Endemic states of integro-differential equation-based disease models

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1 Introduction

As recently demonstrated by the SARS-CoV-2 pandemic, infectious diseases may have a huge impact on society. Mathematical models of infectious diseases allow to predict their behaviour. This process makes it easier to plan mitigation actions. Moreover, by studying the long-term behaviour of a model mathematically, one can see when disease dynamics start to stabilize around an equilibrium or under which circumstances the disease dies out.

Often, ordinary differential equation models, also called ODE-based models, are used to describe and study the behaviour of infectious diseases. Mathematically, ordinary differential equations are well understood, and there are many numerical solvers to handle them. However, these models assume exponentially distributed stay-times in the infected states, which was found to be rather unrealistic according to [1, 2, 3]. Models based on integro-differential equations, also called IDE-based models, generalize ODE-based models and allow for arbitrary stay-time distributions. In 1927, Kermack and McKendrick presented their integro-differential model [4]. Over the last decades, many models based on the Kermack and McKendrick model were published, see for example [5, 6, 7, 8, 9].

Previously, the analysis of models based on integro-differential equations focused on the short-term effects. On the other hand, for models based on ordinary differential equations, many results on the long-term behaviour, such as the stability of equilibria, are available, see for example [10, 11, 12]. Furthermore, the results on the long-term behaviour of models based on integro-differential equations are usually restricted to models without disease deaths and assuming constant population size [13, 14].

Our contribution is the study of an IDE-based model with varying population size which does allow for endemic behaviour. In order to derive an endemic model based on integro-differential equations, we will include the possibility of natural birth and death in a model similar to the one presented in [15]. Compared to other IDE-based models, this model is rather complex, also allowing for disease death. The fact that we have a varying population size influenced by both the natural birth and death rate, as well as the disease-induced mortality, make the model analysis more involved. Moreover, the definition of equilibria is unclear when considering non-constant population size. In order to study the model behaviour independently of the population size, we will introduce a normalized version of our model. While this technique was already applied to ODE-based models, this seems to be a novel approach to IDE-based models. As a main result, we show the stability of the disease-free equilibrium whenever the reproduction number is smaller than one. Moreover, we derive conditions under which the disease-free equilibrium becomes unstable for a reproduction number larger than one.

The thesis is structured as follows. In Section 2, we will start by introducing our model. We will first define a model without the possibility of natural birth and death and then extend it by adding the birth and the death rate to the model formulation. As already mentioned, we will then introduce a normalized model version in order to analyse the equilibria. Then, in Section 3, we will analyse the long-term behaviour of the model. Therefore, we will introduce some parameters that indicate the behaviour of the disease, such as the concept of reproduction

numbers. Then, we compute the equilibria and analyse their existence in dependence of the parameters computed before. Afterwards, we analyse the stability of the equilibria that depends, for example, on the size of the reproduction number. Finally, we will comment on the behaviour of the population size. In order to analyse the model numerically we will introduce a numerical scheme in Section 4. To avoid the runtime-heavy Newton Algorithm and to preserve the main features of the model, we will use a non-standard scheme, as given in [8, 15]. We will then give some proofs to the properties of the numerical scheme. In Section 5, we will then use our own implementation of the numerical scheme to confirm our results from Section 3 in the numerical experiments. Moreover, we will discuss the effect of different birth and death rates on the model.

2 Model formulation

In this section, we introduce an age-of-infection SECIR-type model that also includes births and natural deaths. To do this, we first present the SECIR-type IDE-based model from [15] in Section 2.1, which does not yet include natural births or deaths. Then, in Section 2.2 we add the possibility of birth and death to the model given in Section 2.1. As we will need a normalized model to analyse the long-term behaviour we will then introduce a normalization of the SECIR-type birth-and-death model in Section 2.3.

SECIR-type models are a form of compartmental models in which the entire population is partitioned into different compartments. The simplest compartmental model is a SIR-model, where the population is divided into the compartments: Susceptible (S); Infected (I); and Recovered (R). SECIR-type models are a generalization of the classic SIR-models. In our case, SECIR-type means that we consider eight different compartments: Susceptible (S) consisting of individuals that can potentially become infected; Exposed (E) consisting of individuals that are infected but not yet infectious; Carrier (C) consisting of individuals that are infectious but not symptomatic; Infected (I) consisting of individuals that are infectious and symptomatic; Hospitalized (H) consisting of individuals with a severe case; In Intense Care Unit (U); Dead(D) consisting of all individuals that have died from the disease; Recovered (R), consisting of individuals that have recovered from the disease. We consider individuals in (R) to have full immunity, since we do not allow reinfection. Moreover, we assume that only individuals in the compartments (C) and (I) are infectious, as we assume individuals in (H) and (U) to be isolated either at home or in a hospital. Then, we define the set of compartments as $\mathcal{Z} = \{S, E, C, I, H, U, R, D\}$.

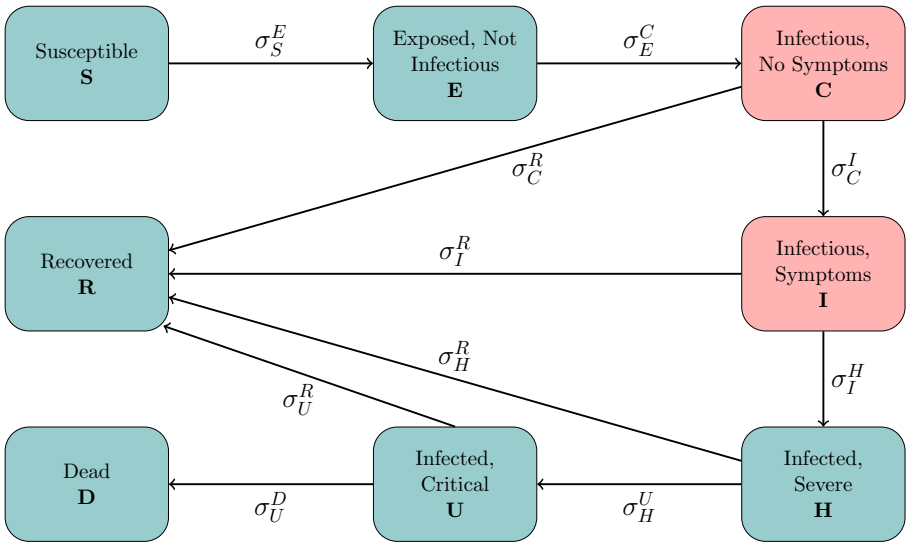

Figure 1: **Structure of the SECIR-type IDE model.** Schematic representation of the compartments and the transitions between the compartments in the SECIR-type IDE model. The states in which individuals are infectious are highlighted in red. As given in [15].

We will formulate the model using integro-differential equations. Therefore, we call the model

SECIR-type IDE-based birth-and-death model. The general structure of a SECIR-type IDE model is given in Figure 1. As the general structure for all models, to be introduced, is the same and we use the same parameters, we introduce them at this point.

We describe by $\sigma_{z_1}^{z_2}(t)$ the number of individuals who transition from $z_1 \in \mathcal{Z}$ to $z_2 \in \mathcal{Z}$ at time t. These transitions are only defined for consecutive compartments, as indicated by the arrows in Figure 1. Moreover, $0 \leq \phi(t) \leq c$, for $c \in (0, \infty)$, gives the average daily contacts of an individual at time t, and $\rho(t) \in [0, 1]$ gives the average transmission probability. By $\xi_C(\tau) \in [0, 1]$ and $\xi_I(\tau) \in [0, 1]$, we denote the mean proportion of individuals in compartments C and I which are not isolated after time τ in the respective compartment. For $z_1, z_2 \in \mathcal{Z}$, we denote by $\mu_{z_1}^{z_2} \in [0, 1]$ the expected proportion of people who move from z_1 to z_2 in the course of their infection. The expression $\gamma_{z_1}^{z_2}(\tau)$, with $\gamma_{z_1}^{z_2} : \mathbb{R} \to [0, 1]$, denotes the expected proportion of individuals who are still in compartment z_1 after time τ in this compartment and who will move to compartment z_2 over the course of their infection. This proportion as used in [15] does not take into account the possibility of natural death. For theoretical purposes, we need some assumptions about these functions.

Assumption 2.1. *For all $z_1, z_2 \in \mathcal{Z}$, we assume the following*

a) $\gamma_{z_1}^{z_2}$ *is continuously differentiable on* $(0, \infty)$,

b) $\gamma_{z_1}^{z_2}(\tau)$ *is monotonically decreasing with* $\gamma_{z_1}^{z_2}(\tau) = 1$ *for* $\tau \leq 0$,

c) $\gamma_{z_1}^{z_2} \in L^1((0, \infty))$,

d) $\lim_{t\to\infty} \gamma_{z_1}^{z_2}{}' = 0$.

A combination of these assumptions implies $\lim_{\tau\to\infty} \gamma_{z_1}^{z_2}(\tau) = 0$. In [15] they only have Assumption 2.1 a)-c), but for the long-term analysis of the model we will also need Assumption 2.1 d). Moreover, we want to emphasize that Assumption 2.1 d) is not trivial, as can be seen in the following lemma.

Lemma 2.2. *There is a function γ satisfying Assumption 2.1 a)-c), but not Assumption 2.1 d).*

Proof. We start by constructing the derivative of γ. For every $i \in \mathbb{N}$, we define for $x \in (i, i+2^{-i})$

$$f_i(x) \coloneqq \begin{cases} 2^{i+1}(x - i) & \text{for } x \leq i + 2^{-(i+1)} \\ 1 - 2^{i+1}\left(x - i - 2^{-(i+1)}\right) & \text{for } x > i + 2^{-(i+1)}. \end{cases}$$

A plot for $f_i(x)$ is given in Figure 2. Using this, we define for all $x \in \mathbb{R}$

$$f(x) \coloneqq \begin{cases} f_i(x) & \text{for } x \in (i, i + 2^{-i}) \text{ for some } i \in \mathbb{N} \\ 0 & \text{else.} \end{cases}$$

Then, we define

$$\gamma(t) \coloneqq 1 - \int_{-\infty}^{t} f(x)\, dx.$$

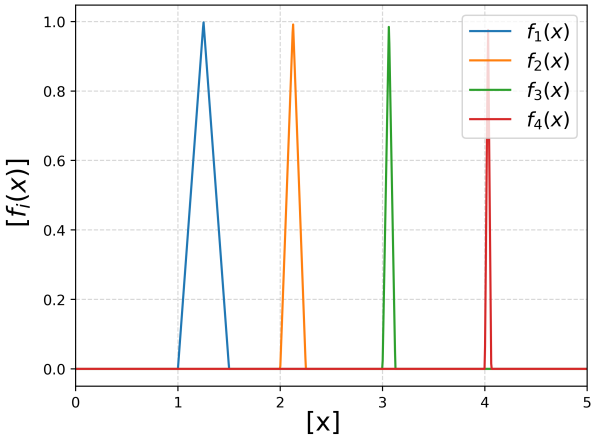

Figure 2: **The function** $f_i(x)$ for $i \in \{1, 2, 3, 4\}$.

Then $\gamma \in C^1((0, \infty)$ is obvious, and we also have $\gamma(t) = 0$ for $t \leq 0$. Moreover, we compute

$$\begin{aligned}\int_{-\infty}^{\infty} f(x)\ dx &= \sum_{i=0}^{\infty} \int_{i}^{i+2^{-i}} f_i(x)\ dx \\ &= \sum_{i=0}^{\infty} 2^{-(i+1)} = 1.\end{aligned}$$

This immediately implies

$$\lim_{t\to\infty} \gamma(t) = \lim_{t\to\infty} \left(1 - \int_{-\infty}^{t} f(x)\ dx\right) = 0.$$

Lastly, we show that $\gamma \in L^1((0, \infty))$

$$\begin{aligned}\int_{\mathbb{R}} \left(1 - \int_{-\infty}^{t} f(x)\ dx\right)\ dt &\leq \int_{\mathbb{R}} \left(1 - \int_{-\infty}^{\lceil t \rceil} f(x)\ dx\right)\ dt \\ &= \int_{\mathbb{R}} \left(\sum_{i=0}^{\infty} 2^{-(i+1)} - \sum_{i=0}^{\lceil t \rceil} 2^{-(i+1)}\right)\ dt \\ &= \int_{\mathbb{R}} \left(\sum_{i=\lceil t \rceil + 1}^{\infty} 2^{-(i+1)}\right)\ dt \\ &= \int_{\mathbb{R}} \left(2^{-\lceil t \rceil} \sum_{j=0}^{\infty} 2^{-(j+1)}\right)\ dt \\ &\leq \int_{\mathbb{R}} 2^{-t}\ dt < +\infty.\end{aligned}$$

Therefore, γ satisfies Assumption 2.1 a)-c), but $\gamma' = -f$ is not converging. □

Remark 2.3. *From Assumption 2.1 it follows that there exists a cumulative distribution function* $1 - \gamma_{z_1}^{z_2}(\tau)$ *that describes the distribution of the stay-time. This means that* $\gamma_{z_1}^{z_2}$ *is the survival function of a probability distribution. Therefore,* $-\gamma_{z_1}^{z_2\prime} : \mathbb{R} \to \mathbb{R}$ *is a probability density function that is continuous on* $(0, \infty)$ *and satisfies* $-\gamma_{z_1}^{z_2\prime}(\tau) = 0$ *for all* $\tau < 0$*. It is also obvious that* $-\gamma_{z_1}^{z_2\prime} \in L^1(\mathbb{R})$.

Lastly, we introduce the natural birth rate ν_b and the natural death rate ν_d. The natural death rate does not include those individuals who die from the considered disease. The meaning of the parameters is summarized in Table 1.

Parameter	Description
$\phi(t)$	Average daily contacts at time t.
$\rho(t)$	Risk of transmission on contact at time t.
$\xi_C(\tau)$	Proportion of Carrier individuals with infection age τ that are not isolated.
$\xi_I(\tau)$	Proportion of infected individuals with infection age τ that are not isolated.
$\mu_{z_1}^{z_2}$	Expected transition probability from compartment z_1 to z_2.
$\gamma_{z_1}^{z_2}(\tau)$	Expected proportion of individuals who are in compartment z_1 τ days after entering this compartment and who eventually move to compartment z_2.
ν_b	Birth rate.
ν_d	Natural death rate.

Table 1: **Description of the parameters used to define the model.**

2.1 A SECIR-type IDE-based model

Now we want to explicitly define the compartments, the transitions and the force of infection term, described above, in order to get a SECIR-type IDE model, similar to the model from [15]. As this model does not include any endemic dynamics, the natural birth and death rate is set to zero, meaning $\nu_b = \nu_d = 0$. The total population in this model is given by

$$N(t) = \sum_{Z \in \mathcal{Z}} Z(t). \tag{2.1}$$

Since this sum also counts the deaths, no one can drop out of the model and the total population is constant over time. We will also see this fact later on in this section.

We define the model equations starting with the force of infection term λ. The force of infection gives the rate at which susceptibles become infected. We assume that only people in the compartments C and I are infectious. Therefore, these are the only compartments that have an

influence on the force of infection term. After seeing the explicit definition of the compartments, we will further comment on this. For now, we define

$$\begin{aligned}\lambda(t) = \frac{\phi(t)\,\rho(t)}{N(t) - D(t)} \int_{-\infty}^{t} & \xi_C(t-s)\left(\mu_C^I\,\gamma_C^I(t-s) + \left(1-\mu_C^I\right)\gamma_C^R(t-s)\right)\sigma_E^C(s) \\ & + \xi_I(t-s)\left(\mu_I^H\,\gamma_I^H(t-s) + \left(1-\mu_I^H\right)\gamma_I^R(t-s)\right)\sigma_C^I(s)\;ds.\end{aligned} \tag{2.2}$$

The equations for the compartments write

$$\begin{aligned}
S'(t) &= -S(t)\lambda(t) \\
E(t) &= \int_{-\infty}^{t} \gamma_E^C(t-s)\,\sigma_S^E(s)\;ds, \\
C(t) &= \int_{-\infty}^{t} \left(\mu_C^I\,\gamma_C^I(t-s) + \left(1-\mu_C^I\right)\gamma_C^R(t-s)\right)\sigma_E^C(s)\;ds, \\
I(t) &= \int_{-\infty}^{t} \left(\mu_I^H\,\gamma_I^H(t-s) + \left(1-\mu_I^H\right)\gamma_I^R(t-s)\right)\sigma_C^I(x)\;ds, \\
H(t) &= \int_{-\infty}^{t} \left(\mu_H^U\,\gamma_H^U(t-s) + \left(1-\mu_H^U\right)\gamma_H^R(t-s)\right)\sigma_I^H(s)\;ds, \\
U(t) &= \int_{-\infty}^{t} \left(\mu_U^D\,\gamma_U^D(t-s) + \left(1-\mu_U^D\right)\gamma_U^R(t-s)\right)\sigma_H^U(s)\;ds, \\
R(t) &= \int_{-\infty}^{t} \sigma_C^R(s) + \sigma_I^R(s) + \sigma_H^R(s) + \sigma_U^R(s)\;ds, \\
D(t) &= \int_{-\infty}^{t} \sigma_U^D(s)\;ds.
\end{aligned} \tag{2.3}$$

Remark 2.4. *Given the definition of the compartments, one can see that the definition of the force of infection is a modificated version of* $\frac{C+I}{N}$*. Where, we weighted the function inside the integrals of* C *and* I *with the terms* ξ_C *and* ξ_I*, in order to only count of individuals that are not isolated within the force of infection term. Moreover, we multiplied the sum by the number of contacts* ϕ *times the risk of transmission* ρ*.*

In general, it is not clear whether this model admits a unique solution since the integrals start at $-\infty$. To ensure the existence of a unique solution, we need to add initial conditions. We assume that we know the values for the compartments in $t = 0$, i.e., we assume $S(0) = S_0$, $E(0) = E_0$, $C(0) = C_0$, $I(0) = I_0$, $H(0) = H_0$, $U(0) = U_0$, $R(0) = R_0$, $D(0) = D_0$. Moreover, we let $Z_0(t)$ for $Z \in \mathcal{Z}$ be the functions that give the number of individuals that were in compartment Z at $t = 0$ and are still in compartment Z at time $t \in [0, \infty)$. It is clear that $R_0(t) = R_0$ and $D_0(t) = D_0$ are constant as no individual can exit these compartments. Then for $t \in [0, \infty)$, the

equations for the compartments become

$$\begin{aligned}
S'(t) &= -S(t)\lambda(t)\\
E(t) &= \int_0^t \gamma_E^C(t-s)\,\sigma_S^E(s)\;ds + E_0(t),\\
C(t) &= \int_0^t \left(\mu_C^I\,\gamma_C^I(t-s) + \left(1-\mu_C^I\right)\gamma_C^R(t-s)\right)\sigma_E^C(s)\;ds + C_0(t),\\
I(t) &= \int_0^t \left(\mu_I^H\,\gamma_I^H(t-s) + \left(1-\mu_I^H\right)\gamma_I^R(t-s)\right)\sigma_C^I(x)\;ds + I_0(t),\\
H(t) &= \int_0^t \left(\mu_H^U\,\gamma_H^U(t-s) + \left(1-\mu_H^U\right)\gamma_H^R(t-s)\right)\sigma_I^H(s)\;ds + H_0(t),\\
U(t) &= \int_0^t \left(\mu_U^D\,\gamma_U^D(t-s) + \left(1-\mu_U^D\right)\gamma_U^R(t-s)\right)\sigma_H^U(s)\;ds + U_0(t),\\
R(t) &= \int_0^t \sigma_C^R(s) + \sigma_I^R(s) + \sigma_H^R(s) + \sigma_U^R(s)\;ds + R_0,\\
D(t) &= \int_0^t \sigma_U^D(s)\;ds + D_0.
\end{aligned} \tag{2.4}$$

With the following assumption, we can write down $Z_0(t)$ for $Z \in \{E, C, I, H, U\}$ explicitly.

Assumption 2.5. *We assume that all individuals who are in an infected compartment after time $t = 0$, meaning they are in {E,C,I,H,U}, entered this compartment at $t = 0$. In other words, they have infection age zero.*

This assumption is not made in [15], as they take into account the whole history of the disease and analyse the model mainly numerically. This assumptions leads to different formulas for the compartments and the flows, therefore this model is not exactly the same model as given in [15]. We now write

$$\begin{aligned}
E_0(t) &= E_0\gamma_E^C(t),\\
C_0(t) &= C_0(\mu_C^I\gamma_C^I(t) + (1-\mu_C^I)\gamma_C^R(t)),\\
I_0(t) &= I_0(\mu_I^H\gamma_I^H(t) + (1-\mu_I^H)\gamma_I^R(t)),\\
H_0(t) &= H_0(\mu_H^U\gamma_H^U(t) + (1-\mu_H^U)\gamma_H^R(t)),\\
U_0(t) &= U_0(\mu_U^D\gamma_U^D(t) + (1-\mu_U^D)\gamma_U^R(t)).
\end{aligned} \tag{2.5}$$

Then $Z_0(0) = Z_0$. For the force of infection term we write

$$\begin{aligned}
\lambda(t) = \lambda_0(t) + \frac{\phi(t)\,\rho(t)}{N(t)-D(t)} \int_0^t \xi_C(t-s)\left(\mu_C^I\,\gamma_C^I(t-s) + \left(1-\mu_C^I\right)\gamma_C^R(t-s)\right)\sigma_E^C(s)\\
+ \xi_I(t-s)\left(\mu_I^H\,\gamma_I^H(t-s) + \left(1-\mu_I^H\right)\gamma_I^R(t-s)\right)\sigma_C^I(s)\;ds.
\end{aligned} \tag{2.6}$$

With Assumption 2.5 we get for $\lambda_0(t)$

$$\lambda_0(t) = \phi(t)\,\rho(t)\frac{C_0(t)\xi_C(t) + I_0(t)\xi_I(t)}{N(t)-D(t)}. \tag{2.7}$$

To fully describe the model, we need formulas for the transitions $\sigma_{z_1}^{z_2}$. To compute them, we use the fact that the derivatives of the compartments should be determined by the in- and outflows. Therefore, we can derive

$$\begin{aligned}
S'(t) &= -\sigma_S^E(t),\\
E'(t) &= \sigma_S^E(t) - \sigma_E^C(t),\\
C'(t) &= \sigma_E^C(t) - \sigma_C^I(t) - \sigma_C^R(t),\\
I'(t) &= \sigma_C^I(t) - \sigma_I^H(t) - \sigma_I^R(t),\\
H'(t) &= \sigma_I^H(t) - \sigma_H^U(t) - \sigma_H^R(t),\\
U'(t) &= \sigma_H^U(t) - \sigma_U^D(t) - \sigma_U^R(t),\\
R'(t) &= \sigma_C^R(t) + \sigma_I^R(t) + \sigma_H^R(t) + \sigma_U^R(t),\\
D'(t) &= \sigma_U^D(t).
\end{aligned} \tag{2.8}$$

By computing the derivatives of the equations (2.3), one can derive the formulas for the transitions. For the explicit computations, we refer to the computations for the birth and death model in Section 2.2. Here, we only give the transitions, that write

$$\begin{aligned}
\sigma_S^E(t) &= -S'(t) = S(t)\,\lambda(t),\\
\sigma_E^C(t) &= -\int_0^t \gamma_E^{C\prime}(t-s)\,\sigma_S^E(s)\,ds - E_0\gamma_E^{C\prime}(t),\\
\sigma_C^I(t) &= -\int_0^t \gamma_C^{I\prime}(t-s)\,\mu_C^I\,\sigma_E^C(s)\,ds - C_0\mu_C^I\gamma_C^{I\prime}(t),\\
\sigma_C^R(t) &= -\int_0^t \gamma_C^{R\prime}(t-s)\,\left(1-\mu_C^I\right)\sigma_E^C(s)\,ds - C_0(1-\mu_C^I)\gamma_C^{R\prime}(t),\\
\sigma_I^H(t) &= -\int_0^t \gamma_I^{H\prime}(t-s)\,\mu_I^H\,\sigma_C^I(s)\,ds - I_0\mu_I^H\gamma_I^{H\prime}(t),\\
\sigma_I^R(t) &= -\int_0^t \gamma_I^{R\prime}(t-s)\,\left(1-\mu_I^H\right)\sigma_C^I(s)\,ds - I_0(1-\mu_I^H)\gamma_I^{R\prime}(t),\\
\sigma_H^U(t) &= -\int_0^t \gamma_H^{U\prime}(t-s)\,\mu_H^U\,\sigma_I^H(s)\,ds - H_0\mu_H^U\gamma_H^{U\prime}(t),\\
\sigma_H^R(t) &= -\int_0^t \gamma_H^{R\prime}(t-x)\,\left(1-\mu_H^U\right)\sigma_I^H(x)\,ds - H_0(1-\mu_H^U)\gamma_H^{R\prime}(t),\\
\sigma_U^D(t) &= -\int_0^t \gamma_U^{D\prime}(t-s)\,\mu_U^D\,\sigma_H^U(s)\,ds - U_0\mu_U^D\gamma_U^{D\prime}(t),\\
\sigma_U^R(t) &= -\int_0^t \gamma_U^{R\prime}(t-s)\,\left(1-\mu_U^D\right)\sigma_H^U(s)\, - U_0(1-\mu_U^D)\gamma_U^{R\prime}(t)ds.
\end{aligned} \tag{2.9}$$

Now, we stated the model with initial conditions. The goal of this was to make sure that there exists a non-negative solution, we will further comment on this in the next section. For now we just assume that there exists a non-negative solution to our equations and therefore assume that all compartments and transitions are non-negative.

Remark 2.6. *We already stated in the introduction of the model that we expect the total population to be constant over time. Together with the non-negativity of the compartments, this fact can be directly derived from* (2.8)*, as this implies* $N'(t) = 0$.

The following remark shows that the initial conditions do not have an influence on the long-term behaviour of our model.

Remark 2.7. *By Assumption 2.1, it is easy to see that,*

1. *for* $Z \in \{E, C, I, H, U\}$ *it holds* $\lim_{t\to\infty} Z_0(t) = 0$,
2. *for suitable combinations* $Z, X \in \mathcal{Z}$ *there holds* $\lim_{t\to\infty} Z_0 \mu_Z^X \gamma_Z^{X\,\prime}(t) = 0$,
3. $\lim_{t\to\infty} \lambda_0(t) = 0$.

2.2 A SECIR-type IDE-based birth-and-death model

We now generalize the model from the previous section to endemic scenarios by including the possibility of natural birth and death. Therefore, from now on we assume that the natural birth rate and the natural death rate are positive, i.e $\nu_b, \nu_d > 0$. Moreover, we assume that the probability of surviving natural death is given by $e^{-\nu_d t}$. Then for this model we define the total population as

$$N(t) = \sum_{Z\in\mathcal{Z}\setminus D} Z(t). \tag{2.10}$$

We note that in Model 2.3, we included the death compartment in the total population N (2.1). In (2.10) we do not include the death compartment as this time we only want to account for living individuals. Moreover, we will assume the same initial conditions as before to ensure the existence of a solution. This means we assume that $S(0) = S_0$, $E(0) = E_0$, $C(0) = C_0$, $I(0) = I_0$, $H(0) = H_0$, $U(0) = U_0$, $R(0) = R_0$, $D(0) = D_0$. In addition, we assume that Assumption 2.5 still holds true. Moreover, let $Z_0(t)$ for $Z \in \mathcal{Z}$ be the functions that give the number of individuals that were in compartment Z at $t = 0$ and are still in compartment Z at time $t \in [0, \infty)$. The functions $E_0(t), C_0(t), I_0(t), H_0(t)$ and $U_0(t)$ are given by

$$\begin{aligned} E_0(t) &= e^{-\nu_d t} E_0 \gamma_E^C(t), & C_0(t) &= e^{-\nu_d t} C_0 \gamma_C(t), \\ I_0(t) &= e^{-\nu_d t} I_0 \gamma_I(t), & H_0(t) &= e^{-\nu_d t} H_0 \gamma_H(t), \\ U_0(t) &= e^{-\nu_d t} U_0 \gamma_U(t), & R_0(t) &= e^{-\nu_d t} R_0, \end{aligned} \tag{2.11}$$

using

$$\begin{aligned} \gamma_C(t) &= \mu_C^I \gamma_C^I(t) + (1-\mu_C^I)\gamma_C^R(t), & \gamma_I(t) &= \mu_I^H \gamma_I^H(t) + (1-\mu_I^H)\gamma_I^R(t), \\ \gamma_H(t) &= \mu_H^U \gamma_H^U(t) + (1-\mu_H^U)\gamma_H^R(t), & \gamma_U(t) &= \mu_U^D \gamma_U^D(t) + (1-\mu_U^D)\gamma_U^R(t). \end{aligned} \tag{2.12}$$

Then, we have that $Z_0(0) = Z_0 = Z(0)$. Again, we start by introducing the force of infection term λ. In our model, only living individuals can be infectious to others, hence we need to add

the probability of surviving natural death. We do this by by multiplying $\gamma_{z_1}^{z_2}(\tau)$ with $e^{-\nu_d \tau}$. Then, $\lambda(t)$ at time $t \in [0, \infty)$ is defined by

$$\begin{aligned}\lambda(t) &= \lambda_0(t) \\ &\quad + \frac{\phi(t)\,\rho(t)}{N(t)} \int_0^t \xi_C(t-s)\gamma_C(t)\sigma_E^C(s)e^{-\nu_d(t-s)} + \xi_I(t-s)\gamma_I(t)\sigma_C^I(s)e^{-\nu_d(t-s)}\ ds.\end{aligned} \tag{2.13}$$

With Assumption 2.5 we get

$$\lambda_0(t) = \phi(t)\,\rho(t)\frac{C_0(t)\xi_C(t) + I_0(t)\xi_I(t)}{N(t)}. \tag{2.14}$$

In addition, the equations for the compartments look quite similar to those of (2.4). To every equation, we add the probability of surviving by multiplying $\gamma_{z_1}^{z_2}(\tau)$ with $e^{-\nu_d \tau}$. To the definition of the susceptibles, we add the births and subtract the deaths. Therefore, we get

$$\begin{aligned}
S'(t) &= \nu_b N(t) - S(t)\lambda(t) - \nu_d S(t) \\
E(t) &= \int_0^t \gamma_E^C(t-s)e^{-\nu_d(t-s)}\sigma_S^E(s)\ ds + E_0(t), \\
C(t) &= \int_0^t \gamma_C(t-s)e^{-\nu_d(t-s)}\sigma_E^C(s)\ ds + C_0(t), \\
I(t) &= \int_0^t \gamma_I(t-s)e^{-\nu_d(t-s)}\sigma_C^I(s)\ ds + I_0(t), \\
H(t) &= \int_0^t \gamma_U(t-s)e^{-\nu_d(t-s)}\sigma_I^H(s)\ ds + H_0(t), \\
U(t) &= \int_0^t \gamma_H(t-s)e^{-\nu_d(t-s)}\sigma_H^U(s)\ ds + U_0(t), \\
R(t) &= \int_0^t e^{-\nu_d(t-s)}\left(\sigma_C^R(s) + \sigma_I^R(s) + \sigma_H^R(s) + \sigma_U^R(s)\right)\ ds + R_0(t), \\
D(t) &= \int_0^t \sigma_U^D(s)\ ds + D_0.
\end{aligned} \tag{2.15}$$

Again, we make the assumption that all individuals who are in an infected compartment at time $t = 0$ entered this compartment at $t = 0$, that is Assumption 2.5. In the further analysis of the model, it will be useful to have the equation for S as an integral equation. Therefore, the following lemma will be useful.

