > 0 \mid \forall x \in \mathcal{V} : \|f(x)\|_{\mathcal{W}} \leq c\|x\|_{\mathcal{V}}\}) .\end{aligned}$$

Proof. See [5], Theorem 8.9.7, Theorem 8.9.9 and Definition 8.9.8. ■

Theorem A.3.5 (Banach)**.** *If the bounded linear operator $\mathcal{F}$ over a real or complex Banach space is bijective, then the inverse operator $\mathcal{F}^{-1}$ is also bounded.*

Proof. See [2], Theorem 1.2.3. ■

Definition A.3.6. The **spectrum** $\text{spec}(\mathcal{F})$ of a bounded linear operator $\mathcal{F}$ over a real or complex Banach space $\mathcal{V}$ is defined as the set of all $\lambda \in \mathbb{C}$ where $\lambda \cdot \text{id} - \mathcal{F}$ does not have an inverse that is a bounded linear operator. A value $\lambda \in \text{spec}(\mathcal{F})$ is called a **spectral value**. In particular, the spectrum contains all $\lambda \in \mathbb{C}$ with $\mathcal{F}(f) = \lambda f$ for some $f \in \mathcal{V}\backslash\{0\}$, also called **eigenvalues**. A corresponding element $f \in \mathcal{V}\backslash\{0\}$ is called an **eigenfunction**. The **spectral radius** is defined as

$$\varrho(\mathcal{F}) \coloneqq \{|\lambda| \mid \lambda \in \text{spec}(\mathcal{F})\} .$$

Theorem A.3.7. *Every bounded linear operator $\mathcal{F}$ on a Banach space has a non-empty, closed, bounded spectrum, which satisfies*

$$\text{spec}(\mathcal{F}) \subseteq \{\lambda \in \mathbb{C} \mid |\lambda| \leq \|\mathcal{F}\|_{\text{op}}\} .$$

Proof. See [2], Theorem 1.2.11. ■

Theorem A.3.8. *For a bounded linear operator $\mathcal{F}$ on a Hilbert space $(\mathcal{V}, \langle\cdot,\cdot\rangle)$ there is a unique bounded linear operator $\mathcal{F}^*$, also operating on $\mathcal{V}$ such that $\langle \mathcal{F}f, g\rangle = \langle f, \mathcal{F}^* g\rangle$ for all $f, g \in \mathcal{V}$. We call $\mathcal{F}^*$ the **adjoint operator** of $\mathcal{F}$.*

Proof. See [2], Section 1.2. ■

Definition A.3.9. A bounded linear operator $\mathcal{F}$ is called **self-adjoint** if $\mathcal{F} = \mathcal{F}^*$.

Theorem A.3.10. *For a bounded linear operator $\mathcal{F}\colon \mathcal{V} \to \mathcal{V}$ operating on a Banach space $\mathcal{V}$ we have*

$$\operatorname{spec}(\mathcal{F}) = \operatorname{spec}(\mathcal{F}^*)\,.$$

Proof. See [2], Problem 1.2.14. ■

Definition A.3.11. A bounded linear operator $\mathcal{F}\colon \mathcal{V} \to \mathcal{V}$ on a Hilbert space $(\mathcal{V}, \langle\cdot,\cdot\rangle)$ is called **positive semi-definit** if for all $f \in \mathcal{V}$ one has

$$\langle \mathcal{F}(f), f\rangle \geq 0\,.$$

Theorem A.3.12. *A bounded linear and positive semi-definit operator $\mathcal{F}\colon \mathcal{V} \to \mathcal{V}$ on a Hilbert space $(\mathcal{V}, \langle\cdot,\cdot\rangle)$ admits only non-negative eigenvalues.*

Proof. By convention, assume that $\langle\cdot,\cdot\rangle$ is linear in the first component and semilinear in the second one. One has for an eigenvalue $\lambda \in \mathbb{C}$ and a corresponding eigenfunction $f \in \mathcal{V}$ that

$$0 \leq \langle \mathcal{F}(f), f\rangle = \langle \lambda f, f\rangle = \lambda \langle f, f\rangle = \lambda \|f\|\,.$$

As $\|f\| > 0$, we get $\lambda \geq 0$, . ■

Definition A.3.13. A linear operator $\mathcal{F}\colon \mathcal{V} \to \mathcal{V}$ operating on a Banach space $(\mathcal{V}, \|\cdot\|)$ is said to be **compact**, if the image of the open unit ball $B_1(0) \coloneqq \{f \in \mathcal{V} \,|\, \|f\| < 1\}$ has compact closure in $\mathcal{V}$.