Lemma 2.8. *It holds*

$$S(t) = \int_0^t \nu_b N(s)e^{-\nu_d(t-s)}\ ds - \int_0^t \lambda(s)S(s)e^{-\nu_d(t-s)}\ ds + S_0 e^{-\nu_d t}. \tag{2.16}$$

Proof. Integrating the equation for S and applying the integration by parts formula yields

$$\int_0^t S'(s)e^{-\nu_d(t-s)}\ ds = \int_0^t \nu_b N(s)e^{-\nu_d(t-s)}\ ds$$

$$
\begin{aligned}
& - \int_0^t S(s)\lambda(s)e^{-\nu_d(t-s)}\ ds - \int_0^t \nu_d S(s)e^{-\nu_d(t-s)}\ ds. \\
\Leftrightarrow \qquad & \left[S(s)e^{-\nu_d(t-s)}\right]_0^t = \int_0^t \nu_b N(s)e^{-\nu_d(t-s)}\ ds - \int^t S(s)\lambda(s)e^{-\nu_d(t-s)}\ ds \\
\Leftrightarrow \qquad & S(t) = \int_0^t \nu_b N(s)e^{-\nu_d(t-s)}\ ds - \int_0^t S(s)\lambda(s)e^{-\nu_d(t-s)} + S_0 e^{-\nu_d t}\ ds.
\end{aligned}
$$

□

As in Section 2.1, the change of the compartment sizes should be determined partially by the in- and outflow, but for model (2.15) they should also be determined by the births and deaths. Therefore, the following relations between the derivatives of the compartments and the transitions should be true

$$
\begin{aligned}
S'(t) &= -\sigma_S^E(t) + \nu_b N(t) - \nu_d S(t), \\
E'(t) &= \sigma_S^E(t) - \sigma_E^C(t) - \nu_d E(t) \\
C'(t) &= \sigma_E^C(t) - \sigma_C^I(t) - \sigma_C^R(t) - \nu_d C(t), \\
I'(t) &= \sigma_C^I(t) - \sigma_I^H(t) - \sigma_I^R(t) - \nu_d I(t), \\
H'(t) &= \sigma_I^H(t) - \sigma_H^U(t) - \sigma_H^R(t) - \nu_d H(t), \\
U'(t) &= \sigma_H^U(t) - \sigma_U^D(t) - \sigma_U^R(t) - \nu_d U(t), \\
R'(t) &= \sigma_C^R(t) + \sigma_I^R(t) + \sigma_H^R(t) + \sigma_U^R(t) - \nu_d R(t), \\
D'(t) &= \sigma_U^D(t).
\end{aligned}
\tag{2.17}
$$

We now want to derive the formulas for the transitions $\sigma_{z_1}^{z_2}$ using (2.17). Therefore, we take the derivative of the compartment formulas in (2.15) . For simplicity we only consider the compartment C. The equations for the other compartments can be derived analogously. By using the Leibniz rule for integrals and the assumption that $\gamma_{z_1}^{z_2}(0) = 1$, we compute for $C'(t)$

$$
\begin{aligned}
C'(t) &= \frac{d}{dt}\left(\int_0^t \left(\mu_C^I\,\gamma_C^I(t-s) + \left(1-\mu_C^I\right)\gamma_C^R(t-s)\right)\sigma_E^C(s)e^{-\nu_d(t-s)}\ ds\right) + C_0'(t) \\
&= \left(\mu_C^I\,\gamma_C^I(0) + \left(1-\mu_C^I\right)\gamma_C^R(0)\right)\sigma_E^C(t)e^0 \\
&\quad + \int_0^t \left(\mu_C^I\,\gamma_C^{I\prime}(t-s) + \left(1-\mu_C^I\right)\gamma_C^{R\prime}(t-s)\right)\sigma_E^C(s)e^{-\nu_d(t-s)}\ ds \\
&\quad - \int_0^t \left(\mu_C^I\,\gamma_C^I(t-s) + \left(1-\mu_C^I\right)\gamma_C^R(t-s)\right)\sigma_E^C(s)\nu_d e^{-\nu_d(t-s)}\ ds \\
&\quad - \nu_d e^{-\nu_d t}C_0\gamma_C(t) + C_0 e^{-\nu_d t}\gamma_C'(t) \\
&= \sigma_E^C(t) - \nu_d C(t) \\
&\quad + \int_0^t \left(\mu_C^I\,\gamma_C^{I\prime}(t-s) + \left(1-\mu_C^I\right)\gamma_C^{R\prime}(t-s)\right)\sigma_E^C(s)e^{-\nu_d(t-s)}\ ds
\end{aligned}
$$

$$
\begin{aligned}
&+ C_0 e^{-\nu_d t}\left(\mu_C^I \gamma_C^{I\prime}(t) + (1-\mu_C^I)\gamma_C^{R\prime}(t)\right) \\
&= \sigma_E^C(t) + \underbrace{\int_0^t \mu_C^I \gamma_C^{I\prime}(t-s)\sigma_E^C e^{-\nu_d(t-s)}\, ds + e^{-\nu_d t} C_0 \mu_C^I \gamma_C^{I\prime}(t)}_{=-\sigma_C^I(t)} \\
&\quad + \underbrace{\int_0^t (1-\mu_C^I)\gamma_C^{R\prime}(t-s)\sigma_E^C e^{-\nu_d(t-s)}\, ds + e^{-\nu_d t} C_0 (1-\mu_C^I)\gamma_C^{R\prime}(t)}_{=-\sigma_C^R(t)} - \nu_d C(t)
\end{aligned}
$$

The equations for the transitions can then be written

$$
\begin{aligned}
\sigma_S^E(t) &= \lambda(t)S(t), \\
\sigma_E^C(t) &= -\int_0^t \sigma_S^E(s) e^{-\nu_d(t-s)} \gamma_E^{C\prime}(t-s) ds - e^{-\nu_d t} E_0 \gamma_E^{C\prime}(t), \\
\sigma_C^I(t) &= -\int_0^t \sigma_E^C(s) e^{-\nu_d(t-s)} \mu_C^I \gamma_C^{I\prime}(t-s)\, ds - e^{-\nu_d t} C_0 \mu_C^I \gamma_C^{I\prime}(t), \\
\sigma_C^R(t) &= -\int_0^t \sigma_E^C(s) e^{-\nu_d(t-s)} (1-\mu_C^I) \gamma_C^{R\prime}(t-s)\, ds - e^{-\nu_d t} C_0 (1-\mu_C^I) \gamma_C^{R\prime}(t), \\
\sigma_I^H(t) &= -\int_0^t \sigma_C^I(s) e^{-\nu_d(t-s)} \mu_I^H \gamma_I^{H\prime}(t-s)\, ds - e^{-\nu_d t} I_0 \mu_I^H \gamma_I^{H\prime}(t), \\
\sigma_I^R(t) &= -\int_0^t \sigma_C^I(s) e^{-\nu_d(t-s)} (1-\mu_I^H) \gamma_I^{R\prime}(t-s)\, ds - e^{-\nu_d t} I_0 (1-\mu_I^H) \gamma_I^{R\prime}(t), \\
\sigma_H^U(t) &= -\int_0^t \sigma_I^H(s) e^{-\nu_d(t-s)} \mu_H^U \gamma_H^{U\prime}(t-s)\, ds - e^{-\nu_d t} H_0 \mu_H^U \gamma_H^{U\prime}(t), \\
\sigma_H^R(t) &= -\int_0^t \sigma_I^H(s) e^{-\nu_d(t-s)} (1-\mu_H^U) \gamma_H^{R\prime}(t-s)\, ds - e^{-\nu_d t} H_0 (1-\mu_H^U) \gamma_H^{R\prime}(t), \\
\sigma_U^D(t) &= -\int_0^t \sigma_H^U(s) e^{-\nu_d(t-s)} \mu_U^D \gamma_U^{D\prime}(t-s)\, ds - e^{-\nu_d t} U_0 \mu_U^D \gamma_U^{D\prime}(t), \\
\sigma_U^R(t) &= -\int_0^t \sigma_H^U(s) e^{-\nu_d(t-s)} (1-\mu_U^D) \gamma_U^{R\prime}(t-s)\, ds - e^{-\nu_d t} U_0 (1-\mu_U^D) \gamma_U^{R\prime}(t).
\end{aligned}
\tag{2.18}
$$

Before proving some properties of the model, we want to introduce the concept of the mean infectivity.

Definition 2.1. *We first define*

$$
\begin{aligned}
B_C(s) &= \xi_C(s)\gamma_C(s), \\
B_I(s) &= \xi_I(s)\gamma_I(s), \quad \textit{and} \\
B(s) &= \int_0^s B_I(v)\mu_C^I \gamma_C^{I\prime}(s-v)\, dv.
\end{aligned}
\tag{2.19}
$$

Then let a_1, a_2 be defined as

$$\begin{aligned} a_1(\tau) &= -e^{-\nu_d \tau} \int_0^\tau B_C(u) \gamma_E^{C\,\prime}(\tau - u)\, du, \\ a_2(\tau) &= e^{-\nu_d \tau} \int_0^\tau \gamma_E^{C\,\prime}(\tau - u) B(u)\ du. \end{aligned} \tag{2.20}$$

Finally, we define the mean infectivity

$$A(\tau) = (a_1(\tau) + a_2(\tau)). \tag{2.21}$$

Remark 2.9. *Then, A is non-negative as both a_1 and a_2 are non-negative. This is true, since $\gamma_E^{C\,\prime}(t) \leq 0$ for all t.*

2.2.1 Properties of the SECIR-type birth-and-death model

In this section, we will prove some helpful results about Model (2.15), that we are going to use in the further analysis of the model.

In the following, we will show an alternative version of the force of infection term. This version will be useful for the further analysis of equilibria in Section 3.

Lemma 2.10. *We can write $\lambda(t)$ from (2.13) as*

$$\lambda(t) = \lambda_0(t) + \frac{\phi(t)\,\rho(t)}{N(t)} \int_0^t \lambda(s) S(s) A(t-s)\, ds + \frac{\phi(t)\,\rho(t)}{N(t)} f(t), \tag{2.22}$$

with

$$f(t) = E_0 A(t) - C_0 e^{-\nu_d t} B(t) \tag{2.23}$$

Here, $B(t)$ and $A(t)$ are given by (2.19) and (2.21).

Proof. By applying a change of variables s to $t - \tau$, we compute for the first term of λ (2.13)

$$\begin{aligned} &\int_0^t e^{-\nu_d(t-s)} B_C(t-s) \sigma_E^C(s) ds \\ &= -\int_0^t B_C(t-s) e^{-\nu_d(t-s)} \left(\int_0^s \lambda(u) S(u) e^{-\nu_d(s-u)} \gamma_E^{C\,\prime}(s-u) du + e^{-\nu_d s} E_0 \gamma_E^{C\,\prime}(s) \right) ds \\ &= -\int_0^t B_C(\tau) e^{-\nu_d \tau} \left(\int_0^{t-\tau} \lambda(u) S(u) e^{-\nu_d(t-\tau-u)} \gamma_E^{C\,\prime}(t-\tau-u) du \right) d\tau \\ &\quad - \int_0^t B_C(\tau) e^{-\nu_d t} E_0 \gamma_E^{C\,\prime}(t-\tau)\ d\tau \\ &= -\int_0^t \lambda(u) S(u) e^{-\nu_d(t-u)} \left(\int_0^{t-u} B_C(\tau) \gamma_E^{C\,\prime}(t-\tau-u) d\tau \right) du \\ &\quad - \int_0^t B_C(u) E_0 e^{-\nu_d t} \gamma_E^{C\,\prime}(t-u)\ du \end{aligned}$$

Similarly, for the second term of λ (2.13) we compute

$$\begin{aligned}
&\int_0^t e^{-\nu_d(t-s)} B_I(t-s)\sigma_C^I(s)ds \\
&= -\int_0^t e^{-\nu_d(t-s)} B_I(t-s)\left(\int_0^s \sigma_E^C(u)e^{-\nu_d(s-u)}\mu_C^I\gamma_C^{I\prime}(s-u)\ du + e^{-\nu_d s}C_0\mu_C^I\gamma_C^{I\prime}(s)\right)\ ds \\
&= -\int_0^t e^{-\nu_d\tau} B_I(\tau)\left(\int_0^{t-\tau} \sigma_E^C(u)e^{-\nu_d(t-\tau-u)}\mu_C^I\gamma_C^{I\prime}(t-\tau-u)\ du\right)d\tau \\
&\quad -\int_0^t B_I(\tau)C_0e^{-\nu_d t}\mu_C^I\gamma_C^{I\prime}(t-\tau))\ d\tau \\
&= -\int_0^t \sigma_E^C(u)e^{-\nu_d(t-u)}\underbrace{\left(\int_0^{t-u} B_I(\tau)\mu_C^I\gamma_C^{I\prime}(t-\tau-u)\ d\tau\right)}_{=:B(t-u)}\ du \\
&\quad -\int_0^t B_I(u)C_0e^{-\nu_d t}\mu_C^I\gamma_C^{I\prime}(t-u)\ du.
\end{aligned}$$

We now take a closer look at the first integral above

$$-\int_0^t \sigma_E^C(u)e^{-\nu_d(t-u)}B(t-u)\ du.$$

We can see that it has the same form as the first part of λ (2.13) with $B(t-u)$ instead of $B_C(t-u)$. Therefore, applying the same computations to this as to the first part of λ, yields

$$\begin{aligned}
&\int_0^t e^{-\nu_d(t-s)} B_I(t-s)\sigma_C^I(s)ds \\
&= \int_0^t \lambda(u)S(u)e^{-\nu_d(t-u)}\left(\int_0^{t-u} B(\tau)\gamma_E^{C\prime}(t-\tau-u)d\tau\right)\ du \\
&\quad +\int_0^t B(u)E_0e^{-\nu_d t}\gamma_E^{C\prime}(t-u)du \\
&\quad -\int_0^t B_I(u)C_0e^{-\nu_d t}\mu_C^I\gamma_C^{I\prime}(t-u)\ du.
\end{aligned}$$

Putting the formulas we computed for the first and second term of the force of infection λ (2.13) together yields

$$\begin{aligned}
&\int_0^t e^{-\nu_d(t-s)} B_C(t-s)\sigma_E^C(s) + e^{-\nu_d(t-s)} B_I(t-s)\sigma_C^I(s)ds \\
&\quad = \int_0^t \lambda(u)S(u)e^{-\nu_d(t-u)}\left(\int_0^{t-u} \gamma_E^{C\prime}(t-\tau-u)(B(\tau)-B_C(\tau))\ d\tau\right)du \\
&\qquad -\int_0^t B_C(u)E_0e^{-\nu_d t}\gamma_E^{C\prime}(t-u)\ du
\end{aligned}$$

$$
\begin{aligned}
&+ \int_0^t B(u) E_0 e^{-\nu_d t} \gamma_E^{C\,\prime}(t-u) du \\
&- \int_0^t B_I(u) C_0 e^{-\nu_d t} \mu_C^I \gamma_C^{I\,\prime}(t-u)\ du \\
&= \int_0^t \lambda(u) S(u) A(t-u)\ du + f(t).
\end{aligned}
$$

What finishes the proof. □

That new version of the force of infection term λ is going to be useful for later analysis. Moreover, it allows us to comment on the existence of a solution for our model. From a biological point of view, it only makes sense to work with non-negative solutions, as we cannot have a negative amount of individuals in a compartment. From the equations for the compartments (2.15) and the transition (2.18) we cannot directly show that every solution to these equations has to be non-negative. Therefore, we want to talk briefly about the existence of solutions. First of all, we realize that we have a Volterra integral equation for S (2.16) and λ (2.22). Volterra integral equations have the following form

$$
X(t) = F(t) + \int_0^t K(t,\tau) G(X(\tau))\ d\tau. \tag{2.24}
$$

Then in our case we set

$$
X(t) = \begin{pmatrix} S(t) \\ \lambda(t) \end{pmatrix}, \qquad F(t) = \begin{pmatrix} S_0 e^{-\nu_d t} + \int_0^t \nu_b N(s) e^{-\nu_d (t-s)}\ ds \\ \lambda_0(t) + \frac{\phi(t)\rho(t)}{N(t)} f(t) \end{pmatrix},
$$

$$
K(t,\tau) = \begin{pmatrix} 0 & -e^{-\nu_d(\tau)} \\ 0 & \frac{\phi(t)\rho(t)}{N(t)} A(\tau) \end{pmatrix}, \qquad G(X(\tau)) = \begin{pmatrix} S(\tau) \\ \lambda(\tau) S(\tau) \end{pmatrix}.
$$

There is plenty of literature about Volterra equations and the existence of solutions of such equations, see for example [16, 17, 18]. We assume from now on that there exists a non-negative solution to our equations, as negative solutions void of biological meaning. However, non-negativity of solutions is a non-trivial property of a solution. Nevertheless, from now on we assume that all the compartments and transitions are non-negative. This also implies that all compartments are smaller than the population size $N(t)$, by definition.

Now we want to show a bound for the force of infection term.

Lemma 2.11. *For all $t \in (-\infty, \infty)$, it holds*

$$
\lambda(t) \leq \phi(t)\rho(t). \tag{2.25}
$$

Proof. We will use $\xi_C(s), \xi_I(s) \leq 1$ for all $t, s \in (-\infty, \infty)$ and $C(t) + I(t) \leq N(t)$. Then, defining λ as in (2.6) we can compute

$$
\begin{aligned}
\lambda(t) &\leq \frac{\phi(t)\,\rho(t)(C_0(t)+I_0(t))}{N(t)} \\
&\quad + \frac{\phi(t)\,\rho(t)}{N(t)} \int_0^t \left(\mu_C^I\,\gamma_C^I(t-s) + \left(1-\mu_C^I\right)\gamma_C^R(t-s)\right)\sigma_E^C(s)e^{-\nu_d(t-s)} \\
&\qquad\qquad + \left(\mu_I^H\,\gamma_I^H(t-s) + \left(1-\mu_I^H\right)\gamma_I^R(t-s)\right)\sigma_C^I(s)e^{-\nu_d(t-s)}\;ds \\
&= \frac{\phi(t)\,\rho(t)}{N(t)}\,(C(t)+I(t)) \\
&\leq \phi(t)\rho(t).
\end{aligned}
$$

□

Lemma 2.12. *For fixed $t \in (0,\infty)$, it holds*

1. $0 \leq A(t) \leq 2$ *for all* $t \in [0,\infty)$,
2. $\int_0^\infty A(\tau)\;d\tau < \infty$,
3. $\lim_{t\to\infty} B(t) = 0$ *and* $\lim_{t\to\infty} A(t) = 0$.

To prove this lemma, we need some properties of convolutions. First, we recall the definition of a convolution, that is for $p, q : \mathbb{R} \to \mathbb{R}$ defined as

$$
(p * q)(t) = \int_{\mathbb{R}} p(t-s)q(s)\;ds. \tag{2.26}
$$

Then we have the following lemma.

Lemma 2.13. *It holds for all $p, q : \mathbb{R} \to \mathbb{R}$*

$$
||p * q||_{L_1(\mathbb{R})} \leq ||p||_{L_1(\mathbb{R})}||q||_{L_1(\mathbb{R})}.
$$

Moreover, if $p \in L^1(\mathbb{R})$ and $q \in L^1(\mathbb{R}) \cap L^\infty(\mathbb{R})$ it holds

$$
\lim_{t\to\infty} (p * q)(t) = 0.
$$

Proof. The first statement is proven in [19] and is a special case of Young's convolution inequality. The second statement is an exercise of [19], therefore we will present the proof here.

We first assume that $p \in C_c^\infty(\mathbb{R})$, then we know that there is some $R > 0$ such that $\text{supp}(p) \subset B_R(0)$. Then, for $|t| > R$, we have that $p(t-s)q(s) = 0$ if $|s| < |t| - R$. This implies for $|t| > R$

$$
\begin{aligned}
(p * q)(t) &= \int_{\mathbb{R}} p(t-s)q(s)ds \\
&\leq \left(\max_{t\in\mathbb{R}} |p(t)|\right) \int_{\mathbb{R}\setminus B_{|t|-R}(0)} q(s)\;ds \to 0 \quad \text{for } |t| \to \infty.
\end{aligned}
$$

Here we used that $q \in L^1(\mathbb{R})$. This proves the statement for all $p \in C_c^\infty(\mathbb{R})$. Now, we proof the statement for all $p \in L^1(\mathbb{R})$. We choose a sequence $p_n \in C_c^\infty(\mathbb{R})$ that converges to p in L^1, this sequence exists by density. We compute

$$\begin{aligned}|(p_n * q)(t) - (p * q)(t)| &= \left| \int_{\mathbb{R}} (p_n - p)(t-s) q(s) \, ds \right| \\ &\leq ||p_n - p||_{L^1(\mathbb{R})} ||g||_{L^\infty(\mathbb{R})} \to 0 \quad \text{as } n \to \infty.\end{aligned}$$

Here we used the Hölder inequality. This shows that the convolutions $p_n * q$ converge uniformly to $p * q$. This implies that $(p * q)(t) \to 0$ as $t \to \infty$, which concludes the proof. □

Using Lemma 2.13 we are now able to prove Lemma 2.12.

Proof of Lemma 2.12. In Remark 2.9 we already stated that A is non-negative. For the first statement we easily compute

$$\begin{aligned}a_1(\tau) &= -e^{-\nu_d \tau} \int_0^\tau \xi_C(u) \left(\mu_C^I \, \gamma_C^I(u) + \left(1 - \mu_C^I\right) \gamma_C^R(u) \right) \gamma_E^{C\prime}(\tau - u) \, du \\ &\leq \int_0^\tau (-\gamma_E^{C\prime}(\tau - u)) \, du \\ &\leq \int_{-\infty}^\infty -\gamma_E^{C\prime}(s) \, ds = 1,\end{aligned}$$

and

$$\begin{aligned}a_2(\tau) &= e^{-\nu_d \tau} \int_0^\tau \left(\int_0^u \xi_I(v) \left(\mu_I^H \, \gamma_I^H(v) + \left(1 - \mu_I^H\right) \gamma_I^R(v) \right) \mu_C^I \gamma_C^{I\prime}(u - v) \, dv \right) \gamma_E^{C\prime}(\tau - u) \, du \\ &\leq \int_0^\tau \left(\int_0^u (-\gamma_C^{I\prime}(u - v)) \, dv \right) (-\gamma_E^{C\prime}(\tau - u)) \, du \\ &\leq \int_0^\tau (-\gamma_E^{C\prime}(\tau - u)) \, du \leq 1.\end{aligned}$$

In both estimates we used that $-\gamma_E^{C\prime}(\tau)$ is a probability density function. Then together we have

$$A(\tau) = (a_1(\tau) + a_2(\tau)) \leq 2.$$

Now, we show the other statements. We start with a_1, where we want to make use of Lemma 2.13. Therefore, we define

$$\begin{aligned}q(u) &\coloneqq \begin{cases} \xi_C(u) \left(\mu_C^I \, \gamma_C^I(u) + \left(1 - \mu_C^I\right) \gamma_C^R(u) \right) & \text{if } u \geq 0 \\ 0 & \text{if } u < 0 \end{cases} \\ p(u) &\coloneqq \begin{cases} -\gamma_E^{C\prime}(u) & \text{if } u \geq 0 \\ 0 & \text{if } u < 0. \end{cases}\end{aligned}$$

Then, by assumption $p \in L^1(\mathbb{R})$ and $q \in L^1(\mathbb{R})$, and Lemma 2.13 gives us that

$$\begin{aligned} a_1(\tau) &= -e^{-\nu_d \tau} \int_0^\tau \xi_C(u) \left(\mu_C^I \gamma_C^I(u) + \left(1 - \mu_C^I\right) \gamma_C^R(u)\right) \gamma_E^{C\,\prime}(\tau - u)\, du \\ &\leq -\int_{-\infty}^{\infty} p(u) q(\tau - u)\, du, \end{aligned}$$

and therefore $a_1 \in L^1((0,\infty))$. Moreover, we have that $q \in L^\infty(\mathbb{R})$ and, therefore, we can also apply the second part of Lemma 2.13 and get

$$\lim_{\tau \to \infty} a_1(\tau) = 0.$$

Now, we take a look at a_2 and start with the inner integral

$$B(u) = \int_0^u \xi_I(v) \left(\mu_I^H \gamma_I^H(v) + \left(1 - \mu_I^H\right) \gamma_I^R(v)\right) \mu_C^I \gamma_C^{I\,\prime}(\tau - v)\, dv.$$

With the same trick as above we see that $B(u) \in L^1(0,\infty)$ and $\lim_{u\to\infty} B(u) = 0$. Moreover, we know that $B(u) \in L^\infty((0,\infty))$. Then we apply the trick from above again and get that $a_2 \in L^1((0,\infty))$ and $\lim_{\tau\to 0} a_2(\tau) = 0$. A combination of both results yields the claim of the lemma. □

The following lemma shows that we can neglect the initial conditions in the long-term analysis of the model.

Lemma 2.14. *Let $Z \in \{E, C, I, H, U, R\}$, the following statements hold true.*

1. $\lim_{t\to\infty} e^{-\nu_d t} Z_0(t) = 0$,
2. *for every $X \in \{E, C, I, H, U, R, D\}$ such that there exists a transition from Z to X there holds* $\lim_{t\to\infty} e^{-\nu_d t} Z_0 \gamma_Z^{X\,\prime}(t) = 0$,
3. $\lim_{t\to\infty} f(t) = 0$ *and if we furthermore assume that* $\lim_{t\to\infty} N(t) > 0$ *we also have* $\liminf_{t\to\infty} \lambda_0(t) = 0$.

Proof. We show each claim separately.

1. For $Z \in \{E, C, I, H, U, \}$ we already saw in Remark 2.7 that $Z_0(t) \to 0$ as $t \to \infty$. Then we obviously have $e^{-\nu_d t} Z_0(t) \to 0$ as $t \to \infty$. Since $D_0(t) = D_0$ is constant, we also have $e^{-\nu_d t} D_0(t) \to 0$ as $t \to \infty$.
2. By Assumption 2.1 we know that $\lim_{t\to\infty} \gamma_Z^{X\,\prime}(t) = 0$, and we have $\lim_{t\to\infty} e^{-\nu_d t} = 0$. This shows the claim.
3. For $\lambda_0(t)$, we again use that $C_0(t), I_0(t) \to 0$ as $t \to \infty$. For $f(t)$, we directly see that the first term $E_0 A(t)$ converges to zero by Lemma 2.12.