Theorem A.3.14 (Riesz)**.** *Let $\mathcal{F}$ be a compact operator operating on a Banach space $\mathcal{V}$ of infinite dimension. Then the spectrum of $\mathcal{F}$ contains 0 and is finite or countable. If $\operatorname{spec}(\mathcal{F})$ is infinite countable, then*

$$\operatorname{spec}(\mathcal{F}) = \{0\} \cup \{\lambda_n \,|\, n \in \{1, 2, ...\}\}$$

where $\lim_{n\to\infty} \lambda_n = 0$, assuming that the λ_n are, starting at some $N \in \mathbb{N}$, sorted by descending norm.

Proof. See [2], Theorem 4.3.19. ■

Theorem A.3.15. *Let $\mathcal{A}$ be a compact set in $\mathbb{R}$. Assume that for $f \in \mathcal{C}(\mathcal{A})$ the condition $\|f\|_2 = 0$ implies $f(a) = 0$ for all $a \in \mathcal{A}$. If g is a continuous function on $\mathcal{A} \times \mathcal{A}$, then the formula*

$$\mathcal{F}(f)(a) \coloneqq \int_{\mathcal{A}} g(a, \tilde{a}) f(\tilde{a})\, \mathrm{d}\tilde{a} \tag{A.1}$$

*defines a compact linear operator on $\mathcal{C}(\mathcal{A})$. Such an operator is called **Hilbert-Schmidt operator**.*
If g is symmetric, then $\mathcal{F}$ is self-adjoint.

Proof. See [2], Theorem 4.2.20. ■

The following definition is from [3], Chapter I, Definition 3.1.

Definition A.3.16. A bounded linear operator $\mathcal{F}\colon \mathcal{V} \to \mathcal{W}$ between two Banach spaces $\mathcal{V}$ and $\mathcal{W}$ is said to be a **Fredholm operator** if its kernel $\mathrm{Ker}(\mathcal{F})$ and cokernel

$$\mathrm{Coker}(\mathcal{F}) \coloneqq \mathcal{W}/\mathrm{Im}(\mathcal{F})$$

are both finite-dimensional and the range $\mathcal{F}(\mathcal{V})$ is closed.

Theorem A.3.17. *A bounded linear operator on a Banach space with finite-dimensional cokernel has closed range. In particular, in the definition of a Fredholm operator, the last condition is redundant.*

Proof. See [3], Chapter I, Theorem 3.2. ■

Theorem A.3.18. *If $\mathcal{F}$ is a compact operator on $\mathcal{V}$, then $(\lambda \cdot \mathrm{id} - \mathcal{F})$ is a Fredholm operator for all $\lambda \neq 0$.*

Proof. See [2], Lemma 4.3.3. ■

There exist various definitions of the essential spectrum. However, we will only use the following version from [3], Chapter I, Section 4:

Definition A.3.19. Let $\mathcal{F}$ be a bounded linear operator operating on a Banach space. We say that $\lambda \in \mathbb{C}$ lies in the **essential spectrum** $\mathrm{spec}_e(\mathcal{F})$ if $\lambda \cdot \mathrm{id} - \mathcal{F}$ is not a Fredholm operator.
The **radius of the essential spectrum** is defined as

$$\varrho_e(\mathcal{F}) \coloneqq \max\{|\lambda| \,|\, \lambda \in \mathrm{spec}_e^{(i)}(\mathcal{F})\}\,.$$

Remark. The kernel and cokernel of an invertible, bounded operator on a Banach space have dimension zero. Hence, such an operator is also a Fredholm operator.
In particular, the essential spectrum of a bounded linear operator is included in its spectrum.

Theorem A.3.20. *If $\mathcal{F}\colon \mathcal{V} \to \mathcal{V}$ is a bounded linear operator and $\tilde{\mathcal{F}} \coloneqq \mathcal{F} + \mathcal{T}$ where $\mathcal{T}$ is compact, then*

$$\mathrm{spec}_e(\mathcal{F}) = \mathrm{spec}_e(\tilde{\mathcal{F}})\,.$$

Proof. See [3], Chapter I, Theorem 4.1. ■

Theorem A.3.21. *Let $\mathcal{F}\colon \mathcal{V} \to \mathcal{V}$ be a bounded linear operator on a Banach space $\mathcal{V}$. Then*

$$\mathrm{spec}_e(\mathcal{F}) = \mathrm{spec}_e(\mathcal{F}^*)\,.$$

Proof. See [3], Chapter IX, Theorem 1.1. ■

Theorem A.3.22 (square root lemma)**.** *Let $\mathcal{F}$ be a bounded, non-negative, self-adjoint operator. Then there exists a bounded, non-negative and self-adjoint operator $\mathcal{G}$ such that*

$$\mathcal{G} \circ \mathcal{G} = \mathcal{F} .$$

This operator is denoted by $\mathcal{F}^{\frac{1}{2}} := \mathcal{G}$.