□

2.3 A normalized SECIR-type birth-and-death model

The goal of this thesis is to study the long-term behaviour of the SECIR-type birth-and-death model, an important part of this is the stability analysis of equilibria. In most cases, we do not have a constant population size for the SECIR-type birth-and-death model given in Section 2.2. This makes the long-term analysis very complicated, and it is not clear how an equilibrium in this case is defined. In this Section, we will therefore introduce a normalized model, in order to study the dynamics of the disease independently of the change in the population size. When normalizing a model, we divide every compartment by the population size N. In [11] and [12], the authors study a model based on ordinary differential equations with a non-constant population size. The ordinary differential equations allow for a direct derivation of the normalized model. However, when using IDE-based formulations as introduced before, the procedure is more complicated. In our case the integro-differential equations make this more complicated, since the factor $\frac{1}{N(t)}$ cannot be taken into the integrand. We therefore suggest the following model for which we we are not able to show that it is the correct normalized formulation of model (2.15). Later on in Section 5, we will demonstrate numerically that the corresponding discretized model provides qualitatively and quantitatively similar outcomes.

To initialize our normalized model we use $z_0 = \frac{Z_0}{N_0}$, with Z_0 as in the SECIR-type birth-and-death model in Section 2.2. Moreover, we define

$$\begin{aligned} e_0(t) &= e^{-\nu_d t} e_0 \gamma_E^C(t), & c_0(t) &= e^{-\nu_d t} c_0 \gamma_C(t), \\ i_0(t) &= e^{-\nu_d t} i_0 \gamma_I(t), & h_0(t) &= e^{-\nu_d t} h_0 \gamma_H(t), \\ u_0(t) &= e^{-\nu_d t} u_0 \gamma_U(t), & r_0(t) &= e^{-\nu_d t} r_0. \end{aligned} \tag{2.27}$$

As already mentioned, in models based on ordinary differential equations, it is easy to derive the normalized version of the model. Therefore, we will start by recalling that the derivatives of (2.15) are given by (2.17), that is

$$\begin{aligned} S'(t) &= -\sigma_S^E(t) + \nu_b N(t) - \nu_d S(t), \\ E'(t) &= \sigma_S^E(t) - \sigma_E^C(t) - \nu_d E(t) \\ C'(t) &= \sigma_E^C(t) - \sigma_C^I(t) - \sigma_C^R(t) - \nu_d C(t), \\ I'(t) &= \sigma_C^I(t) - \sigma_I^H(t) - \sigma_I^R(t) - \nu_d I(t), \\ H'(t) &= \sigma_I^H(t) - \sigma_H^U(t) - \sigma_H^R(t) - \nu_d H(t), \\ U'(t) &= \sigma_H^U(t) - \sigma_U^D(t) - \sigma_U^R(t) - \nu_d U(t), \\ R'(t) &= \sigma_C^R(t) + \sigma_I^R(t) + \sigma_H^R(t) + \sigma_U^R(t) - \nu_d R(t) \\ N'(t) &= \nu_b N(t) - \nu_d N(t) - \sigma_U^D(t). \end{aligned}$$

To compute the derivatives of the normalized compartments, we make use of the quotient rule

$$\begin{aligned} z'(t) &= \frac{d}{dt}\left(\frac{Z(t)}{N(t)}\right) = \frac{Z'(t)N(t) - Z(t)N'(t)}{N^2(t)} \\ &= \frac{Z'(t)}{N(t)} - z(t)\frac{N'(t)}{N(t)}. \end{aligned}$$

This yields

$$\begin{aligned} s'(t) &= -\lambda(t)s(t) + (1-s(t))\nu_b + s(t)\frac{\sigma_U^D(t)}{N(t)}, \\ e'(t) &= \lambda(t)s(t) - \frac{\sigma_E^C(t)}{N(t)} - \nu_b e(t) + e(t)\frac{\sigma_U^D(t)}{N(t)}, \\ c'(t) &= \frac{\sigma_E^C(t)}{N(t)} - \frac{\sigma_C^I(t) + \sigma_C^R(t)}{N(t)} - \nu_b c(t) + c(t)\frac{\sigma_U^D(t)}{N(t)}, \\ i'(t) &= \frac{\sigma_C^I(t)}{N(t)} - \frac{\sigma_I^H(t) + \sigma_I^R(t)}{N(t)} - \nu_b i(t) + i(t)\frac{\sigma_U^D(t)}{N(t)}, \\ h'(t) &= \frac{\sigma_I^H(t)}{N(t)} - \frac{\sigma_H^U(t) + \sigma_H^R(t)}{N(t)} - \nu_b h(t) + h(t)\frac{\sigma_U^D(t)}{N(t)}, \\ u'(t) &= \frac{\sigma_H^U(t)}{N(t)} - \frac{\sigma_U^D(t) + \sigma_U^R(t)}{N(t)} - \nu_b u(t) + u(t)\frac{\sigma_U^D(t)}{N(t)}, \\ r'(t) &= \frac{\sigma_C^R(t) + \sigma_I^R(t) + \sigma_H^R(t) + \sigma_U^R(t)}{N(t)} - \nu_b r(t) + r(t)\frac{\sigma_U^D(t)}{N(t)}. \end{aligned} \tag{2.28}$$

We directly see that in the normalized version of the derivatives (2.28), the force of infection term λ from Model (2.15) still appears in the same form. There is no obvious way to get rid of the term $\frac{1}{N(t)}$ in the definition of the force of infection term of the SECIR-type birth-and-death model in (2.13). But, as we cannot predict the population size without knowing the behaviour of the compartments which again depends on the force of infection term, the long-term analysis of the model would be very complicated. Therefore, we slightly change the definition of the force of infection term and call it l. As its definition depends on the definitions of c and i we will give it after defining the compartments. Then, in order to define the compartments we guess an

integral formulation that suits the derivatives for the compartments given in (2.28). This yields

$$
\begin{aligned}
s'(t) &= -l(t)s(t) + (1-s(t))\nu_b + s(t)\sigma_u^d(t),\\
e(t) &= \int_0^t \gamma_E^C(t-\tau)e^{-\nu_d(t-\tau)}l(\tau)s(\tau)\ d\tau + e_0(t)\\
&\quad + \int_0^t \gamma_E^C(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d + \sigma_u^d(\tau) - \nu_b\right)e(\tau)\ d\tau,\\
c(t) &= \int_0^t \gamma_C(t-\tau)e^{-\nu_d(t-\tau)}\sigma_e^c(\tau)\ d\tau + c_0(t)\\
&\quad + \int_0^t \gamma_C(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d + \sigma_u^d(\tau) - \nu_b\right)c(\tau)\ d\tau,\\
i(t) &= \int_0^t \gamma_I(t-\tau)e^{-\nu_d(t-\tau)}\sigma_c^i(\tau)\ d\tau + i_0(t)\\
&\quad + \int_0^t \gamma_I(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d + \sigma_u^d(\tau) - \nu_b\right)i(\tau)\ d\tau,\\
h(t) &= \int_0^t \gamma_H(t-\tau)e^{-\nu_d(t-\tau)}\sigma_i^h(\tau)\ d\tau + h_0(t)\\
&\quad + \int_0^t \gamma_H(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d + \sigma_u^d(\tau) - \nu_b\right)h(\tau)\ d\tau,\\
u(t) &= \int_0^t \gamma_U(t-\tau)e^{-\nu_d(t-\tau)}\sigma_h^u(\tau)\ d\tau + u_0(t)\\
&\quad + \int_0^t \gamma_U(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d + \sigma_u^d(\tau) - \nu_b\right)u(\tau)\ d\tau,\\
r(t) &= \int_0^t e^{-\nu_d(t-\tau)}\left(\sigma_c^r(\tau) + \sigma_i^r(\tau) + \sigma_h^r(\tau) + \sigma_h^r(\tau)\right)\ d\tau + r_0(t)\\
&\quad + \int_0^t e^{-\nu_d(t-\tau)}\left(\nu_d + \sigma_u^d(\tau) - \nu_b\right)r(\tau)\ d\tau.
\end{aligned}
\tag{2.29}
$$

Before, the force of infection term was given by some modified $\frac{C(t)+I(t)}{N(t)}$, as C and I are the only infectious compartments. The idea now is to modify $\frac{C(t)+I(t)}{N(t)} = c(t) + i(t)$, the same way as described for λ in Remark 2.4. This yields

$$
\begin{aligned}
l(t) = l_0(t) + \phi(t)\rho(t) \int_0^t & B_C(t-\tau)e^{-\nu_d(t-\tau)}\sigma_e^c(\tau)\\
&+B_C(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d + \sigma_u^d(\tau) - \nu_b\right)c(\tau)\\
&+B_I(t-\tau)e^{-\nu_d(t-\tau)}\sigma_c^i(\tau)\\
&+B_I(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d + \sigma_u^d(\tau) - \nu_b\right)i(\tau)\ d\tau,
\end{aligned}
\tag{2.30}
$$

with

$$
l_0(t) = \phi(t)\rho(t)\left(c_0(t)\xi_C(t) + i_0(t)\xi_I(t)\right), \tag{2.31}
$$

and B_C, B_I given in (2.19). At last, we define the transitions by

$$
\begin{aligned}
\sigma_e^c(t) &= -\int_0^t \gamma_E^{C\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}l(\tau)s(\tau)\ d\tau - e^{-\nu_d t}e_0\gamma_E^{C\,\prime}(t) \\
&\quad -\int_0^t \gamma_E^{C\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d+\sigma_u^d(\tau)-\nu_b\right)e(\tau)\ d\tau, \\
\sigma_c^i(t) &= -\int_0^t \mu_C^I\gamma_C^{I\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\sigma_e^c(\tau)\ d\tau - e^{-\nu_d t}c_0\mu_C^I\gamma_C^{I\,\prime}(t) \\
&\quad -\int_0^t \mu_C^I\gamma_C^{I\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d+\sigma_u^d(\tau)-\nu_b\right)c(\tau)\ d\tau, \\
\sigma_c^r(t) &= -\int_0^t (1-\mu_C^I)\gamma_C^{R\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\sigma_e^c(\tau)\ d\tau - e^{-\nu_d t}c_0(1-\mu_C^I)\gamma_C^{R\,\prime}(t) \\
&\quad -\int_0^t (1-\mu_C^I)\gamma_C^{R\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d+\sigma_u^d(\tau)-\nu_b\right)c(\tau)\ d\tau, \\
\sigma_i^h(t) &= -\int_0^t \mu_I^H\gamma_I^{H\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\sigma_c^i(\tau)\ d\tau - e^{-\nu_d t}i_0\mu_I^H\gamma_I^{H\,\prime}(t) \\
&\quad -\int_0^t \mu_I^H\gamma_I^{H\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d+\sigma_u^d(\tau)-\nu_b\right)i(\tau)\ d\tau, \\
\sigma_i^r(t) &= -\int_0^t (1-\mu_I^H)\gamma_I^{R\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\sigma_c^i(\tau)\ d\tau - e^{-\nu_d t}i_0(1-\mu_I^H)\gamma_I^{H\,\prime}(t) \\
&\quad -\int_0^t (1-\mu_I^H)\gamma_I^{R\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d+\sigma_u^d(\tau)-\nu_b\right)i(\tau)\ d\tau, \\
\sigma_h^u(t) &= -\int_0^t \mu_H^U\gamma_H^{U\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\sigma_i^h(\tau)\ d\tau - e^{-\nu_d t}h_0\mu_H^U\gamma_H^{U\,\prime}(t) \\
&\quad -\int_0^t \mu_H^U\gamma_H^{U\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d+\sigma_u^d(\tau)-\nu_b\right)h(\tau)\ d\tau, \\
\sigma_h^r(t) &= -\int_0^t (1-\mu_H^U)\gamma_H^{R\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\sigma_i^h(\tau)\ d\tau - e^{-\nu_d t}h_0(1-\mu_H^U)\gamma_H^{R\,\prime}(t) \\
&\quad -\int_0^t (1-\mu_H^U)\gamma_H^{R\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d+\sigma_u^d(\tau)-\nu_b\right)h(\tau)\ d\tau, \\
\sigma_u^d(t) &= -\int_0^t \mu_U^D\gamma_U^{D\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\sigma_h^u(\tau)\ d\tau - e^{-\nu_d t}u_0\mu_U^D\gamma_U^{D\,\prime}(t) \\
&\quad -\int_0^t \mu_U^D\gamma_U^{D\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d+\sigma_u^d(\tau)-\nu_b\right)u(\tau)\ d\tau, \\
\sigma_u^r(t) &= -\int_0^t (1-\mu_U^D)\gamma_U^{R\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\sigma_h^u(\tau)\ d\tau - e^{-\nu_d t}u_0(1-\mu_U^D)\gamma_U^{R\,\prime}(t) \\
&\quad -\int_0^t (1-\mu_U^D)\gamma_U^{R\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d+\sigma_u^d(\tau)-\nu_b\right)u(\tau)\ d\tau.
\end{aligned}
\tag{2.32}
$$

If we compute the derivatives of the compartments (2.29) using the definition of the trans-

itions (2.32) we get the derivatives from (2.28) with use l instead of λ. We show this exemplary for the compartment c. Using the Leibniz rule for integrals gives us

$$\begin{aligned}
c'(t) &= \gamma_C(0)e^0 \left(\sigma_e^c(t) + \left(\nu_d + \sigma_u^d(t) - \nu_b\right) c(t)\right) \\
&\quad - \nu_d \int_0^t \gamma_C(t-\tau)e^{-\nu_d(t-\tau)} \left(\sigma_e^c(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) c(\tau)\right)\, d\tau \\
&\quad + \int_0^t \gamma_C'(t-\tau)e^{-\nu_d(t-\tau)} \left(\sigma_e^c(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) c(\tau)\right)\, d\tau \\
&\quad + c_0'(t) \\
&= \sigma_e^c(t) + \left(\nu_d + \sigma_u^d(t) - \nu_b\right) c(t) \\
&\quad - \nu_d \int_0^t \gamma_C(t-\tau)e^{-\nu_d(t-\tau)} \left(\sigma_e^c(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) c(\tau)\right)\, d\tau \\
&\quad + \int_0^t \left(\mu_C^I \gamma_C^{I\prime}(t-\tau) + (1-\mu_C^I)\gamma_C^{R\prime}(t-\tau)\right) e^{-\nu_d(t-\tau)} \\
&\qquad \cdot \left(\sigma_e^c(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) c(\tau)\right)\, d\tau \\
&\quad - \nu_d c_0(t) + e^{-\nu_d t} c_0 \left(\mu_C^I \gamma_C^{I\prime}(t) + (1-\mu_C^I)\gamma_C^{R\prime}(t)\right) \\
&= \sigma_e^c(t) + \left(\nu_d + \sigma_u^d(t) - \nu_b\right) c(t) - \nu_d c(t) \\
&\quad + \int_0^t \mu_C^I \gamma_C^{I\prime}(t-\tau)e^{-\nu_d(t-\tau)} \left(\sigma_e^c(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) c(\tau)\right)\, d\tau \\
&\quad + e^{-\nu_d t} c_0 \mu_C^I \gamma_C^{I\prime}(t) \\
&\quad + \int_0^t (1-\mu_C^I)\gamma_C^{R\prime}(t-\tau)e^{-\nu_d(t-\tau)} \left(\sigma_e^c(\tau) \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) c(\tau)\right)\, d\tau \\
&\quad + e^{-\nu_d t} c_0 (1-\mu_C^I)\gamma_C^{R\prime}(t) \\
&= \sigma_e^c(t) + \sigma_u^d(t)c(t) - \nu_b c(t) - \sigma_c^i(t) - \sigma_c^r(t).
\end{aligned}$$

As before, we would like to get a Volterra type equation. Therefore, by integrating the formula for s, as we did for Lemma 2.8, we get

$$\begin{aligned}
s(t) = &- \int_0^t s(\tau)l(\tau)e^{-\nu_d(t-\tau)}\, d\tau + \int_0^t \sigma_u^d(\tau)s(\tau)e^{-\nu_d(t-\tau)}\, d\tau \\
&+ (\nu_d - \nu_b) \int_0^t s(\tau)e^{-\nu_d(t-\tau)}\, d\tau + \nu_b \int_0^t e^{-\nu_d(t-\tau)}\, d\tau + s_0 e^{-\nu_d t}.
\end{aligned} \tag{2.33}$$

2.3.1 Properties of the normalized SECIR-type model

Now we want to show that the normalized model fulfils the same properties as the SECIR-type model (2.15), that we showed in Section 2.2.1.

Remark 2.15. *We see that if we replace λ by l in (2.28), the mass $n(t) = s(t) + e(t) + c(t) + i(t) + h(t) + u(t) + r(t)$ has derivative zero. This means that the mass of the normalized model is preserved. Then, if we start with mass 1, we will always have mass 1.*

Assumption 2.16. *As before, we assume that the compartments, transitions and the force of infection term are non-negative. Together with Remark 2.15 this means that every compartment $z \in \{s, e, c, i, h, u, r, d\}$ fulfils $0 \leq z(t) \leq 1$ for all $t \in [0, \infty)$. Moreover, we assume that the flows are bounded from above by some finite constant.*

We now make sure that the conditions for for the force of infection term λ (2.6) from Section 2.2.1 also hold for the force of infection term l (2.30). First we see that we can derive a similar form for l as for λ as in Lemma 2.10.

Lemma 2.17. *We can write*

$$\begin{aligned} l(t) = l_0(t) &+ \phi(t)\,\rho(t) g(t) \\ &+ \phi(t)\rho(t) \int_0^t \left(l(\tau)s(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) e(\tau) \right) A(t-s)\, d\tau \\ &+ \phi(t)\rho(t) \int_0^t \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) e^{-\nu_d(t-\tau)} \\ &\qquad \cdot \left(c(\tau)B_C(t-\tau) + i(\tau)B_I(t-\tau) - c(\tau)B(t-\tau)\right)\, d\tau \end{aligned} \tag{2.34}$$

with $A(t)$ given by (2.21) *and*

$$g(t) = e_0 A(t) - c_0 e^{-\nu_d t} B(t). \tag{2.35}$$

Proof. If we do the same steps as in the proof of Lemma 2.10, we get

$$\begin{aligned} &\int_0^t B_C(t-\tau) e^{-\nu_d(t-\tau)} \sigma_e^c(\tau)\, d\tau \\ &= -\int_0^t B_C(t-\tau) \int_0^\tau \gamma_E^{C\prime}(\tau-u) e^{-\nu_d(\tau-u)} \left(l(u)s(u) + \left(\nu_d + \sigma_u^d(u) - \nu_b\right) e(u) \right)\, du\, d\tau \\ &\quad - \int_0^t B_C(\tau) e^{-\nu_d t} e_0 \gamma_E^{C\prime}(t-\tau)\, d\tau \\ &= \int_0^t \left(l(u)s(u) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) e(\tau) \right) e^{-\nu_d(t-\tau)} a_1(t-\tau)\, d\tau \\ &\quad - \int_0^t B_C(\tau) e^{-\nu_d t} e_0 \gamma_E^{C\prime}(t-\tau)\, d\tau, \end{aligned}$$

and

$$\begin{aligned} &\int_0^t B_I(t-\tau) e^{-\nu_d(t-\tau)} \sigma_c^i(\tau)\, d\tau \\ &= -\int_0^t B_I(t-\tau) \int_0^\tau \mu_C^I \gamma_C^{I\prime}(\tau-u) e^{-\nu_d(\tau-u)} \left(\sigma_e^c(u) + \left(\nu_d + \sigma_u^d(u) - \nu_b\right) c(u) \right)\, du\, d\tau \\ &\quad - \int_0^t B_I(u) e^{-\nu_d t} c_0 \mu_C^I \gamma_C^{I\prime}(t-u) \\ &= -\int_0^t \left(\sigma_e^c(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) c(\tau) \right) e^{-\nu_d(t-\tau)} B(t-\tau)\, d\tau \end{aligned}$$

$$
\begin{aligned}
&- \int_0^t B_I(u) e^{-\nu_d t} c_0 \mu_C^I \gamma_C^{I\prime}(t-u)\ du \\
&= \int_0^t \left(\lambda(\tau)s(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) e(\tau)\right) e^{-\nu_d(t-\tau)} a_2(t-\tau)\ d\tau \\
&\quad - \int_0^t \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) c(\tau) e^{-\nu_d(t-\tau)} B(t-\tau)\ d\tau \\
&\quad + \int_0^t B(u) e_0 e^{-\nu_d u} \gamma_E^{C\prime}(t-u) du \\
&\quad - \int_0^t B_I(u) e^{-\nu_d t} c_0 \mu_C^I \gamma_C^{I\prime}(t-u)\ du.
\end{aligned}
$$

□

The following version of Lemma 2.11 still holds true.

Lemma 2.18. *For all $t \in (-\infty, \infty)$, it holds*

$$l(t) \leq \phi(t)\rho(t). \tag{2.36}$$

Proof. The proof works analogously to the proof of Lemma 2.11 □

Moreover, we have following version of Lemma 2.14 concerning the influence of the initial conditions for the normalized model.

Lemma 2.19. *Let $z \in \{e, c, i, h, u, r\}$, then the following hold*

1. $\lim_{t\to\infty} z_0(t) = 0$,
2. *for all $x \in \{e, c, i, h, u, r, d\}$ such that the transition z to x exists* $\lim_{t\to\infty} e^{-\nu_d t} z_0 \gamma_Z^{X\prime}(t) = 0$,
3. $\lim_{t\to\infty} l_0(t) = 0$ *and* $\lim_{t\to\infty} g(t) = 0$.

Proof. The proof works analogously to the proof of Lemma 2.14. □

2.4 A normalized SIRD-model

For simplicity, we now reduce the model to a SIRD-model, in order to use it for the long-term analysis in Section 3. A SIRD-model has the same structure as a SECIR-type model, but only has one infected compartment. We will use this model in the mathematical analysis, as it is much simpler, but the main mathematical structure is the same. To simplify the notation, we set

$$\gamma_I(t) = \mu_I^D \gamma_I^D(t) + (1 - \mu_I^D)\gamma_I^R(t), \tag{2.37}$$

$$\tilde{\gamma}_I^Z(t) = \mu_I^Z \gamma_I^{Z\prime}(t) e^{-\nu_d t}, \quad \text{for } z \in \{r, d\}. \tag{2.38}$$

For the initial values, we use $s(0) = s_0, i(0) = i_0$ and $r(0) = r_0$ and define

$$i_0(t) = e^{-\nu_d t} i_0 \gamma_I(t), \quad r_0(t) = e^{-\nu_d t} r_0. \tag{2.39}$$

As always, we start with the definition of the force of infection term

$$l(t) = l_0(t) + \phi(t)\rho(t) \int_0^t (l(\tau)s(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) i(\tau))\xi_I(t-\tau)\gamma_I(t-\tau)e^{-\nu_d(t-\tau)}\, d\tau. \tag{2.40}$$

Here $l_0(t)$ is given by

$$l_0(t) = \phi(t)\rho(t)i_0(t)\xi_I(t). \tag{2.41}$$

Then with

$$A(t) = \xi_I(t)\gamma_I(t)e^{-\nu_d t}, \tag{2.42}$$

we write

$$l(t) = l_0(t) + \phi(t)\rho(t) \int_0^t \left(l(\tau)s(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) i(\tau)\right) A(t-\tau)d\tau. \tag{2.43}$$

Then, we directly see that we have the same mathematical structure for the force of infection as given in Lemma 2.17 for the normalized SECIR-type model. The compartments are written as

$$\begin{aligned}
s'(t) &= -l(t)s(t) + (1 - s(t))\nu_b + s(t)\sigma_i^d(t) \\
i(t) &= \int_0^t \gamma_I(t-\tau)e^{-\nu_d(t-\tau)}l(\tau)s(\tau)\ d\tau \\
&\quad + \int_0^t \gamma_I(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau)\ d\tau + i_0(t), \\
r(t) &= \int_0^t e^{-\nu_d(t-\tau)}\sigma_i^r(\tau)\ d\tau \\
&\quad + \int_0^t e^{-\nu_d(t-\tau)}\left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) r(\tau)\ d\tau + r_0(t),
\end{aligned} \tag{2.44}$$

and flows are given by

$$\begin{aligned}
\sigma_i^d(t) &= -\int_0^t \mu_I^D \gamma_I^{D\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}l(\tau)s(\tau)\ d\tau \\
&\quad - \int_0^t \mu_I^D \gamma_I^{D\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau)\ d\tau + \tilde{\gamma}_I^D(t), \\
\sigma_i^r(t) &= -\int_0^t (1-\mu_I^D)\gamma_I^{R\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}l(\tau)s(\tau)\ d\tau \\
&\quad - \int_0^t (1-\mu_I^D)\gamma_I^{R\,\prime}(t-\tau)e^{-\nu_d(t-\tau)}\left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau)\ d\tau + \tilde{\gamma}_I^R(t).
\end{aligned} \tag{2.45}$$

Integrating the equation for s yields

$$\begin{aligned} s(t) &= -\int_0^t s(\tau)l(\tau)e^{-\nu_d(t-\tau)}\,d\tau + \int_0^t \sigma_i^d(\tau)s(\tau)e^{-\nu_d(t-\tau)}\,d\tau \\ &\quad + (\nu_d-\nu_b)\int_0^t s(\tau)e^{-\nu_d(t-\tau)}\,d\tau + \nu_b\int_0^t e^{-\nu_d(t-\tau)}\,d\tau + s_0e^{-\nu_d t} \\ &= -\int_0^t s(\tau)l(\tau)e^{-\nu_d(t-\tau)}\,d\tau + \int_0^t \sigma_i^d(\tau)s(\tau)e^{-\nu_d(t-\tau)}\,d\tau \\ &\quad + (\nu_d-\nu_b)\int_0^t s(\tau)e^{-\nu_d(t-\tau)}\,d\tau + \frac{\nu_b}{\nu_d} - \frac{\nu_b}{\nu_d}e^{-\nu_d t} + s_0e^{-\nu_d t}. \end{aligned}$$

As before, we will make the following assumption.

Assumption 2.20. *As before, we assume that the compartments, transitions and the force of infection term are non-negative. Together with Remark 2.15 this means that every compartment $z \in \{s, e, c, i, h, u, r, d\}$ fulfils $0 \le z(t) \le 1$ for all $t \in [0, \infty)$. Moreover, we assume that the flows are bounded from above by some finite constant.*

We can again show a bound for the force of infection term l.

Lemma 2.21. *For all $t \in (-\infty, \infty)$, it holds*

$$l(t) \le \phi(t)\rho(t). \tag{2.46}$$

Proof. The proof works analogously to the proof of Lemma 2.11. □

The following Lemma shows the influence of the initial values on the long-term behaviour of the model.

Lemma 2.22. *The following statements hold true.*

1. $\lim_{t\to\infty} i_0(t) = 0$ *and* $\lim_{t\to\infty} r_0(t) = 0$,
2. $\lim \tilde{\gamma}_I^D(t) = 0$ *and* $\lim_{t\to\infty} \tilde{\gamma}_I^D(t) = 0$,
3. $\lim_{t\to\infty} l_0(t) = 0$,
4. $\lim_{t\to\infty} s_0e^{-\nu_d t} - \frac{\nu_b}{\nu_d}e^{-\nu_d t} = 0$.

Proof. The first three statements can be shown analogously to the proof of Lemma 2.14, and the last statement follows from $\lim_{t\to\infty} e^{-\nu_d t} = 0$. □

As for the other models, we have seen that the initial values have no influence on the long-term behaviour of the model. We introduced the normalized SIRD-model mainly for the long-term analysis. Therefore, we will now state a normalized SIRD-model without initial values that we

will use for the long-term analysis in Section 3.

$$
\begin{aligned}
l(t) &= \phi(t)\rho(t)\int_0^t \left(l(\tau)s(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) i(\tau)\right) A(t-\tau)d\tau,\\
s(t) &= -\int_0^t \left(l(\tau)s(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) s(\tau)\right) e^{-\nu_d(t-\tau)}\ d\tau,\\
i(t) &= \int_0^t \left(l(\tau)s(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) i(\tau)\right) \gamma_I(t-\tau)e^{-\nu_d(t-\tau)}\ d\tau,\\
r(t) &= \int_0^t \left(\sigma_i^r(\tau) + \left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) r(\tau)\right) e^{-\nu_d(t-\tau)}\ d\tau,\\
\sigma_i^d(t) &= -\int_0^t \left(l(\tau)s(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) i(\tau)\right) \mu_I^D\gamma_I^{D\prime}(t-\tau)e^{-\nu_d(t-\tau)}\ d\tau,\\
\sigma_i^r(t) &= -\int_0^t \left(l(\tau)s(\tau) + \left(\nu_d + \sigma_u^d(\tau) - \nu_b\right) i(\tau)\right) (1-\mu_I^D)\gamma_I^{R\prime}(t-\tau)e^{-\nu_d(t-\tau)}\ d\tau.
\end{aligned}
\tag{2.47}
$$

3 Analysis of the model's long-term behaviour

In this section we want to analyse the long-term behaviour of our models. We have seen in Section 2.4 that the basic mathematical structures of the normalized SIRD-model and the normalized SECIR-model are very similar, as the integrals of the compartments and the transitions have the same structure. Moreover, the force of infection term can be written in a similar structure by defining the appropriate term A. The interesting features of our model, such as the disease death and the birth and natural death rate, are included in both models. The analysis of the SECIR-model would be very complex, already the computation of the equilibrium for the SECIR-model would be very involved, as one would have to solve a non-linear system of 12 equations. Thus,we decide to restrict the analysis of the equilibria to the SIRD-model. At the end of the section we will then shortly look at the expected behaviour of the population size in the SECIR-type birth-and-death model.

3.1 Introduction of some model parameters

In this section, we introduce some important parameters of the SECIR-type and the SIRD-type model that we will need for the model analysis. Note that the following parameters are the same for the standard and the normalized model. In the definition of the parameters that depend on one or more compartment, we will use small letters for the indices.

First, we introduce the concept of a reproduction number. The basic reproduction number describes the expected number of new infections caused by one infectious individual in a population where everyone is susceptible. The reproduction number is a useful expression for the controllability of a disease. In the literature the reproduction number is found to be a threshold condition for the stability of equilibria; see [13, 11]. In our case we will see that the reproduction number is a threshold condition for the stability of the disease-free equilibrium, Theorem 3.3 and 3.6. Some theory about the computation of reproduction numbers can be found in [20]. There are several types of reproduction numbers. Here we introduce the control reproduction number $\mathcal{R}_c$, where c stands for control, which means that we allow isolation. The reproduction number $\mathcal{R}_c$ is also used in [13]. In contrarison The basic reproduction number $\mathcal{R}_0$, is computed when no control measures exist, i.e in our case this means $\xi_z(t) = 1$ for $Z \in \{c, i\}$. To facilitate the further analysis of our model, we make the following assumption.

Assumption 3.1. *We assume that the transmission rate ρ and the contact rate ϕ are constant with respect to time, i.e we have $\phi(t) = \phi(t_0) = \phi$ and $\rho(t) = \rho(t_0) = \rho$ for all $t \in (-\infty, \infty)$.*

Then we can define

$$\mathcal{R}_c = \phi\rho \int_0^\infty A(s)\, ds, \tag{3.1}$$

where one can plug in different choices for A. We use A given by (2.21) for the SECIR-type model and A given by (2.42) for the SIRD-model. One would derive the basic reproduction number by setting $\xi_C, \xi_I = 1$ in the definition of A (2.21), (2.42), as this means no control measures are implemented.

Next, we define for suitable $z_1, z_2 \in \{s, e, c, i, h, u, r, d\}$

$$\mathcal{T}_{z_1}^{z_2} = -\int_0^\infty e^{-\nu_d \tau} \mu_{z_1}^{z_2} \gamma_{z_1}^{z_2\,\prime}(\tau)\, d\tau. \tag{3.2}$$

Then $\mathcal{T}_{z_1}^{z_2}$ gives the probability that an individual transitions at some point from compartment z_1 into compartment z_2 . Since $-\gamma_{z_1}^{z_2\,\prime}$ is a probability density function, we can compute

$$\begin{aligned}\mathcal{T}_{z_1}^{z_2} &= -\int_0^\infty e^{-\nu_d \tau} \mu_{z_1}^{z_2} \gamma_{z_1}^{z_2\,\prime}(\tau)\, d\tau \leq \int_0^\infty (-\gamma_{z_1}^{z_2\,\prime}(\tau))\, d\tau \\ &= \int_{-\infty}^\infty (-\gamma_{z_1}^{z_2\,\prime}(\tau))\, d\tau = 1.\end{aligned}$$

In particular for $\mu_I^D < 1$ we even have $\mathcal{T}_i^d < 1$.

In the SECIR-type model, we also define

$$\begin{aligned}\mathcal{V}^c &= \mathcal{T}_e^c, \\ \mathcal{V}^i &= \mathcal{V}^c \mathcal{T}_c^i, \\ \mathcal{V}^h &= \mathcal{V}^i \mathcal{T}_i^h, \\ \mathcal{V}^u &= \mathcal{V}^h \mathcal{T}_h^u, \\ \mathcal{V}^d &= \mathcal{V}^u \mathcal{T}_u^d, \\ \mathcal{V}^r &= \mathcal{V}^c \mathcal{T}_c^r + \mathcal{V}^i \mathcal{T}_i^r + \mathcal{V}^h \mathcal{T}_h^r + \mathcal{V}^u \mathcal{T}_u^r.\end{aligned} \tag{3.3}$$

Here $\mathcal{V}^z$ gives the probability that an individual that was in compartment e at some point will at some point arrive in compartment $z \in \{c, i, h, u, r, d\}$. Moreover, we define

$$\mathcal{W}_z \coloneqq \int_0^\infty \gamma_z(\tau) e^{-\nu_d \tau}\, d\tau. \tag{3.4}$$

Then $\mathcal{W}_z$ is the mean stay-time in compartment z. We have the following bound

$$\mathcal{W}_z = \int_0^\infty \gamma_z(\tau) e^{-\nu_d \tau}\, d\tau \leq \int_0^\infty e^{-\nu_d \tau} d\tau = \frac{1}{\nu_d}. \tag{3.5}$$

We realize that for the SIRD-model, we have the following relation between $\mathcal{R}_c$ and $\mathcal{W}_i$

$$\mathcal{R}_c = \phi\rho \int_0^\infty \xi_I(t) \gamma_I(t) e^{-\nu_d t}\, dt \leq \phi\rho \int_0^\infty \gamma_I(t) e^{-\nu_d t}\, dt = \phi\rho \mathcal{W}_i. \tag{3.6}$$

3.2 Analysis of the normalized SIRD-model

We now analyse the long-term behaviour of the normalized SIRD-model introduced in Section 2.4.

3.2.1 Assumption on the birth and death rates

In the normalized model (2.44) the factor $\nu_d + \sigma_i^d(\tau) - \nu_b$ appears several times. Later on, in the analysis of the model it will be important to control this factor. We note that this factor is just the term $\frac{N'(t)}{N(t)}$. Therefore, it would be alogical assumption that $\nu_d + \sigma_i^d(\tau) < \nu_b$ in order to make sure that the population does not die out. The assumption that the population size is increasing is also made in [11]. In the case of [11] this assumption is straightforward as they have a constant rate for the disease death. However, in our case we do not have some given rate for the disease death, instead we compute the number of disease deaths as a transition for every time. Moreover, the assumption $\nu_d + \sigma_i^d(\tau) - \nu_b < 0$ does not necessarily need to be true for every time τ to guarantee that the population does not die out. For example he term σ_i^d could also be oscillating. Moreover, in our proofs later we need that $\nu_d + \sigma_i^d(\tau) - \nu_b < 0$ for τ large enough. We now show that it is possible to ensure this by deriving an assumption that implies that $\nu_d + \sigma_i^d(\tau) - \nu_b < 0$ for all τ.

As $\sigma_i^d(t)$ is bounded from below by 0 and above by some constant m by Assumption 2.16, we know that the supremum exists. Therefore, we define

$$\sigma_{\sup} \coloneqq \sup_{t \geq T} \sigma_i^d(t).$$

Using this we get the following estimate for σ_i^d

$$\begin{aligned}
\sigma_i^d(t) &= -\int_0^t \mu_I^D \gamma_I^D{}'(t-\tau) e^{-\nu_d(t-\tau)} \left(l(\tau)s(\tau) + \left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau) \right) \, d\tau \\
&\leq -\int_0^t \mu_I^D \gamma_I^D{}'(t-\tau) e^{-\nu_d(t-\tau)} \left(\phi\rho + (\nu_d + m) \right) \, d\tau \\
&= \left(\phi\rho + (\nu_d + m) \right) \mathcal{T}_i^d.
\end{aligned}$$

Then, as the right-hand side is independent of t, this inequality also holds if we take the supremum on the left-hand side. This yields

$$\sigma_{\sup} \leq \left(\phi\rho + (\nu_d + m) \right) \mathcal{T}_i^d.$$

Using this, we know that

$$\nu_d + \left(\phi\rho + (\nu_d + m) \right) \mathcal{T}_i^d - \nu_b \leq 0$$

implies $\nu_d + \sigma_i^d(\tau) - \nu_b \leq 0$ for $t \geq T$. From this we now derive a condition for the birth-and-death rate.

$$\begin{aligned}
& \nu_d + \left(\phi\rho + \nu_d + m \right) \mathcal{T}_i^d \leq \nu_b \\
\Leftrightarrow \quad & \nu_d(1 + \mathcal{T}_i^d) + \mathcal{T}_i^d \phi\rho + \mathcal{T}_i^d m \leq \nu_b.
\end{aligned}$$

We used really rough estimates in order to get to this point. This assumption is probably very unrealistic and might not be possible to achieve. But, we wanted to show that it is possible to derive an assumption that ensures $\nu_d + \sigma_i^d(\tau) - \nu_b \leq 0$ for large τ. Our numerical experiments in Section 5 justify to make this as an assumption.

Assumption 3.2. *We assume that $\nu_d + \sigma_i^d(\tau) - \nu_b < 0$ for all τ large enough.*

3.2.2 Computation of the equilibria

Now we compute the possible equilibria points of model (2.47). Let $(l^*, s^*, i^*, r^*, \sigma_i^{d\,*}, \sigma_i^{r\,*})$ denote an equilibrium for model (2.47). In particular, an equilibrium is always defined for all $t \in \mathbb{R}$ and does not have initial values. By definition an equilibrium is a constant solution to the following system of equations

$$
\begin{aligned}
l(t) &= \phi\rho \int_0^t \Big(l(t)s(t) + (\nu_d + \sigma_u^d(t) - \nu_b) i(\tau) \Big) A(t-\tau) d\tau, \\
s(t) &= -\int_{-\infty}^t \Big(l(t)s(t) - (\nu_d + \sigma_u^d(t) - \nu_b) s(t) \Big) e^{-\nu_d(t-\tau)}\, d\tau + \frac{\nu_b}{\nu_d}, \\
i(t) &= \int_{-\infty}^t \Big(l(t)s(t) + (\nu_d + \sigma_u^d(t) - \nu_b) i(t) \Big) \gamma_I(t-\tau) e^{-\nu_d(t-\tau)}\, d\tau, \\
r(t) &= \int_{-\infty}^t \Big(\sigma_i^r(t) + (\nu_d + \sigma_u^d(t) - \nu_b) r(t) \Big) e^{-\nu_d(t-\tau)}\, d\tau, \\
\sigma_i^d(t) &= -\int_{-\infty}^t \Big(l(t)s(t) + (\nu_d + \sigma_u^d(t) - \nu_b) i(t) \Big) \mu_I^D \gamma_I^{D\,\prime}(t-\tau) e^{-\nu_d(t-\tau)}\, d\tau, \\
\sigma_i^r(t) &= -\int_{-\infty}^t \Big(l(t)s(t) + (\nu_d + \sigma_u^d(t) - \nu_b) i(t) \Big) (1-\mu_I^D) \gamma_I^{R\,\prime}(t-\tau) e^{-\nu_d(t-\tau)}\, d\tau.
\end{aligned}
$$

Then, as for an equilibrium $z(t) = z(0) = z^*$, we get the following system of equations

$$
\begin{aligned}
l^* &= \Big(s^* l^* + (\nu_d + \sigma_i^{d\,*} - \nu_b) i^* \Big) \phi\rho \int_{-\infty}^0 A(-\tau)\, d\tau, \\
s^* &= -\Big(s^* l^* - \Big(\nu_d + \sigma_i^{d\,*} - \nu_b \Big) s^* \Big) \int_{-\infty}^0 e^{\nu_d \tau}\, d\tau + \frac{\nu_b}{\nu_d}, \\
i^* &= \Big(s^* l^* + (\nu_d + \sigma_i^{d\,*} - \nu_b) i^* \Big) \int_{-\infty}^0 \gamma_I(-\tau) e^{\nu_d \tau}\, d\tau, \\
r^* &= \Big(\sigma_i^{r\,*} + \Big(\nu_d + \sigma_i^{d\,*} - \nu_b \Big) \Big) r^* \int_{-\infty}^0 e^{\nu_d \tau}\, d\tau, \\
\sigma_i^{d\,*} &= -\Big(s^* l^* + (\nu_d + \sigma_i^{d\,*} - \nu_b) i^* \Big) \int_{-\infty}^0 \mu_I^D \gamma_I^{D\,\prime}(-\tau) e^{\nu_d \tau}\, d\tau, \\
\sigma_i^{r\,*} &= -\Big(s^* l^* + (\nu_d + \sigma_i^{d\,*} - \nu_b) i^* \Big) \int_{-\infty}^0 (1-\mu_I^D) \gamma_I^{R\,\prime}(-\tau) e^{\nu_d \tau}\, d\tau.
\end{aligned}
\tag{3.7}
$$

Then after a change of variables from $-\tau$ to τ, and plugging in the definitions given in Section 3.1 we derive

$$
(I) \qquad s^* = -\Big(s^* l^* - \Big(\nu_d + \sigma_i^{d\,*} - \nu_b \Big) s^* + \nu_b \Big) \frac{1}{\nu_d} \qquad \Rightarrow \qquad s^* = \frac{\nu_b}{l^* - \sigma_i^{d\,*} - \nu_b},
$$

$$
(II) \qquad l^* = \Big(s^* l^* + \Big(\nu_d + \sigma_i^{d\,*} - \nu_b \Big) i^* \Big) \mathcal{R}_c \qquad \Rightarrow \qquad l^* = \frac{(\nu_d + \sigma_i^{d\,*} - \nu_b) i^*}{\frac{1}{\mathcal{R}_c} - s^*},
$$

$$(III) \qquad i^* = \left(s^*l^* + \left(\nu_d + \sigma_i^{d*} - \nu_b\right) i^*\right) \mathcal{W}_i \qquad \Rightarrow \quad i^* = \frac{l^*s^*}{\frac{1}{\mathcal{W}_i} - \nu_d - \sigma_i^{d*} + \nu_b},$$

$$(IV) \qquad \sigma_i^{d*} = \left(s^*l^* + \left(\nu_d + \sigma_i^{d*} - \nu_b\right) i^*\right) \mathcal{T}_i^d \qquad \Rightarrow \quad \sigma_i^{d*} = \frac{l^*s^* + (\nu_d - \nu_b)i^*}{\frac{1}{\mathcal{T}_i^d} - i^*},$$

$$(V) \qquad \sigma_i^{r*} = \left(s^*l^* + \left(\nu_d + \sigma_i^{d*} - \nu_b\right) i^*\right) \mathcal{T}_i^r,$$

$$(VI) \qquad r^* = \left(\sigma_i^{r*} + \left(\nu_d + \sigma_i^{d*} - \nu_b\right) r^*\right) \frac{1}{\nu_d} \qquad \Rightarrow \quad r^* = \frac{\sigma_i^{r*}}{-\sigma_i^{d*} + \nu_b}.$$

We see that s^*, l^*, i^* and σ_i^{d*} define a system that is independent of σ_i^{r*} and r^*. Therefore, we start by computing the equilibria for these four variables. Once we have done this, we can derive $\sigma_i^{r^*}$ and r^*. If we solve equations $(I) - (IV)$ for s^*l^*, we get

$$(I) \qquad s^*l^* = \sigma_i^{d*}s^* - \nu_b s^* + \nu_b,$$

$$(II) \qquad s^*l^* = -\nu_d i^* - \sigma_i^{d*}i^* + \nu_b i^* + \frac{l^*}{\mathcal{R}_c},$$

$$(III) \qquad s^*l^* = -\nu_d i^* - \sigma_i^{d*}i^* + \nu_b i^* + \frac{i^*}{\mathcal{W}_i},$$

$$(IV) \qquad s^*l^* = -\nu_d i^* - \sigma_i^{d*}i^* + \nu_b i^* + \frac{\sigma_i^{d*}}{\mathcal{T}_i^d}.$$

If we compute $(II) - (III)$ and $(III) - (IV)$ we get the following two equations

$$(II) - (III): \qquad l^* = i^*\frac{\mathcal{R}_c}{\mathcal{W}_i},$$

$$(III) - (IV): \qquad \sigma_i^{d*} = i^*\frac{\mathcal{T}_i^d}{\mathcal{W}_i}.$$

Plugging them into equation (I) yields for $s^* \neq 0$

$$s^*i^*\frac{\mathcal{R}_c}{\mathcal{W}_i} = s^*i^*\frac{\mathcal{T}_i^d}{\mathcal{W}_i} - \nu_b s^* + \nu_b$$

$$\Leftrightarrow \quad \left(i^*\left(\frac{\mathcal{R}_c}{\mathcal{W}_i} - \frac{\mathcal{T}_i^d}{\mathcal{W}_i}\right) + \nu_b\right) = \frac{\nu_b}{s^*}.$$

For $s^* = 0$, we also get $l^* = 0$ $i^* = 0$ and σ_i^{d*}, which means that the population has died out. This case is not interesting for us; therefore, we will not discuss it further. Now we have expressions for s^*, l^* and σ_i^{d*} only depending on i^*. Therefore, we plug these expressions into the equation for i^* to get an equation only depending on i^*, that is

$$i^*\left(i^*\left(\frac{\mathcal{R}_c - \mathcal{T}_i^d}{\mathcal{W}_i}\right) + \nu_b\right) = \frac{i^*\frac{\mathcal{R}_c}{\mathcal{W}_i}\nu_b}{\frac{1}{\mathcal{W}_i} - \nu_d - i^*\frac{\mathcal{T}_i^d}{\mathcal{W}_i} + \nu_b}.$$

We directly see that $i^* = 0$ is one solution. This yields the disease-free equilibrium

$$(s_1^*, l_1^*, i_1^*, \sigma_{i\,1}^{d*}) = (1, 0, 0, 0).$$

For $i^* \neq 0$ we get the following equation

$$\begin{aligned}
&(i^*)^2 \left(\frac{(\mathcal{R}_c - \mathcal{T}_i^d)\mathcal{T}_i^d}{\mathcal{W}_i} \right) \\
&+ i^* \left((\mathcal{R}_c - \mathcal{T}_i^d) \left(\nu_d - \frac{1}{\mathcal{W}_i} - \nu_b \right) - \frac{\nu_b \mathcal{T}_i^d}{\mathcal{W}_i} \right) + \mathcal{W}_i \nu_b \left(\frac{1}{\mathcal{W}_i} - \nu_d + \nu_b - \mathcal{R}_c \right) \\
&= 0,
\end{aligned}$$

which is equivalent to

$$(i^*)^2 + i^* \underbrace{\left(\frac{\mathcal{W}_i}{\mathcal{T}_i^d} \left(\nu_d - \frac{1}{\mathcal{W}_i} - \nu_b \right) - \frac{\nu_b}{\mathcal{R}_c - \mathcal{T}_i^d} \right)}_{=p} + \underbrace{\frac{\nu_b (\mathcal{W}_i)^2}{(\mathcal{R}_c - \mathcal{T}_i^d)\mathcal{T}_i^d} \left(\frac{1}{\mathcal{W}_i} - \nu_d + \nu_b - \mathcal{R}_c \right)}_{=q} = 0.$$

Then the solutions of this quadratic equation are of the form

$$i^*_{1,2} = -\frac{p}{2} \pm \sqrt{\left(\frac{p}{2}\right)^2 - q}.$$

Depending on the parameters, it might be the case that this equation has no real solution. In fact, we have two real solutions if $\left(\frac{p}{2}\right)^2 - q > 0$, one real solution if $\left(\frac{p}{2}\right)^2 - q = 0$ and two complex solutions if $\left(\frac{p}{2}\right)^2 - q < 0$. For the further analysis we are only interested in the first two cases. Moreover, we only want to account for equilibria that are non-negative and smaller than one. First of all, we see that under the assumption that $\mathcal{R}_c > \mathcal{T}_i^d > 0$ we know that $\left(\frac{1}{\mathcal{W}_i} - \nu_d + \nu_b - \mathcal{R}_c \right) < 0$ directly implies that $\left(\frac{p}{2}\right)^2 - q > 0$ which means we have two real solutions. Under the same assumption and with (3.5) we also get that

$$\begin{aligned}
p &\leq \frac{\mathcal{W}_i}{\mathcal{T}_i^d} \left(\nu_d - \frac{1}{\mathcal{W}_i} - \nu_b \right) \\
&\leq \frac{\mathcal{W}_i}{\mathcal{T}_i^d} (-\nu_b) \leq 0
\end{aligned}$$

This directly implies that

$$i^*_1 = -\frac{p}{2} + \sqrt{\left(\frac{p}{2}\right)^2 - q} \geq 0$$

$i^*_1 \geq 0$ whenever $\mathcal{R}_c > \mathcal{T}_i^d > 0$ and it is real.

The parameters are not independent of each other, as $\mathcal{R}_c$, $\mathcal{T}_i^d$ and $\mathcal{W}_i$ were all defined using the transition distributions $\gamma_{z_1}^{z_2}$ and the death rate ν_b. For now, we will ignore this fact and handle them independently as we want to see for what parameter combinations we have a solution for the equation for i^*. We will come back to this point the Section 5. We will further analyse this problem using MATLAB to generate a grid. As a five dimensional grid is hard to study we fix the parameters ν_b, ν_d and $\mathcal{T}_i^d$ and analyse the plot for varying $\mathcal{R}_c$ and $\mathcal{W}_i$, as we will see a

correlation between these two parameters. We will do the plots for $\mathcal{T}_i^d \in \{0.11, 0.51, 0.99\}$, as $\mathcal{T}_i^d \in [0,1]$. In the MATLAB code we chose the step size such that we will never hit the case $\mathcal{R}_c = \mathcal{T}_i^d$, where division by zero would occur. In the implementation later on we will mostly use $\nu_b = 4 \cdot 10^{-3}$ and $\nu_d = 3 \cdot 10^{-3}$ for the birth and the death rate. Therefore, we will fix them for now. Then for $\mathcal{T}_i^d = 0.11$ the evaluation of i^* can be found in Figure 3. It is clear to see that for $\mathcal{R}_c \in [0,5]$ and $\mathcal{W}_i \in [0,5]$, there always exist two real solutions for i^*, clearly except for $\mathcal{R}_c = \mathcal{T}_i^d = 0.11$. Moreover, one can see that i_1^* is always larger than one in this case. For i_2^* one sees that in most cases $i_2^* < 0$. However, there are some parameter combinations that lead to $0 \leq i_2^* \leq 1$. For $\mathcal{R}_c < \mathcal{T}_i^d$ we have a suitable solution i_2^*, for large $\mathcal{W}_i$, when $\mathcal{R}_c$ gets small. For $\mathcal{R}_c > \mathcal{T}_i^d$, there is a suitable solution i_2^*, for larger $\mathcal{R}_c$, when $\mathcal{W}_i$ gets small. The second case is rather unrealistic, as we have (3.5) and we would need $\phi\rho$ to be very large to ensure that $\mathcal{R}_c < \phi\rho\mathcal{W}_i$. In Figure 4 we see the evaluation of i^* for $\mathcal{T}_i^d = 0,51$. One sees that there is a

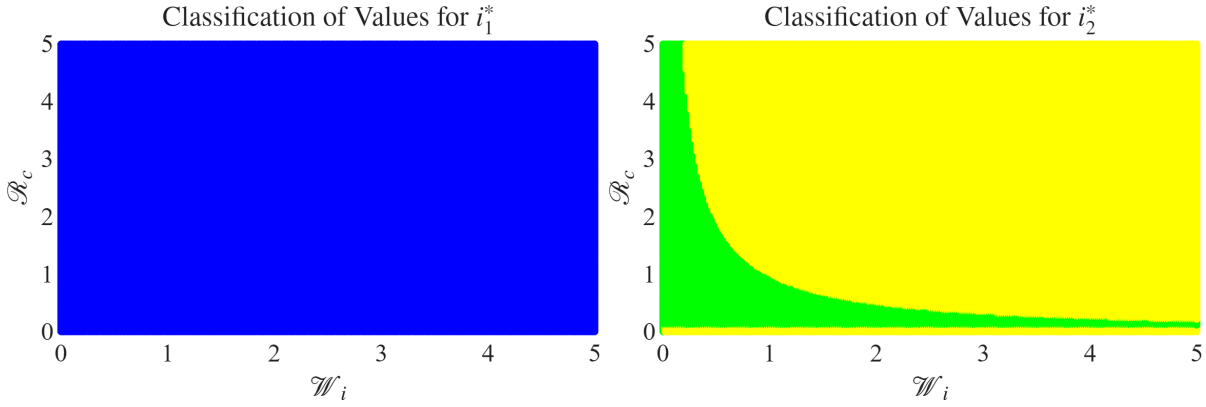

Figure 3: For $\mathcal{T}_i^d = 0.11$, $\nu_b = 4 \cdot 10^{-3}$ and $\nu_d = 3 \cdot 10^{-3}$. Where the colours mean the following, red: only complex solutions exist, yellow: $i^* < 0$, green: $0 < i^* < 1$ and blue: $i^* > 1$.

small area where there is no real solution for i^*. The area where no solution exists is where $\mathcal{W}_i$ is large and $\mathcal{R}_c$ is close to $\mathcal{T}_i^d$. For the other parameter combinations, we have two real solutions for i^*, but there we always have $i_1^* > 1$. One can also observe that for large $\mathcal{W}_i$ and small $\mathcal{R}_c$ we also get $0 \leq i_2^* \leq 1$ for $\mathcal{R}_c < \mathcal{T}_i^d$. But again, for large values of $\mathcal{R}_c$, we need small values of $\mathcal{W}_i$ to have a suitable solution, which is not that realistic. In Figure 5 one can find the evaluation of i^* for $\mathcal{T}_i^d = 0,99$. This time, the area where we have no real solution is a little larger, but still, in this area we find that $\mathcal{R}_c$ is close to $\mathcal{T}_i^d$. Moreover, in this case we have an area where a feasible solution for i_1^* exists, which means $0 \leq i_1^* \leq 1$. We now want to briefly have a look at a case with a larger choice for the birth and the death rate, to see if this has an influence. We set $\mathcal{T}_i^d = 0,51$, $\nu_b = 4 \cdot 10^{-2}$ and $\nu_d = 3 \cdot 10^{-2}$, the evaluation of i^* for this case can be found in Figure 6. One sees that the result is quite similar to Figure 4, but the area where no real solution exists has increased. At this point, one would need to test if the solutions for the other compartments are in the right interval, to know if an equilibrium for the model is feasible. However, we have seen that the existence of an equilibrium for i , that is in the right interval, is quite rare. Therefore, we will omit this point here. All in all the question about the existence of endemic equilibria to the normalized SIRD-model (2.47) needs further work. In Section 5.3

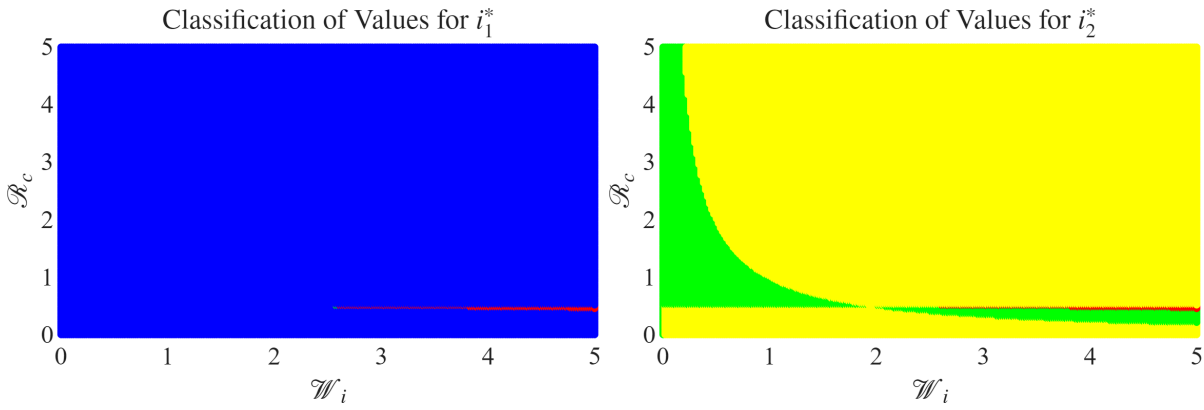

Figure 4: For $\mathcal{T}_i^d = 0.51$, $\nu_b = 4 \cdot 10^{-3}$ and $\nu_d = 3 \cdot 10^{-3}$. Where the colours mean the following, red: only complex solutions exist, yellow: $i^* < 0$, green: $0 < i^* < 1$ and blue : $i^* > 1$.

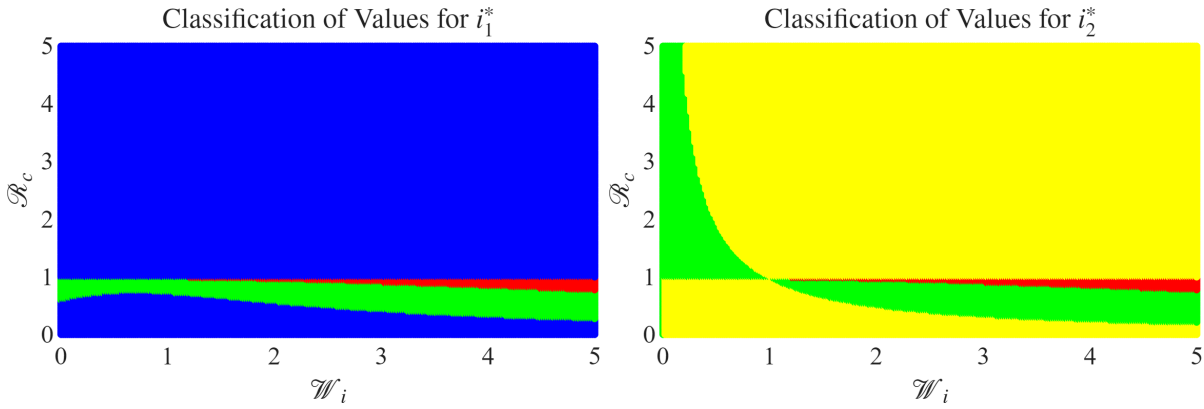

Figure 5: For $\mathcal{T}_i^d = 0.99$, $\nu_b = 4 \cdot 10^{-3}$ and $\nu_d = 3 \cdot 10^{-3}$. Where the colours mean the following, red: only complex solutions exist, yellow: $i^* < 0$, green: $0 < i^* < 1$ and blue: $i^* > 1$.

we will come back to this point.