Proof. See [2], Lemma 5.2.1. ■

Definition A.3.23. Let $\mathcal{V}$ be a Hilbert space and $(e_n)_{n\in\mathbb{N}}$ be a complete orthonormal system in $\mathcal{V}$. The **trace** of a self-adjoint operator $\mathcal{A}$ is defined as

$$\operatorname{tr}(\mathcal{A}) = \sum_{n=1}^{\infty} \langle \mathcal{A}(e_n), e_n \rangle \in [0, \infty[\cup \{\infty\} .$$

A bounded linear operator $\mathcal{F}$ on $\mathcal{V}$ is **trace class** if

$$\operatorname{tr}(|\mathcal{F}|) < \infty$$

where $|\mathcal{F}| \coloneqq (\mathcal{F}^* \circ \mathcal{F})^{\frac{1}{2}}$. In this case, one defines

$$\operatorname{tr}(\mathcal{F}) = \sum_{n=1}^{\infty} \langle \mathcal{F}(e_n), e_n \rangle \in [0, \infty[\cup \{\infty\} .$$

Theorem A.3.24 (Mercer's theorem)**.** *If the non-negative, bounded, self-adjoint operator $\mathcal{F}$ has the continuous integral kernel $g(\cdot,\cdot)$ on $\mathcal{A} \times \mathcal{A}$, i.e., Equation* (A.1) *holds, then*

$$\operatorname{tr}(\mathcal{F}) = \int_{\mathcal{A}} g(a,a) \, \mathrm{d}a ,$$

where, in particular, the finiteness of either side implies the finiteness of the other.

Proof. See [2], Proposition 5.6.9. ■

Theorem A.3.25. *Let $\mathcal{F}_1$ be a trace class operator and $\mathcal{F}_2$ a bounded linear one, both operating on a Hilbert space $\mathcal{V}$. Then $\mathcal{F}_1 \circ \mathcal{F}_2$ and $\mathcal{F}_2 \circ \mathcal{F}_1$ are both trace class operators.*

Proof. See [2], Theorem 5.6.7. ■

Theorem A.3.26. *Let $\mathcal{F}\colon \mathcal{V} \to \mathcal{V}$ be a bounded linear operator on a Banach space $\mathcal{V}$. If $\mathcal{F}$ is trace class, then it is also a Hilbert-Schmidt operator, and hence, compact.*

Proof. See [2], Sections 5.5 and 5.6. ■

The following theorem is from [13], Theorem 2:

Theorem A.3.27 (Lidskii)**.** *Let $\mathcal{F}$ be a linear trace class operator on a Hilbert space with eigenvalues $\lambda_0, \lambda_1, \lambda_2, ...$, listed in order of nonincreasing absolute value and repeated according to algebraic multiplicity. Then*

$$\sum_{n\in\mathbb{N}} \lambda_n = \operatorname{tr}(\mathcal{F}) . \tag{A.2}$$

A.4. Double Sums

For a property P, the so-called Iverson bracket is defined by

$$[P] \coloneqq \begin{cases} 1 & \text{if } P \text{ is true} \\ 0 & \text{otherwise} \end{cases} .$$

Then for all properties $P(k)$ of an integer $k \in \mathbb{Z}$ we can rewrite sums in the following way

$$\sum_{k \in \mathbb{Z}} f(k)[P(k)] = \sum_{\substack{P(k) \\ k \in \mathbb{Z}}} f(k) \,,$$

where f is a function defined at least for the values of $k \in \mathbb{Z}$ where $P(k)$ is true, by convention. This notation allows us to rewrite double sums in a convenient way:

$$\begin{aligned} \sum_{j=0}^{n} \sum_{k=0}^{j} \tilde{f}(j,k) &= \sum_{j,k} f(j,k)[0 \le j \le n][0 \le k \le j] \\ &= \sum_{j,k} f(j,k)[0 \le k \le j \le n] \\ &= \sum_{j,k} f(j,k)[0 \le k \le n][k \le j \le n] \\ &= \sum_{k=0}^{n} \sum_{j=k}^{n} \tilde{f}(j,k) \,, \end{aligned}$$

where $n \in \mathbb{N}$ is an arbitrary non-negative integer.
This technique has been introduced in [11] on page 3.

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