3.2.3 Stability of the equilibria

We have seen that the disease-free equilibrium exists everywhere, independently of the parameter choice. As seen above, an equilibrium corresponding to an endemic state exists only in some area of the parameter space and even if an equilibrium exists often this equilibrium is not feasible for the normalized model, as the values for the compartments and flows might not be between zero and one. Therefore, we will focus on the stability of the disease-free equilibrium. Later on we will make some comments about the stability of endemic equilibria. We start by showing that the disease-free equilibrium is stable if the reproduction number is smaller than one.

Theorem 3.3. *Under the Assumptions 2.20 and 3.2 we have that $\mathcal{R}_c < 1$ implies that*

$$\zeta_1 = (1, 0, 0) \tag{3.8}$$

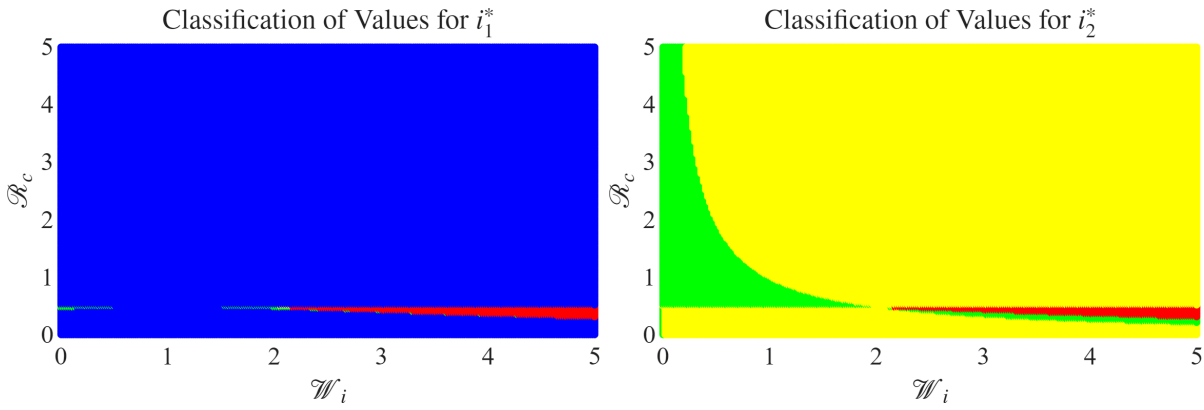

Figure 6: For $\mathcal{T}_i^d = 0.51$, $\nu_b = 4 \cdot 10^{-2}$ and $\nu_d = 3 \cdot 10^{-2}$. Where the colours mean the following, red: only complex solutions exist, yellow: $i^* < 0$, green: $0 < i^* < 1$ and blue: $i^* > 1$.

is a global attractor for model (2.44).

Proof. For the proof we use a similar approach as from [13, Theorem 1]. We start by showing that $l(t) \to 0$ as $t \to \infty$. As $s(\tau) \leq 1$ for all τ we have

$$\begin{aligned} l(t) &= \phi\rho \int_0^t \left(l(\tau)s(\tau) + \left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau) \right) A(t-\tau)\ d\tau \\ &\leq \phi\rho \int_0^t \left(l(\tau) + \left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau) \right) A(t-\tau)\ d\tau. \end{aligned}$$

As by Lemma 2.21 l is bounded we know that the lim sup of l exists. Thus, we let

$$\begin{aligned} l^\infty &= \limsup_{t\to\infty} l(t), \quad \text{i.e} \\ l^\infty &= \lim_{t\to\infty} \Lambda(t), \quad \text{with } \Lambda(t) = \sup_{s\geq t} l(s)\,. \end{aligned}$$

By the definition of the lim sup there exists a sequence $t_n \to \infty$ with $l(t_n) \to l^\infty$ for $n \to \infty$. By choosing a subsequence if necessary, we can assume that $t_{n+1} - t_n \to \infty$ as $n \to \infty$.
Then we can compute

$$\begin{aligned} l(t_{n+1}) \leq\ & \phi\rho \int_0^{t_n} \left(l(\tau) + \left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau) \right) A(t_{n+1}-\tau)\ d\tau \\ & + \phi\rho \int_{t_n}^{t_{n+1}} \left(l(\tau) + \left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau) \right) A(t_{n+1}-\tau)\ d\tau \end{aligned}$$

We first take a closer look at the first part of the right hand side. Then by using Lemma 2.21 and the fact that $\int_0^\infty A(s)\ ds < \infty$ we compute

$$\int_0^{t_n} \left(l(\tau) + \underbrace{\left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau)}_{\leq C < \infty} \right) A(t_{n+1}-\tau)\ d\tau$$

$$
\begin{aligned}
&\leq (\phi\rho + C) \int_0^{t_n} A(t_{n+1} - \tau)\ d\tau \\
&\leq \underbrace{(\phi\rho + C)}_{<\infty} \int_{t_{n+1}-t_n}^{\infty} A(s)\ ds \to 0 \text{ as } n \to \infty,
\end{aligned}
$$

where me may bound $\left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau)$ by some C, as ν_d, σ_i^d and i are bounded from above and ν_b is bounded from below by zero. Moreover, we chose the subsequence such that the lower bound of the integral converges to ∞. Now we consider the second part of the right-hand side. Again, we make use of Assumption 3.2, and we just choose t_n large enough that Assumption 3.2 holds true. This yields

$$
\begin{aligned}
&\phi\rho \int_{t_n}^{t_{n+1}} \left(l(\tau) + \left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau)\right) A(t_{n+1} - \tau)\ d\tau \\
&\leq \phi\rho \int_{t_n}^{t_{n+1}} \Lambda(t_n) A(t_{n+1} - \tau)\ d\tau \\
&= \phi\rho\Lambda(t_n) \int_0^{t_{n+1}-t_n} A(s)\ ds \\
&\leq \Lambda(t_n)\mathcal{R}_c
\end{aligned}
$$

Putting everything together, and letting $n \to \infty$ we get the following result

$$
l^\infty \leq l^\infty \mathcal{R}_c.
$$

The assumption that $\mathcal{R}_c < 1$ implies that $l^\infty = 0$, and since $l(t) \geq 0$ for all t we know that $\lim_{t\to\infty} l(t) = 0$.

Now we show that σ_i^d, σ_i^r and i also converge to zero. As the computations for both can be done in an analogous manner we will only do the proof for σ_i^d. The idea is to just do the same steps as above. First by the fact that $s(\tau) \leq 1$ we have

$$
\sigma_i^d(t) \leq \int_0^t \left(l(\tau) + (\nu_d + \sigma_i^d(\tau) - \nu_b) i(\tau)\right) \mu_I^D \gamma_I^{D\prime}(t - \tau) e^{-\nu_d(t-\tau)}\ d\tau.
$$

We then take the subsequence t_n from above. We have

$$
\begin{aligned}
\sigma_i^d(t_{n+1}) = &- \int_0^{t_n} \left(l(\tau) + (\nu_d + \sigma_i^d(\tau) - \nu_b) i(\tau)\right) \mu_I^D \gamma_I^{D\prime}(t_{n+1} - \tau) e^{-\nu_d(t_{n+1}-\tau)}\ d\tau \\
&- \int_{t_n}^{t_{n+1}} \left(l(\tau) + (\nu_d + \sigma_i^d(\tau) - \nu_b) i(\tau)\right) \mu_I^D \gamma_I^{D\prime}(t_{n+1} - \tau) e^{-\nu_d(t_{n+1}-\tau)}\ d\tau
\end{aligned}
$$

By the same computations as above and the fact that $\int_0^\infty \mu_I^D \gamma_I^{D\prime}(s) e^{-\nu_d s} ds < \infty$ we have that the first term of the right-hand side converges to zero.

For the second part we compute by using Assumption 3.2

$$\begin{aligned}
&-\int_{t_n}^{t_{n+1}} \Big(l(\tau) + (\nu_d + \sigma_i^d(\tau) - \nu_b)i(\tau)\Big)\, \mu_I^D \gamma_I^{D\prime}(t_{n+1} - \tau) e^{-\nu_d(t_{n+1}-\tau)}\, d\tau \\
&\quad \leq -\Lambda(t_n) \int_{t_n}^{t_{n+1}} \mu_I^D \gamma_I^{D\prime}(t_{n+1} - \tau) e^{-\nu_d(t_{n+1}-\tau)}\, d\tau \\
&\quad \leq \Lambda(t_n) \mathcal{T}_i^d
\end{aligned}$$

where we used that the integral is positive, as $-\gamma_I^{D\prime} \geq 0$. This then implies $\sigma_i^d(t) \to 0$ as $t \to \infty$. Again, with the similar computations we can show that $r(t) \to 0$ as $t \to \infty$ using that σ_i^r goes to zero.

Lastly, we use the fact that $s(t) = 1 - i(t) - r(t)$ and see

$$s(t) = 1 - i(t) - r(t) \to 1 \quad \text{as } t \to \infty.$$

□

In order to study the stability of equilibria for the case $\mathcal{R}_c > 1$, we use the approach from [13, 14]. For this we will need some general results about the asymptotic stability of solutions of Volterra integral equations. Explicitly, we will use the following theorem from [21, Theorem 4]

Theorem 3.4. *Assume we have a equation of the form*

$$X(t) = F(t) + \int_0^t K(t - \tau) G(X(\tau))\, d\tau, \quad t \geq 0, \tag{3.9}$$

such that

i) $K \in L^1((0, \infty), \mathbb{R}^{n \times n})$

ii) $F \in C^0((0, \infty), \mathbb{R}^n)$*, bounded and* $F(t) \to 0$ *as* $t \to \infty$*,*

iii) $G \in C^1(\mathbb{R}^n)$ *and* $G(0) = 0$

iv) $J = DG(0)$ *is non-singular.*

Then if and only if

$$\det\left(Id - \int_0^\infty e^{-\tau v} K(\tau) J\, d\tau\right) \neq 0 \tag{3.10}$$

for the right half plane $\Re v \geq 0$ *it holds that* $x(t) \to 0$*.*

Remark 3.5. *The equation* (3.9) *given in the theorem above, is a Volterra equation of convolution type, as the kernel depends on* $t - \tau$*.*

We realize that the following system can be studied independently from the other variables σ_i^r and r

$$\begin{aligned} s(t) &= \int_0^t \left(-s(\tau)l(\tau) + \left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) s(\tau)\right) e^{-\nu_d(t-\tau)}\ d\tau + \frac{\nu_b}{\nu_d}, \\ l(t) &= \phi(t)\rho(t) \int_0^t \left(s(\tau)l(\tau) + \left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau)\right) A(t-\tau)\ d\tau, \\ i(t) &= \int_0^t \left(s(\tau)l(\tau) + \left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau)\right) \gamma_I(t-\tau) e^{-\nu_d(t-\tau)}\ d\tau, \\ \sigma_i^d(\tau) &= -\int_0^t \left(s(\tau)l(t) + \left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) i(\tau)\right) \mu_I^D \gamma_I^{D\prime}(t-\tau) e^{-\nu_d(t-\tau)}\ d\tau. \end{aligned} \tag{3.11}$$

Our goal now is to rewrite this model so that it fits in the scenario of Theorem 3.4. Therefore, we first need to translate the equilibrium

$$(s^*, l^*, i^*, \sigma_i^{d\,*})$$

to the origin. We define $\bar{s} = s - s^*$, $\bar{l} = l - l^*$, $\bar{i} = i - i^*$ and $\bar{\sigma}_i^d = \sigma_i^d - \sigma_i^{d\,*}$, with s^*, l^*, i^* and $\sigma_i^{d\,*}$ given in (3.7). Then, this means that $z = \bar{z} + z^*$ for $z \in \{s, l, i, \sigma_i^d\}$, which allows us to write the equations for $\bar{z}$ without the term z appearing. We now show exemplarily how to write $\bar{s}$ suitable to the Volterra form. Therefore, we compute

$$\begin{aligned} \bar{s}(t) &= \int_0^t \left(-s(\tau)l(\tau) + \left(\nu_d + \sigma_i^d(\tau) - \nu_b\right) s(\tau)\right) e^{-\nu_d(t-\tau)}\ d\tau \\ &\quad - \int_{-\infty}^t \left(-s^*l^* + \left(\nu_d + \sigma_i^{d\,*} - \nu_b\right) s^*\right) e^{-\nu_d(t-\tau)}\ d\tau \\ &= -\int_{-\infty}^0 \left(-s^*l^* + \left(\nu_d + \sigma_i^{d\,*} - \nu_b\right) s^*\right) e^{-\nu_d(t-\tau)}\ d\tau \\ &\quad + \int_0^t \left(-(s(\tau)l(\tau) - s^*l^*) + (\nu_d - \nu_b)(s(\tau) - s^*) + \left(\sigma_i^d(\tau)s(\tau) - \sigma_i^{d\,*}s^*\right)\right) e^{-\nu_d(t-\tau)}\ d\tau \\ &= -\int_{-\infty}^0 \left(-s^*l^* + \left(\nu_d + \sigma_i^{d\,*} - \nu_b\right) s^*\right) e^{-\nu_d(t-\tau)}\ d\tau \\ &\quad + \int_0^t \left(-\bar{l}(\tau)(\bar{s}(\tau) + s^*) - l^*\bar{s}(\tau) + (\nu_d + \sigma_i^{d\,*} - \nu_b)\bar{s}(\tau) + \bar{\sigma}_i^d(\tau)(\bar{s}(\tau) + s^*)\right) e^{-\nu_d(t-\tau)}\ d\tau. \end{aligned}$$

We can derive similar formulations for $\bar{l}$, $\bar{i}$ and $\bar{\sigma_i^d}$, with analogous computations. Now, we can write the system for $\bar{s}, \bar{l}, \bar{i}$ and $\bar{\sigma}_i^d$ as matrix form Volterra integral equation, that is

$$X(t) = F(t) + \int_0^t K(t-\tau)G(X(\tau))\ d\tau, \tag{3.12}$$

with

$$F(t) = \begin{pmatrix} \int_{-\infty}^0 \left(-s^*l^* + \left(\nu_d + \sigma_i^{d\,*} - \nu_b\right) s^*\right) e^{-\nu_d(t-\tau)}\ d\tau \\ \phi\rho \int_{-\infty}^0 \left(s^*l^* + \left(\nu_d + \sigma_i^{d\,*} - \nu_b\right) i^*\right) A(t-\tau)\ d\tau \\ \int_{-\infty}^0 \left(s^*l^* + \left(\nu_d + \sigma_i^{d\,*} - \nu_b\right) i^*\right) \gamma_I(t-\tau) e^{-\nu_d(t-\tau)}\ d\tau \\ \int_{-\infty}^0 \left(s^*l^* + \left(\nu_d + \sigma_i^{d\,*} - \nu_b\right) i^*\right) \mu_I^D \tilde{\gamma}_i^d(t-\tau)\ d\tau \end{pmatrix}, \tag{3.13}$$

$$K(\tau) = \begin{pmatrix} e^{-\nu_d \tau} & -e^{-\nu_d \tau} & 0 & 0 \\ 0 & \phi\rho A(\tau) & \phi\rho A(\tau) & 0 \\ 0 & \gamma_I(\tau)e^{-\nu_d \tau} & \gamma_I(\tau)e^{-\nu_d \tau} & 0 \\ 0 & \tilde{\gamma}_i^d(\tau) & \tilde{\gamma}_i^d(\tau) & 0 \end{pmatrix} \tag{3.14}$$

and

$$G(X(\tau) = \begin{pmatrix} \bar{\sigma}_i^d(\bar{s}(\tau) + s^*) + \sigma_i^{d*}\bar{s}(\tau) + \bar{s}(\tau)(\nu_d - \nu_b) \\ \bar{l}(\bar{s}(\tau) + s^*) + l^*\bar{s}(\tau) \\ \bar{\sigma}_i^d(\tau)(\bar{i}(\tau) + i^*) + \sigma_i^{d*}\bar{i}(\tau) + \bar{i}(\tau)(\nu_d - \nu_b) \\ \bar{\sigma}_i^d(\tau) \end{pmatrix}, \qquad X(t) = \begin{pmatrix} \bar{s}(t) \\ \bar{l}(t) \\ \bar{i}(t) \\ \bar{\sigma}_i^d(t) \end{pmatrix}. \tag{3.15}$$

Where we used γ_I and $\tilde{\gamma}_I^Z$ defined in (2.37). We now want to verify the conditions of Theorem 3.4, in order to apply this theorem later.

i) $K \in L^1((0,\infty), \mathbb{R}^{4\times 4})$ is obviously true.

ii) Clearly $F(t) \in C^0((0,\infty), \mathbb{R}^4)$ and bounded, as all integrals in $F(t)$ exist and are finite. In particular the exponential function is in $L^1 \cap L^\infty$on $(-\infty, 0]$, γ_I is an L^1 function by Assumption 2.1, $\gamma_I^{D\prime} \in L^1$ as it is as probability densitiy function and therefore $\tilde{\gamma}_i^d \in L^1$, and we showed that A is an L^1 function in Lemma 2.12. We show $F(t) \to 0$ as $t \to \infty$ and start with the first component

$$\begin{aligned} &\lim_{t\to\infty} \int_{-\infty}^{0} \left(-s^*l^* + \left(\nu_d + \sigma_i^{d*} - \nu_b\right) s^*\right) e^{-\nu_d(t-\tau)}\, d\tau \\ &= \lim_{t\to\infty} e^{-\nu_d t} \int_{-\infty}^{0} \left(-s^*l^* + \left(\nu_d + \sigma_i^{d*} - \nu_b\right) s^*\right) e^{\nu_d \tau}\, d\tau \\ &= 0 \cdot \underbrace{\int_{-\infty}^{0} \left(-s^*l^* + \left(\nu_d + \sigma_i^{d*} - \nu_b\right) s^*\right) e^{\nu_d \tau}\, d\tau}_{<\infty} = 0. \end{aligned}$$

The convergence for the other three components can be seen similarly.

iii) $G \in C^1(\mathbb{R}^n)$ and $G(0) = 0$ are clear.

iv) We compute $J = DG(0)$

$$DG(0) = \begin{pmatrix} \sigma_i^{d*} + (\nu_d - \nu_b) & 0 & 0 & s^* \\ l^* & s^* & 0 & 0 \\ 0 & 0 & \sigma_i^{d*} + (\nu_d - \nu_b) & i^* \\ 0 & 0 & 0 & 1 \end{pmatrix}. \tag{3.16}$$

Then $\det J = \det DG(0) = (\sigma_i^{d*} + (\nu_d - \nu_b))^2 s^*$. This means $DG(0)$ can only be non-singular if $\nu_d + \sigma_i^{d*} - \nu_b \neq 0$.

Now we want to obtain the characteristic equation

$$\det\left(Id - \int_0^\infty e^{-\tau w} K(\tau) J\, ds\right) = 0. \tag{3.17}$$

The term $K(\tau)J$ is given by

$$\begin{pmatrix} e^{-\nu_d\tau}(\sigma_i^{d*}+\nu_d-\nu_b-l^*) & -e^{-\nu_d\tau}s^* & 0 & e^{-\nu_d\tau}s^* \\ \phi\rho A(\tau)l^* & \phi\rho A(\tau)s^* & \phi\rho A(\tau)(\sigma_i^{d*}+\nu_d-\nu_b) & \phi\rho A(\tau)i^* \\ \gamma_I(\tau)e^{-\nu_d\tau}l^* & \gamma_I(\tau)e^{-\nu_d\tau}s^* & \gamma_I(\tau)e^{-\nu_d\tau}(\sigma_i^{d*}+\nu_d-\nu_b) & \gamma_I(\tau)e^{-\nu_d\tau}i^* \\ \tilde{\gamma}_i^d(\tau)l^* & \tilde{\gamma}_i^d(\tau)s^* & \tilde{\gamma}_i^d(\tau)(\sigma_i^{d*}+\nu_d-\nu_b) & \tilde{\gamma}_i^d(\tau)i^* \end{pmatrix}.$$

With this we get

$$\begin{aligned} M(w) &:= \int_0^\infty e^{-w\tau}K(\tau)Jd\tau \\ &= \begin{pmatrix} \frac{\sigma_i^{d*}+\nu_d-\nu_b-l^*}{\nu_d+w} & -\frac{s*}{\nu_d+w} & 0 & \frac{s*}{\nu_d+w} \\ l^*L(w) & s^*L(w) & (\sigma_i^{d*}+\nu_d-\nu_b)L(w) & i^*L(w) \\ l^*L_I(w) & s^*L_I(w) & (\sigma_i^{d*}+\nu_d-\nu_b)L_I(w) & i^*L_I(w) \\ l^*L_I^D(w) & s^*L_I^D(w) & (\sigma_i^{d*}+\nu_d-\nu_b)L_I^D(w) & i^*L_I^D(w) \end{pmatrix}, \end{aligned}$$

with

$$\begin{aligned} L(w) &= \phi\rho\int_0^\infty e^{-w\tau}A(\tau)d\tau, \\ L_I(w) &= \int_0^\infty e^{-w\tau}\gamma_I(\tau)e^{-\nu_d\tau}d\tau \quad \text{and} \\ L_I^D(w) &= \int_0^\infty e^{-w\tau}\tilde{\gamma}_i^d(\tau)d\tau. \end{aligned}$$

Now we compute the characteristic polynomial

$$\begin{aligned} &\det(I-M(w)) \\ &= \det\begin{pmatrix} 1-\frac{\sigma_i^{d*}+\nu_d-\nu_b-l^*}{\nu_d+w} & \frac{s*}{\nu_d+w} & 0 & -\frac{s*}{\nu_d+w} \\ -l^*L(w) & 1-s^*L(w) & -(\sigma_i^{d*}+\nu_d-\nu_b)L(w) & -i^*L(w) \\ -l^*L_I(w) & -s^*L_I(w) & 1-(\sigma_i^{d*}+\nu_d-\nu_b)L_I(w) & -i^*L_I(w) \\ -l^*L_I^D(w) & -s^*L_I^D(w) & -(\sigma_i^{d*}+\nu_d-\nu_b)L_I^D(w) & 1-i^*L_I^D(w) \end{pmatrix} \\ &= \left(1-\frac{\sigma_i^{d*}+\nu_d-\nu_b-l^*}{\nu_d+w}\right)\det\begin{pmatrix} 1-s^*L(w) & -(\sigma_i^{d*}+\nu_d-\nu_b)L(w) & -i^*L(w) \\ -s^*L_I(w) & 1-(\sigma_i^{d*}+\nu_d-\nu_b)L_I(w) & -i^*L_I(w) \\ -s^*L_I^D(w) & -(\sigma_i^{d*}+\nu_d-\nu_b)L_I^D(w) & 1-i^*L_I^D(w) \end{pmatrix} \\ &\quad -\frac{s*}{\nu_d+w}\det\begin{pmatrix} -l^*L(w) & -(\sigma_i^{d*}+\nu_d-\nu_b)L(w) & -i^*L(w) \\ -l^*L_I(w) & 1-(\sigma_i^{d*}+\nu_d-\nu_b)L_I(w) & -i^*L_I(w) \\ -l^*L_I^D(w) & -(\sigma_i^{d*}+\nu_d-\nu_b)L_I^D(w) & 1-i^*L_I^D(w) \end{pmatrix} \\ &+ \quad \frac{s*}{\nu_d+w}\det\begin{pmatrix} -l^*L(w) & 1-s^*L(w) & -(\sigma_i^{d*}+\nu_d-\nu_b)L(w) \\ -l^*L_I(w) & -s^*L_I(w) & 1-(\sigma_i^{d*}+\nu_d-\nu_b)L_I(w) \\ -l^*L_I^D(w) & -s^*L_I^D(w) & -(\sigma_i^{d*}+\nu_d-\nu_b)L_I^D(w) \end{pmatrix} \\ &= \left(1-\frac{\sigma_i^{d*}+\nu_d-\nu_b-l^*}{\nu_d+w}\right)\left(1-s^*L(w)-i^*L_I^D(w)-\left(\nu_d+\sigma_i^{d*}-\nu_b\right)L_I(w)\right) \end{aligned}$$

$$+\frac{s*}{\nu_d+w}l^*L(w)-\frac{s*}{\nu_d+w}l^*L_I^D(w)$$

Then, the characteristic equation (3.17) becomes

$$\begin{aligned}0=&\left(1-\frac{\sigma_i^{d*}+\nu_d-\nu_b-l^*}{\nu_d+w}\right)\left(1-s^*L(w)-i^*L_I^D(w)-\left(\nu_d+\sigma_i^{d*}-\nu_b\right)L_I(w)\right)\\&+\frac{s*}{\nu_d+w}l^*\left(L(w)-L_I^D(w)\right)=:\mathcal{L}(w).\end{aligned}\tag{3.18}$$

Now we first state the theorem concerning the stability of the disease-free equilibrium.

Theorem 3.6. *If $\mathcal{R}_c>1$, then if $\nu_d<\nu_b$ and $1-\mathcal{R}_c<(\nu_d-\nu_b)\mathcal{W}_i$, the disease-free equilibrium $(s^*,i^*,r^*)=(1,0,0)$ is unstable*

Proof. We first show that the disease-free equilibrium of the smaller model (3.11) is unstable. Then at $(s^*,l^*,i^*,\sigma_i^{d*})=(1,0,0,0)$ the characteristic equation given by (3.18) reduces to

$$0=\left(1-\frac{\nu_d-\nu_b}{\nu_d+w}\right)\left(1-L(w)-(\nu_d-\nu_b)L_I(w)\right).$$

We directly see that $L(0)=\mathcal{R}_c>1$ and $L_I(0)=\mathcal{W}_i$. Then by the assumptions of the theorem we have $\mathcal{L}(0)<0$. We also see that

$$\begin{aligned}\lim_{w\to\infty}L(w)&=\lim_{w\to\infty}\phi\rho\int_0^\infty e^{-w\tau}A(\tau)d\tau\\&=\phi\rho\int_0^\infty\lim_{w\to\infty}e^{-w\tau}\tilde{A}(\tau)d\tau=0,\end{aligned}$$

where we used dominated convergence, as $e^{-w\tau}\tilde{A}(\tau)\le\tilde{A}(\tau)\in L^1((0,\infty))$. The same way one can also see that $L_I(w)\to 0$ as $t\to\infty$. This implies that

$$\lim_{w\to\infty}\mathcal{L}(w)=1>0.$$

□

Remark 3.7. *In the proof we needed the assumption $1-\mathcal{R}_c<(\nu_d-\nu_b)\mathcal{W}_i<0$. This implies that $\nu_b-\nu_d$ cannot become too large, as $\mathcal{W}_i\gg 0$. Without this condition, the birth rate can be large enough that the proportion of infected and recovered individuals in the population vanishes.*

In Section 3.2.2 we have seen that there are many cases where endemic equilibria exist, but we have also seen that the equilibrium points are not always between 0 and 1. To see if the an endemic equilibrium is stable or not, one could again make use of Theorem 3.4. If one has a computed equilibrium one could plug it into the characteristic equation (3.18) to see if it is stable or not. As we could not compute any general formula for the endemic equilibrium we will omit this part here. We will instead look at this numerically in Section 5.

3.3 Analysis of the population size

In this section, we want to take a closer look at the population size and its long-term behaviour. Therefore, we want to have a closer look at the derivative of the population size, as it determines if the population increases, decreases, or is constant over a certain time interval. By (2.17) we get that

$$N'(t) = \nu_b N(t) - \nu_d N(t) - \sigma_U^D(t). \tag{3.19}$$

First of all, we want to take a closer look at the case, where the system is entirely free of the disease. In that case we have $S(t) = N(t)$, i.e

$$N(t) = S(t) = \int_0^t \nu_b N(s) e^{-\nu_d(t-s)} ds = \int_0^t \nu_b S(s) e^{-\nu_d(t-s)} ds. \tag{3.20}$$

First we consider the case where $\nu_b < \nu_d$, then by (3.19) we then know that $N'(t) < 0$. Moreover, this means that N is monotonically decreasing and with $N \geq 0$ we can deduce that N converges to some limit N^*. For this limit point, it should hold

$$N^* = \int_{-\infty}^t \nu_b N^* e^{-\nu_d(t-s)} ds = N^* \frac{\nu_b}{\nu_d}, \tag{3.21}$$

but this is only possible for $N^* = 0$. As one would expect, $\nu_b < \nu_d$ implies that the population is going to die out. In the case $\nu_b \geq \nu_d$ $N(t)$ is monotonically increasing, but is not bounded from above. This means that the population will blow up.

Now we want to take a closer look at the case where the system is not free of disease. This is way more complex as the behaviour of $\sigma_U^D(t)$ cannot be predicted before solving the integro-differential equation for the SECIR-type model given in Section 2.2. However, we want to use our results from the previous part about the analysis of the normalized model. From the previous section, we know how $\sigma_u^d(t)$ behaves. We assume for now on that the relation $\sigma_U^D(t) = N(t)\sigma_u^d(t)$ is true, as this was the idea for the normalization. In the case of the disease-free equilibrium we have seen that $\lim_{t\to\infty} \sigma_u^d(t) = 0$. And as the name already says it is disease-free, therefore, we are in the case of (3.20). We will have a closer look at this later on in the Section about the implementation.

4 Discretization

Before, we have analysed the continuous model. However, we also want to analyse the discretized model numerically. First of all, to validate the results from Section 3. Moreover, we want to get an idea of what happens in the cases, where we were not able to state a theoretical result. In order, to do so we discretize our SECIR-type birth-and-death model given by (2.15) and the normalized model given by (2.29). Later on, in Section 4.4 we are going to show that the numerical scheme preserves the main properties, such as non-negativity. As in [15] and [8], we will use a non-standard discretization scheme to discretize the force of infection term, the transitions and most of the compartments. For the remaining compartments and the other model parameters we will simple use a rectangular rule to approximate the integrals. In our case, non-standard means to mix left and right point approximations. Simply using a standard rectangular or trapezoidal rule would always mean that we have to solve a non-linear system of equations, meaning we would need to use a Newton algorithm. By using a non-standard scheme we can avoid that. Moreover, as shown in [8], the non-standard scheme preserves some properties of the model, as non-negativity, even for large step sizes. In [8], the authors show that this is not necessarily the case if the trapezoidal rule is used. In the following, we will use the notation $\widehat{x}$ for the discretized version of some parameter x.

4.1 Discretization of the parameters used for all models

Here we start by defining the numerical scheme for those parameters that are shared by both models. For a given step size $\Delta t > 0$, we define $t_n \coloneqq n\Delta t$, for $n \in \mathbb{N}$, to define an uniform mesh. We will approximate the derivative of $\gamma_{z_1}^{z_2}$ by a backwards difference scheme, i.e

$$\widehat{\gamma}_{z_1}^{z_2}{}'(t_{n+1}) = \frac{\gamma_{z_1}^{z_2}(t_{n+1}) - \gamma_{z_1}^{z_2}(t_n)}{\Delta t}. \tag{4.1}$$

Then, since by Assumption 2.1 $\gamma_{z_1}^{z_2}(t)$ is decreasing, it holds that $\widehat{\gamma}_{z_1}^{z_2}{}'(t_n) \geq 0$ for all $n \in \mathbb{N}$. The term B used in the definition of the force of infection term is approximated using a standard rectangular rule using a left approximation, as in the non-standard scheme we always use a left-approximation for the functions $\gamma_{z_1}^{z_2}$. Then $\widehat{B}$ is given by

$$\widehat{B}(t_k) = \Delta t \sum_{i=0}^{k-1} \xi_I(t_i)\gamma_I(t_i)\mu_C^I \widehat{\gamma}_C^{I\prime}(t_{k-i}), \tag{4.2}$$

with $\widehat{B}(0) = 0$. Then, as $\widehat{\gamma}_C^{I\prime}(t_{k-i}) \leq 0$, it holds that $B(t_n) \leq 0$ for all $n \in \mathbb{N}$. Finally, the integrals in the definition of A, given in (2.21), are also approximated with a standard rectangular rule using a left approximation. Then for $k > 0$

$$\begin{aligned}
\widehat{a}_1(t_k) &= -\Delta t \sum_{i=0}^{k-1} \xi_C(t_i)\gamma_C(t_i)\widehat{\gamma}_E^{C\prime}(t_{k-i}), \\
\widehat{a}_2(t_k) &= \Delta t \sum_{i=0}^{k-1} \widehat{\gamma}_E^{C\prime}(t_{k-i})B(t_i), \\
\widehat{A}(t_k) &= e^{-\nu_d t_k}(\widehat{a}_1(t_k) + \widehat{a}_2(t_k)),
\end{aligned} \tag{4.3}$$

with $A(0) = 0$. Then, $\widehat{A}(t_n) \geq 0$ for all $n \in \mathbb{N}$. Lastly, we want to discretize the model parameters introduced in Section 3.1. We start with the reproduction number (3.1)

$$\widehat{\mathcal{R}}_c = \phi\rho \sum_{i=0}^{\infty} \widehat{A}(t_i). \tag{4.4}$$

The discretization for $\mathcal{T}_{z_1}^{z_2}$ (3.2) is given by

$$\widehat{\mathcal{T}}_{z_1}^{z_2} = -\sum_{i=0}^{\infty} e^{-\nu_d t_i} \mu_{z_1}^{z_2} \widehat{\gamma}'(t_i). \tag{4.5}$$

Using this the discretization of $\mathcal{V}^z$ (3.3) is given by

$$\begin{aligned}
\widehat{\mathcal{V}}^c &= \widehat{\mathcal{T}}_e^c, \\
\widehat{\mathcal{V}}^i &= \widehat{\mathcal{V}}^c \widehat{\mathcal{T}}_c^i, \\
\widehat{\mathcal{V}}^h &= \widehat{\mathcal{V}}^i \widehat{\mathcal{T}}_i^h, \\
\widehat{\mathcal{V}}^u &= \widehat{\mathcal{V}}^h \widehat{\mathcal{T}}_h^u, \\
\widehat{\mathcal{V}}^d &= \widehat{\mathcal{V}}^u \widehat{\mathcal{T}}_u^d, \\
\widehat{\mathcal{V}}^r &= \widehat{\mathcal{V}}^c \widehat{\mathcal{T}}_c^r + \widehat{\mathcal{V}}^i \widehat{\mathcal{T}}_i^r + \widehat{\mathcal{V}}^h \widehat{\mathcal{T}}_h^r + \widehat{\mathcal{V}}^u \widehat{\mathcal{T}}_u^r.
\end{aligned} \tag{4.6}$$

We discretize $\mathcal{W}_z$ (3.4) by

$$\widehat{\mathcal{W}}_z = \sum_{i=0}^{\infty} \gamma_z(t_i) e^{-\nu_d t_i}. \tag{4.7}$$

These sums are all infite sums, which clearly cannot be evaluated, therefore we need to cut off these sums in the implementation. We will comment on this further in Section 5.1.

4.2 Discretization of the SECIR-type birth-and-death model

In this section we define the numerical scheme for the SECIR-type birth-and-death model from Section 2.2.We start by defining

$$\widehat{\sigma}_S^E(t_{n+1}) = \widehat{S}(t_{n+1}) \widehat{\lambda}(t_n), \tag{4.8}$$

which is a non-standard numerical scheme, which means that we have a right endpoint approximation in $\widehat{S}$ and a left endpoint approximation in $\widehat{\lambda}$. Using a backwards finite difference scheme for $\widehat{S}'$ gives us

$$\widehat{S}'(t_{n+1}) = \frac{\widehat{S}(t_{n+1}) - \widehat{S}(t_n)}{\Delta t}.$$

Moreover, by the definition of S given in (2.15) we have

$$\widehat{S}'(t_{n+1}) = -\widehat{\sigma}_S^E(t_{n+1}) + \nu_b \widehat{N}(t_{n+1}) - \nu_d \widehat{S}(t_{n+1}),$$

but as we will start by computing $\widehat{S}$ in every step we do not know the values for the other compartments at t_{n+1} yet. Therefore, we will use the following formula, where we know the population size $\widehat{N}(t_n)$, from the computations of the previous time step,

$$\widehat{S}'(t_{n+1}) = -\widehat{\sigma}_S^E(t_{n+1}) + \nu_b \widehat{N}(t_n) - \nu_d \widehat{S}(t_{n+1}).$$

All together, this yields

$$\widehat{S}(t_{n+1}) = \frac{\widehat{S}(t_n) + \Delta t \nu_b \widehat{N}(t_n)}{1 + \Delta t(\widehat{\lambda}(t_n) + \nu_d)}. \tag{4.9}$$

In order to discretize the force of infection term we start by discretizing λ_0. Therefore, we define

$$\widehat{\varphi}(t_k) = \phi\rho(C_0(t_k)\xi_C(t_k) + I_0(t_k)\xi_I(t_k)) \tag{4.10}$$

Then the discretization of λ_0 from (2.14) is given by

$$\widehat{\lambda}_0(t_k) = \frac{\widehat{\varphi}(t_k)}{\widehat{N}(t_k)}.$$

Then we discretize f given in (2.23) by

$$\widehat{f}(t_k) = E_0 \widehat{A}(t_k) - C_0 e^{-\nu_d t_k} \widehat{B}(t_k), \tag{4.11}$$

where $\widehat{B}(t_k)$ was given in (4.2) and $\widehat{A}(t_k)$ was given in (4.3). Now we discretize the force of infection term by again using a non-standard discretization, where we use a rectangular rule with a right approximation in $\widehat{S}$ and a left approximation in $\widehat{A}$ and $\widehat{\lambda}$. Then, for $n \geq 0$ we obtain

$$\widehat{\lambda}(t_{n+1}) = \frac{\phi\rho}{\widehat{N}(t_{n+1})} \left(\widehat{\varphi}(t_{n+1}) + \Delta t \sum_{i=0}^{n} \widehat{A}(t_{n+1-j}) \widehat{S}(t_{j+1}) \widehat{\lambda}(t_j) + \widehat{f}(t_{n+1}) \right), \tag{4.12}$$

with $\widehat{\lambda}(0) = \lambda_0(0) = 0$. Analogously, we approximate the integrals of the remaining transitions using a non-standard rectangular rule with a right endpoint approximation in $\widehat{\sigma}_{z_1}^{z_2}$ and a left

endpoint approximation in $e^{-\nu_d \tau}$ and $\widehat{\gamma}_{z_1}^{z_2}{}'$

$$
\begin{aligned}
\widehat{\sigma}_S^E(t_{n+1}) &= \widehat{S}(t_{n+1})\widehat{\lambda}(t_n),\\
\widehat{\sigma}_E^C(t_{n+1}) &= -\Delta t \sum_{i=0}^{n} \widehat{\sigma}_S^E(t_{i+1}) e^{-\nu_d t_{n+1-i}} \widehat{\gamma}_E^{C\,\prime}(t_{n+1-i}) - e^{-\nu_d t_{n+1}} E_0 \widehat{\gamma}_E^{C\,\prime}(t_{n+1}),\\
\widehat{\sigma}_C^I(t_{n+1}) &= -\Delta t \sum_{i=0}^{n} \widehat{\sigma}_E^C(t_{i+1}) e^{-\nu_d t_{n+1-i}} \mu_C^I \widehat{\gamma}_C^{I\,\prime}(t_{n+1-i}) - e^{-\nu_d t_{n+1}} C_0 \mu_C^I \widehat{\gamma}_C^{I\,\prime}(t_{n+1}),\\
\widehat{\sigma}_C^R(t_{n+1}) &= -\Delta t \sum_{i=0}^{n} \widehat{\sigma}_E^C(t_{i+1}) e^{-\nu_d t_{n+1-i}} (1-\mu_C^I) \widehat{\gamma}_C^{R\,\prime}(t_{n+1-i}) - e^{-\nu_d t_{n+1}} C_0 (1-\mu_C^I) \widehat{\gamma}_C^{R\,\prime}(t_{n+1}),\\
\widehat{\sigma}_I^H(t_{n+1}) &= -\Delta t \sum_{i=0}^{n} \widehat{\sigma}_C^I(t_{i+1}) e^{-\nu_d t_{n+1-i}} \mu_I^H \widehat{\gamma}_I^{H\,\prime}(t_{n+1-i}) - e^{-\nu_d t_{n+1}} I_0 \mu_I^H \widehat{\gamma}_I^{H\,\prime}(t_{n+1}),\\
\widehat{\sigma}_I^R(t_{n+1}) &= -\Delta t \sum_{i=0}^{n} \widehat{\sigma}_C^I(t_{i+1}) e^{-\nu_d t_{n+1-i}} (1-\mu_I^H) \widehat{\gamma}_I^{R\,\prime}(t_{n+1-i}) - e^{-\nu_d t_{n+1}} I_0 (1-\mu_I^H) \widehat{\gamma}_I^{R\,\prime}(t_{n+1}),\\
\widehat{\sigma}_H^U(t_{n+1}) &= -\Delta t \sum_{i=0}^{n} \widehat{\sigma}_I^H(t_{i+1}) e^{-\nu_d t_{n+1-i}} \mu_H^U \widehat{\gamma}_H^{U\,\prime}(t_{n+1-i}) - e^{-\nu_d t_{n+1}} H_0 \mu_H^U \widehat{\gamma}_H^{U\,\prime}(t_{n+1}),\\
\widehat{\sigma}_H^R(t_{n+1}) &= -\Delta t \sum_{i=0}^{n+1} \widehat{\sigma}_I^H(t_{i+1}) e^{-\nu_d t_{n+1-i}} (1-\mu_H^U) \widehat{\gamma}_H^{R\,\prime}(t_{n+1-i}) - e^{-\nu_d t_{n+1}} H_0 (1-\mu_H^U) \widehat{\gamma}_H^{R\,\prime}(t_{n+1}),\\
\widehat{\sigma}_U^D(t_{n+1}) &= -\Delta t \sum_{i=0}^{n} \widehat{\sigma}_H^U(t_{i+1}) e^{-\nu_d t_{n+1-i}} \mu_U^D \widehat{\gamma}_U^{D\,\prime}(t_{n+1-i}) - e^{-\nu_d t_{n+1}} U_0 \mu_U^D \widehat{\gamma}_U^{D\,\prime}(t_{n+1}),\\
\widehat{\sigma}_U^R(t_{n+1}) &= -\Delta t \sum_{i=0}^{n} \widehat{\sigma}_H^U(t_{i+1}) e^{-\nu_d t_{n+1-i}} (1-\mu_U^D) \widehat{\gamma}_U^{R\,\prime}(t_{n+1-i}) - e^{-\nu_d t_{n+1}} U_0 (1-\mu_U^D) \widehat{\gamma}_U^{R\,\prime}(t_{n+1}).
\end{aligned}
\tag{4.13}
$$

By Assumption 2.5 we assume that we have infection age $t_0 = 0$, all flows should be 0 at time t_0 and we get the starting value

$$\widehat{\sigma}_{z_1}^{z_2}(t_0) = 0. \tag{4.14}$$

We will discretize the compartments E, C, I, H, U, D and R by directly applying a discretization

scheme to the integral model formulation in (2.15) and obtain for $n \geq 0$

$$\begin{aligned}
\widehat{E}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \gamma_E^C(t_{n+1-i}) e^{-\nu_d t_{n+1-i}} \widehat{\sigma}_S^E(t_{i+1}) + E_0(t_{n+1}),\\
\widehat{C}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \gamma_C(t_{n+1-i}) e^{-\nu_d t_{n+1-i}} \widehat{\sigma}_E^C(t_{i+1}) + C_0(t_{n+1}),\\
\widehat{I}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \gamma_I(t_{n+1-i}) e^{-\nu_d t_{n+1-i}} \widehat{\sigma}_C^I(t_{i+1}) + I_0(t_{n+1}),\\
\widehat{H}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \gamma_H(t_{n+1-i}) e^{-\nu_d t_{n+1-i}} \widehat{\sigma}_I^H(t_{i+1}) + H_0(t_{n+1}),\\
\widehat{U}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \gamma_U(t_{n+1-i}) e^{-\nu_d t_{n+1-i}} \widehat{\sigma}_H^U(t_{i+1}) + U_0(t_{n+1}),\\
\widehat{R}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \left(\widehat{\sigma}_C^R(t_{i+1}) + \widehat{\sigma}_I^R(t_{i+1}) + \widehat{\sigma}_H^R(t_{i+1}) + \widehat{\sigma}_U^R(t_{i+1})\right) e^{-\nu_d t_{n+1-i}} + R_0(t_{n+1}),\\
\widehat{D}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \widehat{\sigma}_U^D(t_{i+1}) + D_0.
\end{aligned} \tag{4.15}$$

For the compartments E, C, I, H, U and R we use the non-standard rectangular rule, with a right approximation for the transitions $\widehat{\sigma}_{z_1}^{z_2}$ and a left approximation for $\widehat{\gamma}_{z_1}^{z_2}$ and the exponential function. For D, we just used a standard rectangular rule with right approximation since the transition to D is the only function in the integral for D. We us the following starting values to initalize the compartments

$$\begin{aligned}
\widehat{S}(t_0) &= S_0, & \widehat{E}(t_0) &= E_0,\\
\widehat{C}(t_0) &= C_0 & \widehat{I}(t_0) &= I_0,\\
\widehat{H}(t_0) &= H_0, & \widehat{U}(t_0) &= U_0,\\
\widehat{R}(t_0) &= R_0, & \widehat{D}(t_0) &= D_0.
\end{aligned} \tag{4.16}$$

Finally, we also want to discretize the reproduction number $\mathcal{R}_c$ defined in (3.1). For this we simply use a standard rectangular rule and the already defined approximation of $\widehat{A}$

$$\widehat{\mathcal{R}}_c = \phi\rho\Delta t \sum_{i=0}^{\infty} \widehat{A}(t_i). \tag{4.17}$$

4.2.1 An update scheme for the compartments

In [15], another approach was used to derive a discretization for the compartments by using the definitions of the derivatives of the compartments. This led to an update scheme which is more efficient in the implementation. Therefore, we want to derive such an update scheme for our

birth-and-death model. To do so, we will make use of (2.8). By using a backwards difference scheme for the derivatives of the compartments we get an update scheme for the compartments E, C, I, H, U, D and R. As we compute the compartments differently than by using the scheme from (4.15) the results for the compartments may be different and therefore we might get another value for the total population. This implies that also the values for the susceptibles $\widehat{S}$, the force of infection $\widehat{\lambda}$ and the transitions $\widehat{\sigma}_{z_1}^{z_2}$ might be different. To clarify the different discretization schemes we will refer to all the variables computed by this discretization scheme as $\check{z}$. Moreover, we will refer to the discretization scheme given by (4.15) as sum-scheme and to the following scheme by update-scheme. The formulas for the compartments are given by

$$\begin{aligned}
\check{E}(t_{n+1}) &= \frac{1}{1+\Delta t\nu_d}\left(\check{E}(t_n) + \Delta t\check{\sigma}_S^E(t_{n+1}) - \Delta t\check{\sigma}_E^C(t_{n+1})\right),\\
\check{C}(t_{n+1}) &= \frac{1}{1+\Delta t\nu_d}\left(\check{C}(t_n) + \Delta t\check{\sigma}_E^C(t_{n+1}) - \Delta t\check{\sigma}_C^I(t_{n+1}) - \Delta t\widehat{\sigma}_C^R(t_{n+1})\right),\\
\check{I}(t_{n+1}) &= \frac{1}{1+\Delta t\nu_d}\left(\check{I}(t_n) + \Delta t\check{\sigma}_C^I(t_{n+1}) - \Delta t\check{\sigma}_I^H(t_{n+1}) - \Delta t\check{\sigma}_I^R(t_{n+1})\right),\\
\check{H}(t_{n+1}) &= \frac{1}{1+\Delta t\nu_d}\left(\check{H}(t_n) + \Delta t\check{\sigma}_I^H(t_{n+1}) - \Delta t\check{\sigma}_H^U(t_{n+1}) - \Delta t\check{\sigma}_H^R(t_{n+1})\right),\\
\check{U}(t_{n+1}) &= \frac{1}{1+\Delta t\nu_d}\left(\check{U}(t_n) + \Delta t\check{\sigma}_H^U(t_{n+1}) - \Delta t\check{\sigma}_U^D(t_{n+1}) - \Delta t\check{\sigma}_U^R(t_{n+1})\right),\\
\check{R}(t_{n+1}) &= \frac{1}{1+\Delta t\nu_d}\left(\check{R}(t_n) + \Delta t\check{\sigma}_C^R(t_{n+1}) + \Delta t\check{\sigma}_I^R(t_{n+1}) + \Delta t\check{\sigma}_H^R(t_{n+1}) + \Delta t\check{\sigma}_U^R(t_{n+1})\right),\\
\check{D}(t_{n+1}) &= \check{D}(t_n) + \Delta t\check{\sigma}_U^D(t_{n+1}).
\end{aligned} \tag{4.18}$$

With the same starting values as used for the sum-scheme. Note that this scheme is more efficient than (4.15), as it is an update formula and we do not need to approximate the integral with a sum, that needs to be computed in every iteration step. On the other hand, the sum-scheme makes it easier to see some nice mathematical properties of this scheme. In [15] it is shown that the two numerical schemes are equivalent, in our case this is not the case. The problem is the exponential function used for the probability of surviving natural death. In [15] they used the fact that the derivatives of the transition distributions $\gamma_{z_1}^{z_2}$ are approximated by a backwards difference scheme to prove that the two schemes are equivalent. We also used a backwards-difference scheme to approximate ${\gamma_{z_1}^{z_2}}'$, but for the exponential function we never needed to approximate its derivative, as we used its explicit form when deriving the formulas for the flows (2.18). However, we are able to show the following result.

Proposition 4.1. *Under the assumption, that for some t_n, we have that $\widehat{Z}(t_n) = \check{Z}(t_n)$ for all $Z \in \{S, E, C, I, H, U, R, D\}$ and that $\widehat{\sigma}_{z_1}^{z_2}(t_{n+1}) = \check{\sigma}_{z_1}^{z_2}(t_{n+1})$ for all suitable $z_1, z_2 \in \{S, E, C, I, H, U, R, D\}$ we can show the following:*

1. *For $Z \in \{E, C, I, H, U, R\}$ it holds $\widehat{Z}(t_{n+1}) \leq \check{Z}(t_{n+1})$,*
2. *$\widehat{D}(t_{n+1}) = \check{D}(t_{n+1})$.*

Proof. We first show the statement for C, the proofs for E, I, H and U follow analogously.

In the following we will use the following estimate of the exponential function

$$e^x \geq 1 + x.$$

We start by computing the difference of two consecutive time steps and get

$$\begin{aligned}
\widehat{C}(t_{n+1}) - \widehat{C}(t_n) &= \Delta t \sum_{i=0}^{n} \left(\mu_C^I \gamma_C^I(t_{n+1-i}) + (1-\mu_C^I)\gamma_C^R(t_{n+1-i})\right) e^{-\nu_d t_{n+1-i}} \widehat{\sigma}_E^C(t_{i+1}) \\
&\quad - \Delta t \sum_{i=0}^{n-1} \left(\mu_C^I \gamma_C^I(t_{n-i}) + (1-\mu_C^I)\gamma_C^R(t_{n-i})\right) e^{-\nu_d t_{n-i}} \widehat{\sigma}_E^C(t_{i+1}) \\
&\quad + \widehat{C}_0(t_{n+1}) - \widehat{C}_0(t_n) \\
&= \Delta t \left(\mu_C^I \gamma_C^I(0) + (1-\mu_C^I)\gamma_C^R(0)\right) e^{-\nu_d t_0} \widehat{\sigma}_E^C(t_{n+1}) \\
&\quad + \Delta t \sum_{i=0}^{n} \left(\mu_C^I \gamma_C^I(t_{n+1-i}) + (1-\mu_C^I)\gamma_C^R(t_{n+1-i})\right) e^{-\nu_d t_{n+1-i}} \widehat{\sigma}_E^C(t_{i+1}) \\
&\quad - \Delta t \sum_{i=0}^{n} \left(\mu_C^I \gamma_C^I(t_{n-i}) + (1-\mu_C^I)\gamma_C^R(t_{n-i})\right) e^{-\nu_d t_{n+1-i}} e^{\nu_d \Delta t} \widehat{\sigma}_E^C(t_{i+1}) \\
&\quad + e^{-\nu_d t_{n+1}} C_0 \left(\mu_C^I \gamma_C^I(t_{n+1-i}) + (1-\mu_C^I)\gamma_C^R(t_{n+1-i})\right) \\
&\quad - e^{-\nu_d t_{n+1}} e^{\nu_d \Delta t} C_0 \left(\mu_C^I \gamma_C^I(t_{n-i}) + (1-\mu_C^I)\gamma_C^R(t_{n-i})\right). \\
&\leq \Delta t \widehat{\sigma}_E^C(t_{n+1}) \\
&\quad + \Delta t \sum_{i=0}^{n} \left(\mu_C^I \gamma_C^I(t_{n+1-i}) + (1-\mu_C^I)\gamma_C^R(t_{n+1-i})\right) e^{-\nu_d t_{n+1-i}} \widehat{\sigma}_E^C(t_{i+1}) \\
&\quad - \Delta t \sum_{i=0}^{n} \left(\mu_C^I \gamma_C^I(t_{n-i}) + (1-\mu_C^I)\gamma_C^R(t_{n-i})\right) e^{-\nu_d t_{n+1-i}} (1+\Delta t \nu_d) \widehat{\sigma}_E^C(t_{i+1}) \\
&\quad + e^{-\nu_d t_{n+1}} C_0 \left(\mu_C^I \gamma_C^I(t_{n+1-i}) + (1-\mu_C^I)\gamma_C^R(t_{n+1-i})\right) \\
&\quad - e^{-\nu_d t_{n+1}} (1+\Delta t \nu_d) C_0 \left(\mu_C^I \gamma_C^I(t_{n+1-i}) + (1-\mu_C^I)\gamma_C^R(t_{n+1-i})\right). \\
&= \Delta t \widehat{\sigma}_E^C(t_{n+1}) - \Delta t \nu_d \widehat{C}(t_n) \\
&\quad + \Delta t \sum_{i=0}^{n} \mu_C^I \left(\widehat{\gamma}_C^I(t_{n+1-i}) - \widehat{\gamma}_C^I(t_{n-i})\right) e^{-\nu_d t_{n+1-i}} \widehat{\sigma}_E^C(t_{i+1}) \\
&\quad + \Delta t \sum_{i=0}^{n} (1-\mu_C^I) \left(\widehat{\gamma}_C^R(t_{n+1-i}) - \widehat{\gamma}_C^R(t_{n-i})\right) e^{-\nu_d t_{n+1-i}} \widehat{\sigma}_E^C(t_{i+1}) \\
&\quad e^{-\nu_d t_{n+1}} C_0 \mu_C^I \left(\widehat{\gamma}_C^I(t_{n+1-i}) - \widehat{\gamma}_C^I(t_{n-i})\right) \\
&\quad e^{-\nu_d t_{n+1}} C_0 (1-\mu_C^I) \left(\widehat{\gamma}_C^R(t_{n+1-i}) - \widehat{\gamma}_C^R(t_{n-i})\right) \\
&= \Delta t \widehat{\sigma}_E^C(t_{n+1}) - \Delta t \nu_d \widehat{C}(t_n) \\
&\quad \Delta t + \sum_{i=0}^{n} e^{-\nu_d t_{n+1-i}} \widehat{\sigma}_E^C(t_{i+1}) \mu_C^I \widehat{\gamma}_C^{I\prime}(t_{n-1})
\end{aligned}$$

$$
\begin{aligned}
&+ e^{-\nu_d t_{n+1}} C_0 \mu_C^I \widehat{\gamma}_C^{I\prime}(t_{n+1}) \\
&+ \Delta t \sum_{i=0}^{n} e^{-\nu_d t_{n+1-i}} \widehat{\sigma}_E^C(t_{i+1})(1-\mu_C^I)\widehat{\gamma}_C^{R\prime}(t_{n-1}) \\
&+ e^{-\nu_d t_{n+1}} C_0 (1-\mu_C^I)\widehat{\gamma}_C^{R\prime}(t_{n+1}) \\
&= -\Delta t \nu_d \widehat{C}(t_n) + \Delta t \widehat{\sigma}_E^C(t_{n+1}) - \Delta t \widehat{\sigma}_C^I(t_{n+1}) - \Delta t \widehat{\sigma}_C^R(t_{n+1})
\end{aligned}
$$

From this and the assumptions of the Propositions that $\widehat{\sigma}_{z_1}^{z_2}(t_{n+1}) = \check{\sigma}_{z_1}^{z_2}(t_{n+1})$, we get

$$
\begin{aligned}
\widehat{C}(t_{n+1}) &\leq \frac{1}{1+\Delta t \nu_d}\left(\widehat{C}(t_n) + \Delta t \widehat{\sigma}_E^C(t_{n+1}) - \Delta t \widehat{\sigma}_C^I(t_{n+1}) - \Delta t \widehat{\sigma}_C^R(t_{n+1})\right) \\
&= \frac{1}{1+\Delta t \nu_d}\left(\check{C}(t_n) + \Delta t \check{\sigma}_E^C(t_{n+1}) - \Delta t \check{\sigma}_C^I(t_{n+1}) - \Delta t \check{\sigma}_C^R(t_{n+1})\right) \\
&= \check{C}(t_{n+1})
\end{aligned}
$$

For the discretizations of R we use that for all $x < 1$, there holds

$$
e^x \leq \frac{1}{1-x}.
$$

With this we can compute

$$
\begin{aligned}
\widehat{R}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \left(\widehat{\sigma}_C^R(t_{i+1}) + \widehat{\sigma}_I^R(t_{i+1}) + \widehat{\sigma}_H^R(t_{i+1}) + \widehat{\sigma}_U^R(t_{i+1})\right) e^{-\nu_d t_{n+1-i}} + e^{-\nu_d t_{n+1}} R_0 \\
&= \Delta t \sum_{i=0}^{n} \left(\widehat{\sigma}_C^R(t_{i+1}) + \widehat{\sigma}_I^R(t_{i+1}) + \widehat{\sigma}_H^R(t_{i+1}) + \widehat{\sigma}_U^R(t_{i+1})\right) e^{-\nu_d t_{n-i}} e^{-\nu_d \Delta t} + e^{-\nu_d t_n} e^{-\nu_d \Delta t} R_0 \\
&\leq \Delta t \sum_{i=0}^{n} \left(\widehat{\sigma}_C^R(t_{i+1}) + \widehat{\sigma}_I^R(t_{i+1}) + \widehat{\sigma}_H^R(t_{i+1}) + \widehat{\sigma}_U^R(t_{i+1})\right) e^{-\nu_d t_{n-i}} \frac{1}{1+\nu_d \Delta t} \\
&\quad + e^{-\nu_d t_n} \frac{1}{1+\nu_d \Delta t} R_0 \\
&= \frac{1}{1+\nu_d \Delta t}\left(\widehat{R}(t_n) + \Delta t \widehat{\sigma}_C^R(t_{n+1}) + \Delta t \widehat{\sigma}_I^R(t_{n+1}) + \Delta t \widehat{\sigma}_H^R(t_{n+1}) + \Delta t \widehat{\sigma}_U^R(t_{n+1})\right) \\
&= \frac{1}{1+\nu_d \Delta t}\left(\check{R}(t_n) + \Delta t \check{\sigma}_C^R(t_{n+1}) + \Delta t \check{\sigma}_I^R(t_{n+1}) + \Delta t \check{\sigma}_H^R(t_{n+1}) + \Delta t \check{\sigma}_U^R(t_{n+1})\right) \\
&= \check{R}(t_{n+1}).
\end{aligned}
$$

For D we simply compute

$$
\begin{aligned}
\widehat{D}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \widehat{\sigma}_U^D(t_{i+1}) + D_0 \\
&= \check{D}(t_n) + \widehat{\sigma}_U^D(t_{n+1})
\end{aligned}
$$

$$
\begin{aligned}
&= \check{D}(t_n) + \check{\sigma}_U^D(t_{n+1}) \\
&= \check{D}(t_{n+1}).
\end{aligned}
$$

□

Remark 4.2. *The result of Proposition 4.1 only holds for one time step, if we initialize both schemes with the same data. The issue in showing the relation for all time steps comes from the definitions of λ and S. With the previous proposition we get for N*

$$
\begin{aligned}
\widehat{N}(t_{n+1}) &= \widehat{S}(t_{n+1}) + \widehat{E}(t_{n+1}) + \widehat{C}(t_{n+1}) + \widehat{I}(t_{n+1}) + \widehat{H}(t_{n+1}) + \widehat{U}(t_{n+1}) + \widehat{R}(t_{n+1}) \\
&\leq \check{S}(t_{n+1}) + \check{E}(t_{n+1}) + \check{C}(t_{n+1}) + \check{I}(t_{n+1}) + \check{H}(t_{n+1}) + \check{U}(t_{n+1}) + \check{R}(t_{n+1}) \\
&= \check{N}(t_{n+1}).
\end{aligned}
$$

But for example, in the formula for S we divide by N which makes it impossible to show the inequality $\widehat{S} \leq \check{S}$.

From now on we will use the sum scheme given by (4.15) if not stated differently.

4.3 Discretization of the normalized SECIR-type birth-and-death model

One way to get normalized compartments is to compute $\widehat{z}(t) = \frac{\widehat{Z}(t)}{\widehat{N}(t)}$ for $\widehat{Z} \in \{\widehat{S}, \widehat{E}, \widehat{C}, \widehat{I}, \widehat{H}, \widehat{U}, \widehat{R}\}$ after computing the nonnormalized compartments $\widehat{Z}$. But, as we were not able to show that our normalized compartments (2.29) are actually $z(t) = \frac{Z(t)}{N(t)}$ we also want to derive a numerical scheme for the normalized model from Section 2.3. In Section 5.4.2 we will compare the two different approaches to compute the normalized compartments and observe that we get similar results. For the initial values of the normalized model we simply use $z_0 = \frac{Z_0}{N_0}$. With similar computations as in Section 4.2 for $\widehat{S}$ (4.9) we get the following discretization of $\widehat{s}$

$$
\widehat{s}(t_{n+1}) = \frac{\widehat{s}(t_n) + \Delta t \nu_b}{1 + \Delta t \left(\widehat{l}(t_n) + \nu_b - \widehat{\sigma}_i^d(t_n) \right)}. \tag{4.19}
$$

We continue with the numerical scheme for the force of infection term l (2.34). First, we describe the numerical scheme for g (2.35), that is similar to $\widehat{f}$ in (4.11)

$$
\widehat{g}(t_k) = e_0 \widehat{A}(t_k) - c_0 e^{-\nu_d t_k} \widehat{B}(t_k). \tag{4.20}
$$

The discretization of l_0 is given by

$$
\widehat{l_0}(t_k) = \phi\rho \left(c_0(t_k)\xi_C(t_k) + i_0(t_k)\xi_I(t_k) \right). \tag{4.21}
$$

The force of infection term given by (2.34) is, similar to (4.12), discretized by a non-standard approximation. We use a rectangular rule, with a right approximation in $\widehat{s}, \widehat{e}, \widehat{i}$ and $\widehat{\sigma}_u^d$ and a

left approximation in $\widehat{A}, \widehat{B}, B_C, B_I$ and $\widehat{l}$. Then for $n \geq 0$

$$\begin{aligned}\widehat{l}(t_{n+1}) &= \widehat{l}_0(t_{n+1})\phi\rho\widehat{g}(t_{n+1}) \\ &\quad + \phi\rho\Delta t \sum_{i=0}^{n} \widehat{A}(t_{n+1-i}) \left(\widehat{s}(t_{i+1})\widehat{l}(t_i) + \left(\nu_d + \widehat{\sigma}_u^d(t_{i+1}) - \nu_b\right)\widehat{e}(t_{i+1})\right) \\ &\quad + \phi\rho \sum_{i=0}^{n} \left(\nu_d + \widehat{\sigma}_u^d(t_{i+1}) - \nu_b\right) e^{-\nu_d t_{n+1-i}} \\ &\qquad\qquad \cdot \left(\widehat{c}(t_{i+1})B_C(t_{n+1-i}) + \widehat{i}(t_{i+1})B_I(t_{n+1-i}) - \widehat{c}(t_{i+1})\widehat{B}(t_{n+1-i})\right),\end{aligned} \tag{4.22}$$

with $\widehat{l}(0) = \widehat{l}_0(0)$.

The flows from s to e and e to c are given by

$$\begin{aligned}\widehat{\sigma}_s^e(t_{n+1}) &= \widehat{l}(t_n)\widehat{s}(t_{n+1}), \\ \widehat{\sigma}_e^c(t_{n+1}) &= -\Delta t \sum_{i=0}^{n} \widehat{\sigma}_s^e(t_{i+1})\widehat{\gamma}_E^{C\,\prime}(t_{n+1-i})e^{-\nu_d t_{n+1-i}} - e^{-\nu_d t_{n+1}} e_0 \widehat{\gamma}_E^{C\,\prime}(t_{n+1}) \\ &\quad - \Delta t \sum_{i=0}^{n} \left(\nu_d + \widehat{\sigma}_u^d(t_i) - \nu_b\right)\widehat{e}(t_i)\widehat{\gamma}_E^{C\,\prime}(t_{n+1-i})e^{-\nu_d t_{n+1-i}}.\end{aligned} \tag{4.23}$$

Now, we define the numerical scheme for the remaining flows. The first integral is approximated with a non-standard rectangular rule as in (4.13), the second integral is approximated with a standard rectangular rule using a left approximation. Given the flow from z_1 to z the flows z to z_2 and z to r are given by

$$\begin{aligned}\widehat{\sigma}_z^{z_2}(t_{n+1}) &= -\Delta t \sum_{i=0}^{n} \widehat{\sigma}_{z_1}^{z}(t_{i+1})\mu_z^{z_2}\widehat{\gamma}_z^{z_2\,\prime}(t_{n+1-i})e^{-\nu_d t_{n+1-i}} - e^{-\nu_d t_{n+1}} z_0 \mu_z^{z_2}\widehat{\gamma}_z^{z_2\,\prime}(t_{n+1}) \\ &\quad - \Delta t \sum_{i=0}^{n} \left(\nu_d + \widehat{\sigma}_u^d(t_i) - \nu_b\right)\widehat{z}(t_i)\mu_z^{z_2}\widehat{\gamma}_z^{z_2\,\prime}(t_{n+1-i})e^{-\nu_d t_{n+1-i}}, \\ \widehat{\sigma}_z^{r}(t_{n+1}) &= -\Delta t \sum_{i=0}^{n} \widehat{\sigma}_{z_1}^{z}(t_{i+1})(1-\mu_z^{z_2})\widehat{\gamma}_z^{z_2\,\prime}(t_{n+1-i})e^{-\nu_d t_{n+1-i}} - e^{-\nu_d t_{n+1}} z_0 (1-\mu_z^{z_2})\widehat{\gamma}_z^{z_2\,\prime}(t_{n+1}) \\ &\quad - \Delta t \sum_{i=0}^{n} \left(\nu_d + \widehat{\sigma}_u^d(t_i) - \nu_b\right)\widehat{c}(t_i)(1-\mu_z^{z_2})\widehat{\gamma}_z^{r\,\prime}(t_{n+1-i})e^{-\nu_d t_{n+1-i}}.\end{aligned} \tag{4.24}$$

As above we have $\widehat{\sigma}_{z_1}^{z_2}(t_0) = 0$, for all suitable combinations z_1, z_2.

Lastly, we define the numerical scheme for the remaining compartments by

$$
\begin{aligned}
\widehat{e}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \gamma_E^C(t_{n+1-i}) e^{-\nu_d t_{n+1-i}} \left(\widehat{\sigma}_s^e(t_{i+1}) + \left(\nu_d + \widehat{\sigma}_u^d(t_i) - \nu_b \right) \widehat{e}(t_i) \right) + e_0(t_{n+1}), \\
\widehat{c}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \gamma_C(t_{n+1-i}) e^{-\nu_d t_{n+1-i}} \left(\widehat{\sigma}_e^c(t_{i+1}) + \left(\nu_d + \widehat{\sigma}_u^d(t_i) - \nu_b \right) \widehat{c}(t_i) \right) + c_0(t_{n+1}), \\
\widehat{i}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \gamma_I(t_{n+1-i}) e^{-\nu_d t_{n+1-i}} \left(\widehat{\sigma}_c^i(t_{i+1}) + \left(\nu_d + \widehat{\sigma}_u^d(t_i) - \nu_b \right) \widehat{i}(t_i) \right) + i_0(t_{n+1}), \\
\widehat{h}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \gamma_H(t_{n+1-i}) e^{-\nu_d t_{n+1-i}} \left(\widehat{\sigma}_i^h(t_{i+1}) + \left(\nu_d + \widehat{\sigma}_u^d(t_i) - \nu_b \right) \widehat{h}(t_i) \right) + h_0(t_{n+1}), \\
\widehat{u}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} \gamma_U(t_{n+1-i}) e^{-\nu_d t_{n+1-i}} \left(\widehat{\sigma}_h^u(t_{i+1}) + \left(\nu_d + \widehat{\sigma}_u^d(t_i) - \nu_b \right) \widehat{u}(t_i) \right) + u_0(t_{n+1}), \\
\widehat{r}(t_{n+1}) &= \Delta t \sum_{i=0}^{n} e^{-\nu_d t_{n+1-i}} \left(\widehat{\sigma}^r(t_{i+1}) + \left(\nu_d + \widehat{\sigma}_u^d(t_i) - \nu_b \right) \widehat{r}(t_i) \right) + r_0(t_{n+1}),
\end{aligned}
\tag{4.25}
$$

with $\widehat{\sigma}^r = \widehat{\sigma}_c^r + \widehat{\sigma}_o^r + \widehat{\sigma}_h^r + \widehat{\sigma}_u^r$.

4.4 Properties of the numerical schemes

In this section we want to show that our numerical scheme preserves all the important properties, such as non-negativity, of model 2.15.We start with the discrete version of Lemma 2.12.

Lemma 4.3. *For $\widehat{A}$ given by* (4.3) *it holds that*

$$
\sum_{k=0}^{\infty} \widehat{A}(t_k) < \infty. \tag{4.26}
$$

As for Lemma 2.12 we are going to need some properties of convolutions. In the discrete case for $p, q : \mathbb{Z} \to \mathbb{R}$, convolutions are defined as follows

$$
(p * q)[n] = \sum_{k=-\infty}^{\infty} p[k] q[n-k]. \tag{4.27}
$$

Lemma 4.4. *For all $p, q : \mathbb{Z} \to \mathbb{R}$ the following inequality holds true*

$$
||p * q||_1 \leq ||p||_1 ||q||_1. \tag{4.28}
$$

Where

$$
||q||_1 \coloneqq \sum_{n=0}^{\infty} |f[n]|.
$$

Proof. We apply Young's convolution inequality to the following $L^1(\mathbb{R},\mathbb{R})$ functions given by the sequences p and q

$$P(t) = \sum_{i\in\mathbb{Z}} p[i]\,\chi_{(i,i+1]}(t),$$
$$Q(t) = \sum_{i\in\mathbb{Z}} q[i]\,\chi_{(i,i+1]}(t).$$

The claim follows because $(P * Q)(k) = (p * q)(k)$ and the L^1 norms agree. □

Now we are able to prove Lemma 4.3.

proof of Lemma 4.3. At first we see

$$\sum_{i=0}^{\infty} \xi_C(t_i)\left(\mu_C^I \gamma_C^I(t_i) + (1-\mu_C^I)\gamma_C^R(t_i)\right) \le \sum_{i=0}^{\infty}\left(\gamma_C^I(t_i) + \gamma_C^R(t_i)\right).$$

Moreover, we know by Assumption 2.1 that $\gamma_C^I, \gamma_C^R \in L^1((0,\infty))$. Then, since γ_C^I and γ_C^R are monotonically decreasing, by the integral criterion for the convergence of sums, we can conclude that

$$\sum_{i=0}^{\infty} \xi_C(t_i)\left(\mu_C^I \gamma_C^I(t_i) + (1-\mu_C^I)\gamma_C^R(t_i)\right) < \infty.$$

With the same argumentation, we also have that

$$\sum_{j=0}^{\infty} \xi_I(t_j)\left(\mu_I^H \gamma_I^H(t_j) + (1-\mu_I^H)\gamma_I^R(t_j)\right) < \infty.$$

Now, we consider $\widehat{\gamma}_E^{C\prime}$ and $\widehat{\gamma}_C^{I\prime}$. As both computations are the same, we only do them for $\widehat{\gamma}_E^{C\prime}$.

$$\begin{aligned}
\sum_{i=0}^{\infty} \widehat{\gamma}_E^{C\prime}(t_{i+1}) &= \sum_{i=0}^{\infty} \frac{\gamma_E^C(t_{i+1}) - \gamma_E^C(t_i)}{\Delta t} \\
&= \lim_{N\to\infty} \sum_{i=0}^{N} \frac{\gamma_E^C(t_{i+1}) - \gamma_E^C(t_i)}{\Delta t} \\
&= \frac{1}{\Delta t}\left(\lim_{N\to\infty} \gamma_E^C(t_{N+1}) - \gamma_E^C(t_0)\right) \\
&= \frac{1}{\Delta t}.
\end{aligned}$$

Now we can show the claim with the same argumentation as in the proof of Lemma 2.12 using Lemma 4.4. □

Remark 4.5. *Lemma 4.3 directly implies that* $\lim_{k\to\infty} \widehat{A}(t_k) = 0$.

As we only consider with non-negative solutions, we now want to make sure that the numerical scheme preserves the non-negativity.

Theorem 4.6. *For non-negative initial data, i.e.* $S_0, E_0, C_0, I_0, H_0, U_0, R_0, D_0 \geq 0$ *we have*

1. $\widehat{S}(t_n) \geq 0$ *for all* $n \in \mathbb{N}$,
2. *for all suitable combinations* $z_1, z_2 \in \{S, E, C, I, H, U, R, D\}$ *we have that* $\widehat{\sigma}_{z_1}^{z_2}(t_n) \geq 0$ *for all* $n \in \mathbb{N}$,
3. *for all* $Z \in \{E, C, I, H, U, R, D\}$ *we have* $\widehat{Z}(t_n) \geq 0$ *for all* $n \in \mathbb{N}$,
4. $\widehat{\lambda}(t_n) \geq 0$ *for all* $n \in \mathbb{N}$.

Proof. We are going to prove this theorem by induction. For $n = 0$, all statements are true by assumption on the initial values. We assume that the statements hold for n and we show them for $n + 1$.

1. By using the induction hypothesis we directly see that, for $\widehat{S}$ given in (4.9), we have
$$\widehat{S}(t_{n+1}) = \frac{\widehat{S}(t_n) + \Delta t \nu_b \widehat{N}(t_n)}{1 + \Delta t(\widehat{\lambda}(t_n) + \nu_d)} \geq 0.$$
2. First of all, by using the induction hypothesis an the estimate above we directly get $\widehat{\sigma}_S^E(t_{n+1}) = \widehat{S}(t_{n+1})\widehat{\lambda}(t_n) \geq 0$. From this we immediately see that all the other transitions are non-negative.
3. As we have just seen, all transitions are non-negative therefore the compartments are also non-negative at time t_{n+1} as we only sum over non-negative parameters and $\widehat{Z}_0 \geq 0$.
4. Moreover we have
$$\widehat{\lambda}(t_{n+1}) = \underbrace{\widehat{\lambda}_0(t_{n+1})}_{\geq 0} + \underbrace{\frac{\phi\rho}{\widehat{N}(t_{n+1})} \Delta t \sum_{i=0}^{n} \widehat{A}(t_{n+1-j})\widehat{S}(t_{j+1})\widehat{\lambda}(t_j)}_{\geq 0} + \underbrace{\frac{\phi\rho}{\widehat{N}(t_{n+1})} \widehat{f}(t_{n+1})}_{\geq 0}$$
$$\geq 0.$$

This concludes the proof. □

Remark 4.7. *By Proposition 4.1 we also get the statements from the previous Theorem 4.6 for the update discretization scheme given by* (4.18)*, but only for one time step. Therefore, we will mainly use the sum-scheme given by* (4.15) *in the implementation.*

Since the normalized compartments are expected to behave like the non-normalized compartments divided by the population size, we expect the discretized normalized compartments to be non-negative as well. However, the proof of Theorem 4.6 does not carry over so easily. The reason for this is that the normalized compartments have the factor
$$\widehat{\sigma}_{z_1}^{z_2}(t_{i+1}) + \left(\nu_d + \widehat{\sigma}_u^d(t_i) - \nu_b\right) \widehat{z}_2(t_i),$$

for which it is not clear why it is non-negative. Nevertheless, the numerical results suggest that the following conjecture holds.

Conjecture 4.8. *For non-negative initial data, i.e.* $s_0, e_0, c_0, i_0, h_0, u_0, r_0, d_0 \geq 0$ *we have*

1. $\widehat{s}(t_n) \geq 0$ *for all* $n \in \mathbb{N}$,
2. *for all suitable combinations* $z_1, z_2 \in \{s, e, c, i, h, u, r, d\}$ *we have that* $\widehat{\sigma}_{z_1}^{z_2}(t_n) \geq 0$ *for all* $n \in \mathbb{N}$,
3. *for all* $z \in \{e, c, i, h, u, r\}$ *we have* $\widehat{z}(t_n) \geq 0$ *for all* $n \in \mathbb{N}$,
4. $\widehat{l}(t_n) \geq 0$ *for all* $n \in \mathbb{N}$.

5 Implementation

Now, we use the numerical scheme described in Section 4 for the implementation of our model. We will shortly describe the implementation structure and then use the implementation for some numerical experiments. We implemented the models in C++ as a part of the high performance modular epidemics simulation software MEmilio [22]. The relevant issue can be found here[1].

5.1 Description of the implementation structure

In this section, we briefly describe the implementation structure for the SECIR-type model. The implementation of the SIRD-type model has the same structure. The class structure can be seen in Figure 7. All in all the idea of the implementation is to iterate over all time steps and compute the compartments, flows and force of infection term in every time step. In the

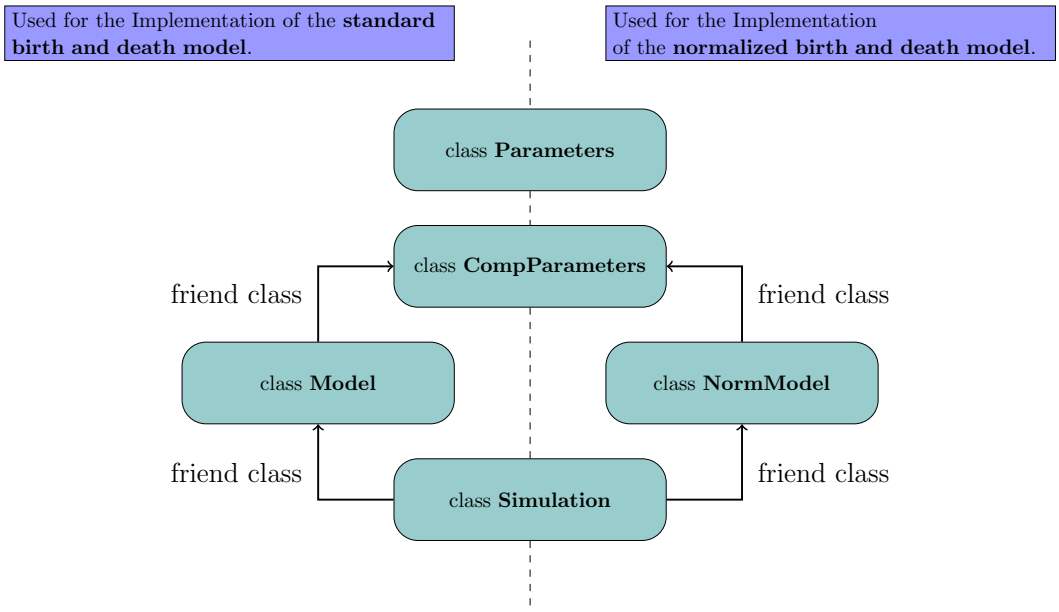

Figure 7: **Class Structure of the Implementation**

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class *Parameters*, all given model parameters, are implemented meaning we set all parameters from Table 1. Then, in the class *CompParameters* we compute all values that can be computed before starting the iteration of the simulation.

1. We start by computing the maximum support of the transition distributions $\gamma_{z_1}^{z_2}$. Either they actually have a maximum support, or we define some tolerance ϵ and the maximum support is the smallest t such that $\gamma_{z_1}^{z_2}(t) < \epsilon$. We know that such a point exist for all possible transition distributions, as Assumption 2.1 gives us that they all converge to zero. We will use this fact in the computation of all functions and parameters calculated in

[1] https://github.com/SciCompMod/memilio/pull/1358

this class, meaning we only evaluate the functions for all time points smaller than the maximum support of the transition distributions.

2. Then, we compute the weighted distributions γ_Z given by (2.12) and the derivatives of the transition distributions using a backwards difference scheme, as given in (4.1).
3. After this, we are able to compute $\widehat{B}$ given by (4.2) and $\widehat{A}$ given by (4.3).
4. Then, we compute the initial value functions used for the force of infection term, meaning the functions $\widehat{\varphi}$ (4.10) and $\widehat{f}$ (4.11) for the standard and the functions $\widehat{l}_0$ (4.21) and $\widehat{g}$ (4.20) for the normalized model.
5. Finally, we can compute the constants $\widehat{\mathcal{R}}_c$ (4.4), $\widehat{\mathcal{T}}_{z_1}^{z_2}$ (4.5), $\widehat{\mathcal{V}}^z$ (4.6) and $\widehat{\mathcal{W}}_z$ (4.7), that are used for the model analysis. These constants are infinite sums, but we make a cut-off and neglect all the terms after the maximum support.

In the classes *Model* and *NormModel* we define all functions needed in the iteration.

1. We start by computing the susceptibles, given by (4.9) and (4.19).
2. After this we compute the transitions given by (4.13) and (4.24).
3. Then, we compute the other compartments. In the class *Model*, we compute the compartments twice, both with the schemes given by (4.15) and (4.18), the scheme for the normalized compartments is given in (4.25).
4. In the class *Model* we then also compute the current population size.
5. At last, we compute the force of infection term given by (4.12) and (4.22).

The class *Simulation* is used to run the actual simulation, by calling the functions defined in the model classes.

Now that we have described the structure of the implementation we want to comment on the computational cost. In general, solvers for models based on integro-differential equations are much less efficient than models based on ordinary differential equations. Also, the Volterra structure of our equations does not allow for an update scheme when evaluating the integrals, as we need to compute the whole sum in every time step. One way to make the implementation more efficient would be to use the update scheme using the equations of the derivatives given in (4.18). We haven given such a scheme in Section 4.2.1. However, we have seen that this scheme is not equivalent to the scheme using sums given in (4.15). Besides, we still need to evaluate the transitions by a sum.

Nevertheless there are some ways to make the implementation more efficient. First off all, the class *CompParameters* computes the parameters in advance that are needed several times in the iterations for both models. Moreover, the use of the maximum support, as described above is an important way to increase the efficiency. First, this means we need to store less values for the parameters computed in the class *CompParameters*. Furthermore, the sums we need to compute in the iterations become shorter. We see this for example in the computation of the

transitions. The transition from E to C is given by

$$\widehat{\sigma}_E^C(t_{n+1}) = -\Delta t \sum_{i=0}^{n} \widehat{\sigma}_S^E(t_{i+1}) e^{-\nu_d t_{n+1-i}} \widehat{\gamma}_E^{C\prime}(t_{n+1-i}) - e^{-\nu_d t_{n+1}} E_0 \widehat{\gamma}_E^{C\prime}(t_{n+1}).$$

Here we can make use of the maximum support $\widehat{\gamma}_E^C$. We evaluate γ_E^C at time point t_{n+1-i}. If the maximum support of $\widehat{\gamma}_E^C$ is t_m this means that the sum starts at $\max(0, n+1-m)$. One other possibility to make the implementation more efficient in terms of storage is not to store the total population for every time step. In the computations we only need the number of the total population of the last time step therefore one could overwrite this number in every time step. In our case, we want to analyse the total population, therefore, it is interesting for us to store it for every time step.

5.2 Choice for transition distributions

Here we introduce some possible choices for the transition distributions $\gamma_{z_1}^{z_2}$. As mentioned in Remark 2.3 the transitions distributions are survival functions of probability distributions. One possibility is to use the survival function of exponential distribution, that depend on some distribution parameter a, and is defined by

$$exp_a(x) = e^{-ax}. \tag{5.1}$$

However, as already mentioned, the exponential distribution is rather unrealistic for the stay-time distributions $\gamma_{z_1}^{z_2}$. But we are going to use it for demonstration purposes and other parameters, such as ξ_I. Another possibility is to use a "smoother" cosine function. It is constructed as a C^1 transition from zero to one, and was introduced in [23] for similar purposes. The "smoother" cosine depends on some distribution parameter a and is defined by

$$smoothcos_a(x) = \begin{cases} 1 & \text{if } x \leq 0 \\ \frac{1}{2}\cos\left(\frac{\pi}{ax} + \frac{1}{2}\right) & \text{if } 0 < x < a \\ 0 & \text{if } x \geq a \end{cases}. \tag{5.2}$$

In [24], the authors use the lognormal distribution as a stay-time distribution to model COVID-19. Therefore, we will also use the survival function of a lognormal distribution, as a possible transition distribution. The probability density function of the lognormal distribution looks as follows

$$f_{a;b}(x) = \frac{b}{ax\sqrt{2\pi}} \exp\left(-\frac{\log^2(\frac{x}{b})}{2a^2}\right),$$

with a some shape parameter and b some scale parameter. For the survival function of the lognormal distribution we write $lognorm_{a;b}(x)$.

5.3 Results for the normalized SIRD-model

First we set all the given parameters we use in the implementation of the normalized SIRD-model. As initial values for the compartments, we set $S_0 = 100000$, $I_0 = 30$, $R_0 = 0$, and $D_0 = 0$. We recall that $z_0 = \frac{Z_0}{N(0)}$. Moreover, we use $\mu_I^D = 0.1$, $\phi = 10$, $\rho = 0,1$ and $\xi_I(t) = exp_{0.5}(t)$. If not stated otherwise, we will use $\nu_b = 4 \cdot 10^{-3}$ and $\nu_d = 3 \cdot 10^{-3}$. In order to derive different values for the parameters $\widehat{\mathcal{R}}_c$, $\widehat{\mathcal{T}}_i^d$ and $\widehat{\mathcal{W}}_i$ we will use different functions for the transition distributions $\gamma_{z_1}^{z_2}$. In Section 3 we have seen that the existence and stability of equilibria strongly depends on these parameters. We start with $\gamma_I^D(\tau) = \gamma_I^R(\tau) = smoothcos_5(\tau)$. This yields $\widehat{\mathcal{R}}_c = 0.875477$, $\widehat{\mathcal{T}}_i^d = 0.0991046$ and $\widehat{\mathcal{W}}_i = 2.98914$. For this case we have seen that the disease-free equilibrium is stable, as $\widehat{\mathcal{R}}_c < 1$. The results for this case can be found in Figure 8 and as expected one directly sees that the model converges to the disease-free equilibrium.

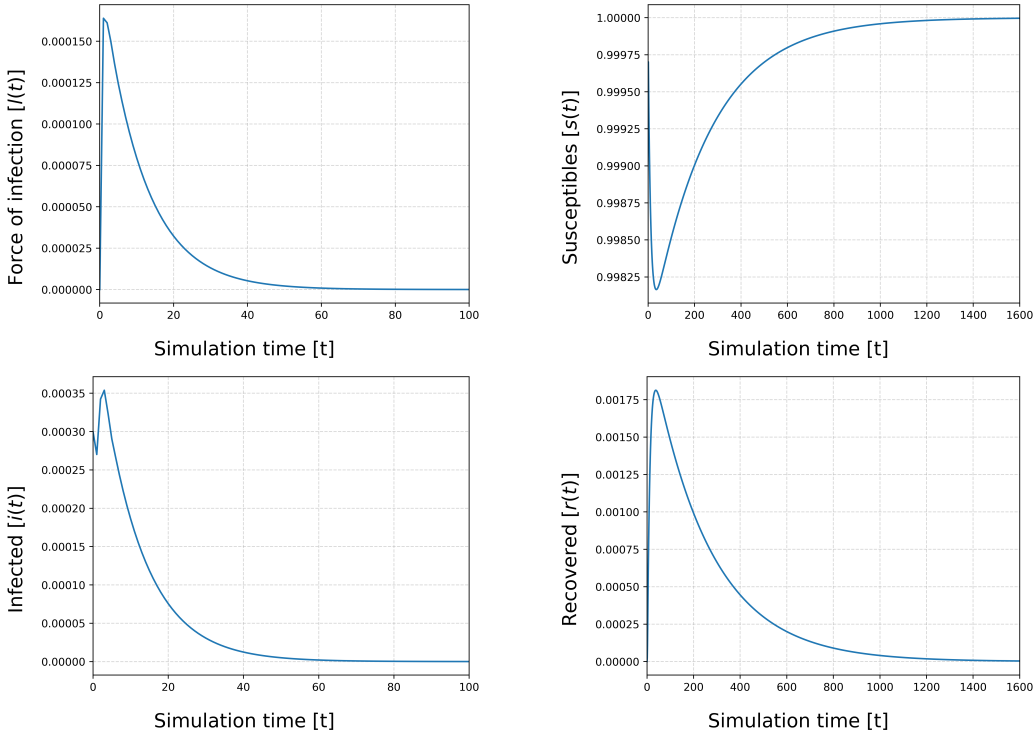


Figure 8: **Evaluation of the normalized SIRD-model:** force of infection term and compartments of the normalized SIRD-model, using $\nu_b = 4 \cdot 10^{-3}$, $\nu_d = 3 \cdot 10^{-3}$ and $\gamma_I^D(\tau) = \gamma_I^R(\tau) = smoothcos_5(\tau)$. In this scenario the reproduction number is smaller than one.

Now we want to use $\gamma_I^D(\tau) = \gamma_I^R(\tau) = smoothcos_8(\tau)$. Then we have $\widehat{\mathcal{R}}_c = 1,14681$, $\widehat{\mathcal{T}}_i^d = 0.0986605$ and $\widehat{\mathcal{W}}_i = 4.47186$. In this case we expect the disease-free equilibrium to be unstable as $1 - \widehat{\mathcal{R}}_c = -0.14681 < -0.00447186 = (\nu_d - \nu_b)\widehat{\mathcal{W}}_i$ and $\widehat{\mathcal{R}}_c > 1$. If we compute the equilibrium for these parameters, we get $i_1^* = 10.2006$ and $i_2^* = -0.0156379$, which are not feasible equilibria for a normalized model. Nevertheless, surprisingly, in Figure 9 one can see that the model is

converging to some endemic state. A possible explanation for this might be that the model is converging to a state that is not an equilibrium of the model.

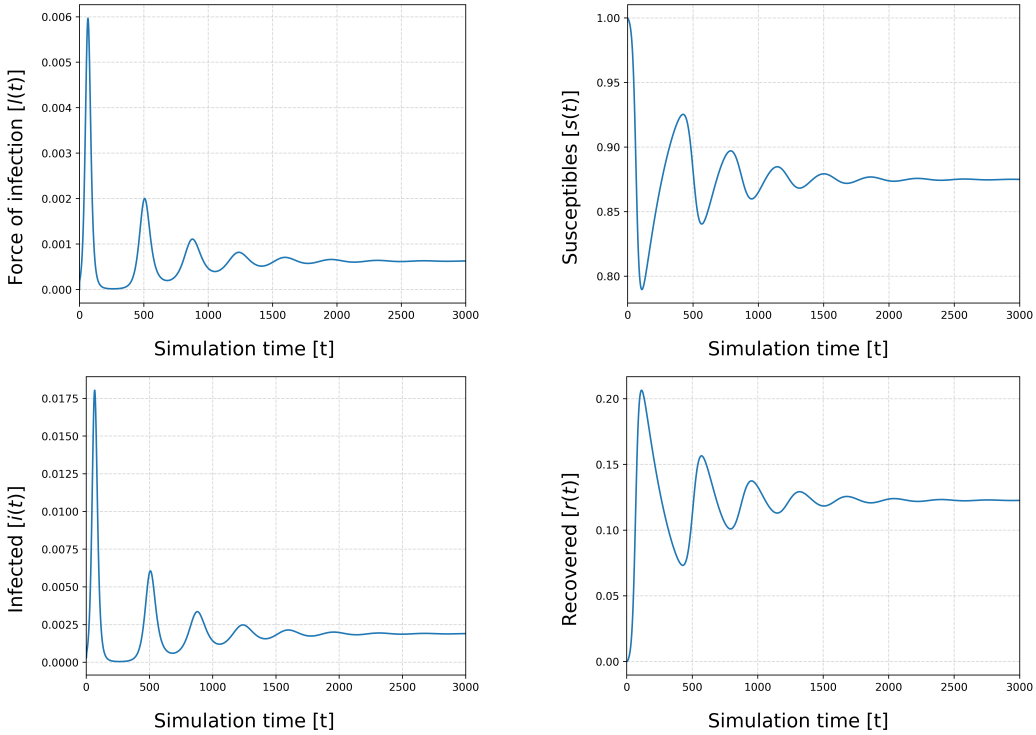


Figure 9: **Evaluation of the normalized SIRD-model:** force of infection and compartments of the normalized SIRD-model, using $\nu_b = 4 \cdot 10^{-3}$, $\nu_d = 3 \cdot 10^{-3}$ and $\gamma_I^D(\tau) = \gamma_I^R(\tau) = smoothcos_8(\tau)$. In this scenario we have a reproduction number larger than one and $\mathcal{R}_c > (\nu_d - \nu_b)\mathcal{W}_i$.

Now we set $\nu_b = 0,1$ and $\nu_d = 0,02$ and choose $\gamma_I^D(\tau) = \gamma_I^R(\tau) = smoothcos_{12}(\tau)$. Here we get $\mathcal{R}_c = 1,27147$, $\mathcal{T}_i^d = 0,0879308$ and $\mathcal{W}_i = 6,09514$, then $1 - \mathcal{R}_c = -0,127147 > -0,4876112 = (\nu_d - \nu_b)\mathcal{W}_i$. For this case, we were not able to show that the disease-free equilibrium is unstable, but we also did not show that it is stable. In Figure 10 one can observe that the model converges to the disease-free state.

5.4 Results for the SECIR-type birth-and-death model

In this section, we want to use our implemented numerical scheme to analyse the SECIR-type model numerically. The theoretical results were only formulated and proven for the SIRD-model, in the section above we already investigated at the SIRD-model numerically. For the SECIR-type model, we expect to get similar results. We introduced the SIRD-model as the theoretical analysis of it is less complex. However, the disease dynamics of the SECIR-type models are more interesting than the dynamics for the SIRD-model, as it is way more detailed. Therefore, the

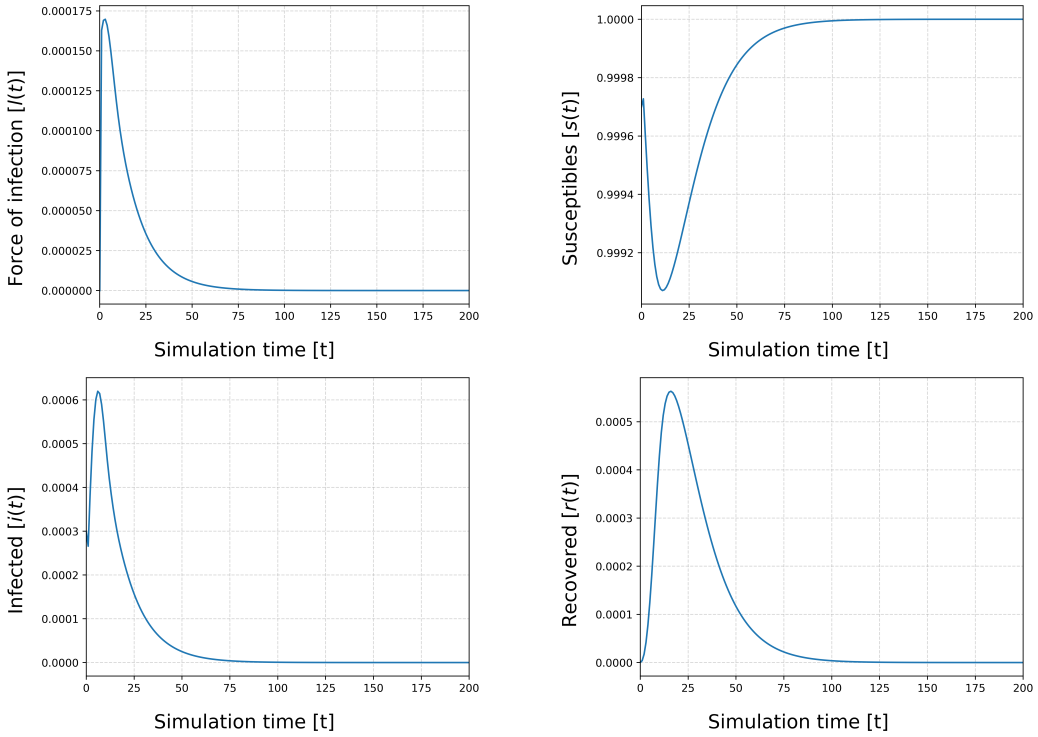


Figure 10: **Evaluation of the normalized SIRD-model:** force of infection and compartments of the normalized SIRD-model, using $\nu_b = 0.1$, $\nu_d = 0.02$ and $\gamma_I^D(\tau) = \gamma_I^R(\tau) = smoothcos_{12}(\tau)$. In this scenario we have a reproduction number larger than one, but $\mathcal{R}_c > (\nu_d - \nu_b)\mathcal{W}_i$.

main goal of this section is to see the long-term behaviour of the SECIR-type model. However, in a first step, we compare the two numerical schemes, the sum scheme (4.15) and the update scheme (4.18) for the compartments, and want to show numerically that the normalized model from Section 2.3 is a suitable normalization of our model from Section 2.2. Then we start by analysing the results for the normalized model, and then we consider the non-normalized birth-and-death model. In the theoretical part, we shortly discussed the influence of different choices for the birth-and-death rates on the model. Therefore, we then study this question numerically. At last, we will make some comments about the convergence of the numerical scheme.

5.4.1 Choice of parameters

In this section we provide initial values and parameters used in the SECIR-type model. In all examples, we will use $S_0 = 100000$, $E_0 = 0$, $C_0 = 10$, $I_0 = 20$, $H_0 = 0$, $U_0 = 0$, $R_0 = 0$ and $D_0 = 0$ as initial values for the compartments. Moreover, we will use the parameters given in Table 2. The birth rate given in Table 2 is larger than the death rate, in Section 5.4.6 we will discuss different choices for the birth and death rate with varying difference, to see the influence of them on the model behaviour. As we will model many time steps, we chose $\Delta t = 1$. In Section 5.4.7, we will briefly discuss the behaviour of the numerical scheme when Δt becomes

Parameter	Choice for Parameter	Parameter	Choice for Parameter
μ_C^I	0.8	ϕ	10
μ_I^H	0.1	ρ	0.1
μ_H^U	0.2	$\xi_C(t)$	$exp_{0.5}(t)$
μ_U^D	0.4	$\xi_I(t)$	$exp_{0.5}(t)$
ν_b	$4 \cdot 10^{-3}$	ν_d	$3 \cdot 10^{-3}$

Table 2: Choice of the parameters used in the examples.

smaller. If not stated differently, we will use the parameters in this section in the following. Moreover, in Table 3 we give three different choices of the transition distributions, that we will use several times in the following. We will refer to them as three different scenarios. Then

Survival function	Distribution		
	Scenario 1	Scenario 2	Scenario 3
$\gamma_E^C(t)$	$smoothcos_2(t)$	$smoothcos_6(t)$	$lognorm_{0.3;4.2}(t)$
$\gamma_C^I(t)$	$smoothcos_2(t)$	$smoothcos_6(t)$	$lognorm_{0.7;0.8}(t)$
$\gamma_C^R(t)$	$smoothcos_2(t)$	$smoothcos_6(t)$	$lognorm_{0.2;7.7}(t)$
$\gamma_I^H(t)$	$smoothcos_2(t)$	$smoothcos_6(t)$	$lognorm_{0.7;5.3}(t)$
$\gamma_I^R(t)$	$smoothcos_2(t)$	$smoothcos_6(t)$	$lognorm_{0.2;7.8}(t)$
$\gamma_H^U(t)$	$smoothcos_2(t)$	$smoothcos_6(t)$	$lognorm_{1;0.9}(t)$
$\gamma_H^R(t)$	$smoothcos_2(t)$	$smoothcos_6(t)$	$lognorm_{0.3;17.1}(t)$
$\gamma_U^D(t)$	$smoothcos_2(t)$	$smoothcos_6(t)$	$lognorm_{0.4;9.8}(t)$
$\gamma_U^R(t)$	$smoothcos_2(t)$	$smoothcos_6(t)$	$lognorm_{0.3;17.1}(t)$

Table 3: Different choices for the survival functions.

Scenario 1 yields $\widehat{\mathcal{R}}_c = 0.498502$, Scenario 2 $\widehat{\mathcal{R}}_c = 1.73317$ and Scenario 3 $\widehat{\mathcal{R}}_c = 3.42176$.

5.4.2 Comparison of the two different discretization schemes

In Section 4 we introduced two different discretization schemes for the compartments. The purpose of this section is to see the results of Proposition 4.1. We will use the parameters given in Table 2. In Table 4 we can see that as expected by Proposition 4.1 we find that after one time step $\widehat{S} = \check{S}$ and $\widehat{D} = \check{D}$ and for the other compartments we have $\widehat{Z} \leq \check{Z}$. We also see that after ten time steps we still have $\widehat{Z} \leq \check{Z}$ for all $Z \in \{S, E, C, I, H, U, R\}$. But for D we see that in this case $\widehat{Z} \geq \check{Z}$ after ten time steps.

5.4.3 Comparison of the normalized compartments

We were unable to rigorously prove that the normalized compartments defined in (2.29) actually match the compartments defined in (2.15), meaning that $z = \frac{Z}{N}$. In particular, we did not use the same force of infection term, therefore it is unclear how closely both models match. Moreover, we were not able to use the exact same numerical scheme due to the second integral

$\gamma = smoothcos(4.0)$

	$n = 1$		$n = 10$	
Compartment	$\widehat{Z}(t_1)$	$\check{Z}(t_1)$	$\widehat{Z}(t_{10})$	$\check{Z}(t_{10})$
S	100069.89833907	100069.89833907	100653.95494754	100653.98511122
E	25.54007998	25.55332099	72.46965325	73.29714526
C	12.23901983	12.24536504	62.85941093	63.52566862
I	18.44952649	18.45909148	43.82889354	44.28739667
H	0.26937771	0.26951737	3.80991366	3.84421183
U	0.00786626	0.00787033	0.64438970	0.64929654
R	3.29675025	3.29676505	191.54494683	191.54775729
D	0.00053985	0.00053985	0.65830792	0.65830723

Table 4: Comparison of the two discretization schemes for the compartments, with $smoothcos(4.0)$ as Transition Distribution.

in the definition of the compartments of the normalized model. Due to this and approximation errors, we do not expect to obtain the exact same results numerically, for both approaches. We define the normalization error for the compartments as $z_{\text{error}} = \left|\frac{Z(t)}{N(t)} - z(t)\right|$. The errors and the compartments S, I, U and R, in Scenario 2, can be seen in Figure 11. The structure of the compartments E, C, I, H and U is the same and we expect to the get errors of the same magnitude. In the plots on the right of Figure 11 where both versions for the normalized compartments are plotted one can see directly that the behaviour of both is very similar. In the errors on the left one can see that the error is always one or two magnitudes smaller than the size of the compartment. In the plots of both normalizations for the compartments one can moreover see that the long-term behaviour of the normalization versions for compartments is the same.

Moreover we want to take a look at the force of infection, as this was the challenging part in the normalization. Since we have used two different definitions, we now want to see if they are similar. We define the error for the force of infection as $\text{FoI}_{\text{error}} = |\lambda(t) - l(t)|$. Again we plot the error for Scenario 2, that can be seen in Figure 12. Here we can see again that the behaviour of both force of infection terms is very similar and also the error is at least two orders of magnitude smaller than the actual force of infection terms. Moreover, we take into account that we used step size $\Delta t = 1$ and expect a rather large approximation error. All in all we conclude that the normalized model from Section 2.3 with the force of infection term l (2.30) is a good choice to model the endemic dynamic of the birth-and-death model introduced in Section 2.2.

5.4.4 Analysis of the normalized model

In this section we want to analyse the normalized SECIR-type model from Section 2.2 numerically. We are interested to see if similar results as from Section 3, where we mainly focused on the normalized SIRD, also hold for the SECIR-type model.

First, we want to look at the force of infection term, as it is a good way to see the disease

dynamics in one term. The plots for the force of infection terms, in the three different scenarios from Table 3, are given in Figure 13. In the plot for Scenario 1, one can see that the disease dies already out after about 10 time steps. This is also what one would expect as in for scenario 1 the reproduction number is smaller than one and we observed this behaviour also for the SIRD-model. Then for both Scenarios 2 and 3 the force of infection term is converging to some fixed value. For the SIRD-model we observed convergence to a positive value if the reproduction number is smaller than one and the difference of ν_b and ν_d is not too large. Both is the case for Scenario 2 and 3, therefore the convergence to some fixed positive values is what we would have expected. Moreover, one can see that the force of infection term is oscillating with waves getting smaller until it gets constant. We are going to analyse why this happens after we take a closer look at the behaviour of the compartments.

We start with the compartments for Scenario 1 that are given in 14. As expected, the compartments e, c, i, h and u tend to zero quickly, as it is the case for the force of infection term. Also, one can see that the proportion of individuals that get infected is very small. As the behaviour of the force of infection term for Scenario 2 and 3 was similar we now only have a look at the compartments in Scenario 3; see Figure 15. All compartments converge to some constant value. Where the largest proportion of individuals are in the compartments s and r and a quite small proportion of individuals is in an infected compartment. As already for the force of infection term we can obverse waves in the behaviour of the compartments. The reason for this might be that the proportion of susceptibles becomes very small at the beginning, therefore only few individuals can become infected and the force of infection term gets smaller. Then after new susceptibles are born more individuals can become infected again, this effects repeats itself until the disease becomes stable.

5.4.5 Analysis of the non-normalized model

In the previous section we have seen the behaviour of the normalized model. In this section we look at the non-normalized SECIR-type model introduced in Section 2.2 numerically. We have already seen in Figure 12 that both force of infection terms, λ and l show very similar dynamics. Therefore, we assume that the results for the force of infection term λ are very similar to those of l seen in 13. Thus, we will directly focus on the non-normalized compartments. First of all we have a look at the compartments in Scenario 1. The plots can be found in Figure 16. Before, we have seen that the disease dies out very fast Scenario 1, here we observe the same. The amount of individuals in the compartments E, C, I, H and U goes to zero very fast. The amount of recovered individuals is also decreasing as now new individuals will enter this compartments. The number of susceptibles is decreasing, as more new individuals are born than die and no new infections take place. Now we take a look at a case where we have seen endemic behaviour of the disease. Therefore, we look at the compartments in Scenario 3. The plots can be found in Figure 17. It can be seen that all compartment sizes are increasing after a certain point. This happens around the same time when the compartments of the normalized model become stable. The increase of the compartment sizes comes from the increasing total population size. Before this, one sees again the wave dynamic of the disease as we already observed before.

5.4.6 Effect of different birth and death rates

Before we analysed the model always for the same birth-and-death rate, where we had a larger birth than death rate. In this section we want to see what effect different choices of birth and death rates might have on the simulation results. We will set the birth and death rate differently from 2, but the other parameters remain the same. Here we use the non-normalized model given in Section 4.3.

We start by discussing the effect of varying birth and death rates on the population size. First of all, we want to make sure that our model behaves as expected in the absence of an infectious disease. Therefore, we set all parameters and initial values to zero except S, which we initialize with 10000. The results of this simulation can be seen in Figure 18. As expected, for $\nu_b > \nu_d$ the population grows, for $\nu_b = \nu_d$ we have a constant population, and for $\nu_b < \nu_d$ the population size decreases. Now, we go to the case where we actually have an infectious disease. Here we use again the parameters and initial values given in Section 3.1. In Figure 19 we modelled the population size and its derivative for Transition Distributions as in Scenario 2. We remember that the derivative of the total population is given by $\widehat{N}'(t) = \nu_b \widehat{N}(t) - \nu_d \widehat{N}(t) - \widehat{\sigma}_U^D(t)$. As seen before in Figure 13 in this Scenario the force of infection term converges to some constant larger than zero. Then also the compartments and transitions converge to some constant larger than zero, explicitly saying $\lim_{n\to\infty} \widehat{\sigma}_u^d(t_n) = \sigma_u^{d*} > 0$. Then as we assume that $\widehat{\sigma}_u^d(t) \approx \widehat{N}(t)\widehat{\sigma}_U^D(t)$, we expect that $\lim_{t\to\infty} \widehat{\sigma}_U^D(t) > 0$. We see that for $\nu_b > \nu_d$ the population size explodes. This means that $\widehat{\sigma}_U^D(t_n)$ is small enough, that $\widehat{N}'(t_n) \geq 0$ at all time points. In the cases $\nu_b = \nu_d$ and $\nu_b < \nu_d$ the population size decreases. This is also what we would expect as for always positive $\widehat{\sigma}_U^D$ the derivative $\widehat{N}'(t_n)$ has to be negative at all time points. This means in these to cases the population will die out at some time point.

We have seen the influence of the relation between the birth and the death rate. As we have seen above that for $\nu_b \leq \nu_d$ the population will always die out, we will now focus on the case $\nu_b > \nu_d$ for different choices of these parameters. In Figure 20 one can find the plots of the population size and its derivative for Scenario 3. Before we have seen that this means we are again in a scenario where the model stabilizes around some constant state. Here we used birth and death rates where the difference between them gets smaller. As one would expect the smaller the difference gets the slower the population size grows. For the case where $\nu_b = 4 \cdot 10^{-3}$ and $\nu_d = 3.99 \cdot 10^{-3}$ the population size is decreasing in the long-term. This means that the number transition to the disease death compartment is larger than the difference between the birth and the death rate in this case, as $\widehat{N}'(t) < 0$.

We now discussed the influence of the choice of the birth and the death rate on the population size. We also want to talk about the influence of different birth and death rates on the disease dynamics. We will do this for the normalized SECIR-type model introduced in Section 2.3. First of all, it is clear that the death rate has an influence on the reproduction number, as it is part of $A(t)$. Moreover, we have seen in the theoretical analysis of the equilibria that the disease-free equilibrium might be stable for $\mathcal{R}_c > 1$, if the difference between the birth and the death rate is too large, see Remark 3.7. In Figure 21 one can see the behaviour of the force of infection term and the susceptibles of the normalized model in Scenario 2, for birth

and death rates getting smaller. Here, the proportion of the birth and the death rate stays the same. The reproduction number for $\nu_b = 0.4$ and $\nu_d = 0.3$ is 0.611289. Therefore, we expect convergence to the disease-free equilibrium, what also can be observed in Figure 21. In the cases $\nu_b = 4 \cdot 10^{-2}, \nu_d = 3 \cdot 10^{-2}$ and $\nu_b = 4 \cdot 10^{-3}, \nu_d = 3 \cdot 10^{-3}$, we see a convergence to some endemic state as one would expect as we have a reproduction number larger than one in these cases. In the case $\nu_b = 4 \cdot 10^{-4}, \nu_d = 3 \cdot 10^{-4}$, we see that the disease dies out, although we have reproduction number $\mathcal{R}_c = 1.75065$. There is no direct explanation for this from the theoretical results. A reason might be that the number of new susceptibles increases too slow and therefore less new infections take place. In other words, for a too small birth rate we are in a epidemic scenario.

For the SIRD-model we have seen in Theorem 3.3 and Figure 10 that if the difference of the birth and the death rate becomes to large we might converge to the disease-free equilibrium, although the reproduction number is larger then one. We now want to see if and when this is the case in the SECIR-type model. In Figure 22 one can find the behaviour of the force of infection term and the susceptibles for the normalized model in Scenario 2. Again we made the plot different birth and death rates, in this case we wanted chose them to have a large different. As expected for $\nu_b = 1 \cdot 10^{-1}$ and $\nu_d = 2 \cdot 10^{-3}$ we converge to a disease-free state.

5.4.7 Convergence of the scheme

Up to this point we did not discuss convergence of the non-standard scheme, we just assumed that it is converging to the continuous model. In [8] they show that the non-standard scheme is consistent with their theoretical model of order 1. Moreover, in [15] they show numerically linear convergence for the compartments using the non-standard scheme. We will not go into the question of convergence in detail but we want to have a short look at the behaviour of the scheme as the step size Δt decreases. We will do the computations for $\Delta t = 10^0, 10^{-1}, 10{-}2, 10^{-3}$ and 10^{-4}. The computations are prohibitively time-consuming for smaller step sizes, and the other computations already give an idea of convergence. In the following, we again use the parameters given in Table 2 and for the transition distributions we use the scenarios from Table 3. The exponential distribution is also a possible choice for the transition distributions. Therefore, we will define a fourth scenario in which we set $\gamma_{z_1}^{z_2}(t) = exp_3(t)$, for all suitable $z_1, z_2 \in \mathcal{Z}$.

In Table 5 you can find the values for the reproduction number $\widehat{\mathcal{R}}_c$, in Table 6 the values for $\widehat{S}(1)$ and in Table 7 the values for $\widehat{\lambda}(1)$. All in all, one can see that the difference between the values for $\widehat{\mathcal{R}}_c$, $\widehat{S}(1)$ and $\widehat{\lambda}(1)$ gets smaller as the step size gets smaller. But to be absolutely sure that the discretization scheme converges, one would need to evaluate more time step sizes. Moreover, we observe that the difference between the values is the largest in Scenario 4, where we used the exponential distribution. These results give the idea that the numerical scheme converges to some point. However, the question of convergence needs to be discussed further.

Δt	$\widehat{\mathcal{R}}_c$			
	Scenario 1	**Scenario 2**	**Scenario 3**	**Scenario 4**
10^0	0.49850225	1.73316892	3.42175268	1.84678163
10^{-1}	0.74321558	1.60493265	2.55310533	0.60805238
10^{-2}	0.75022827	1.58533925	2.47309137	0.52211513
10^{-3}	0.75068752	1.58331490	2.46515471	0.51398559
10^{-4}	0.75073094	1.58311182	2.46436169	0.51317728

Table 5: Values of the reproduction number of the different scenarios for a decreasing step size Δt.

Δt	$\widehat{S}(1)$			
	Scenario 1	**Scenario 2**	**Scenario 3**	**Scenario 4**
10^0	100099.82053838	100099.82053838	100099.82053838	100099.82053838
10^{-1}	100080.47529549	100079.17675936	100078.63759302	100088.47616227
10^{-2}	100078.31900395	100077.04831483	100076.50513239	100087.04372800
10^{-3}	100078.10081657	100076.83471108	100076.29195296	100086.90164288
10^{-4}	100078.07897303	100076.81334308	100076.27063571	100086.88744536

Table 6: Number of susceptibles at time $t = 1$ of the different Scenarios for a decreasing step size Δt.

Δt	$\widehat{\lambda}(1)$			
	Scenario 1	**Scenario 2**	**Scenario 3**	**Scenario 4**
10^0	0.00013038	0.00017437	0.00020062	0.00008464
10^{-1}	0.00015757	0.00017819	0.00019236	0.00007407
10^{-2}	0.00016109	0.00017872	0.00019145	0.00006847
10^{-3}	0.00016144	0.00017878	0.00019135	0.00006788
10^{-4}	0.00016147	0.00017878	0.00019135	0.00006782

Table 7: Force of Infection at time $t = 1$ for different scenarios for a decreasing step size Δt.

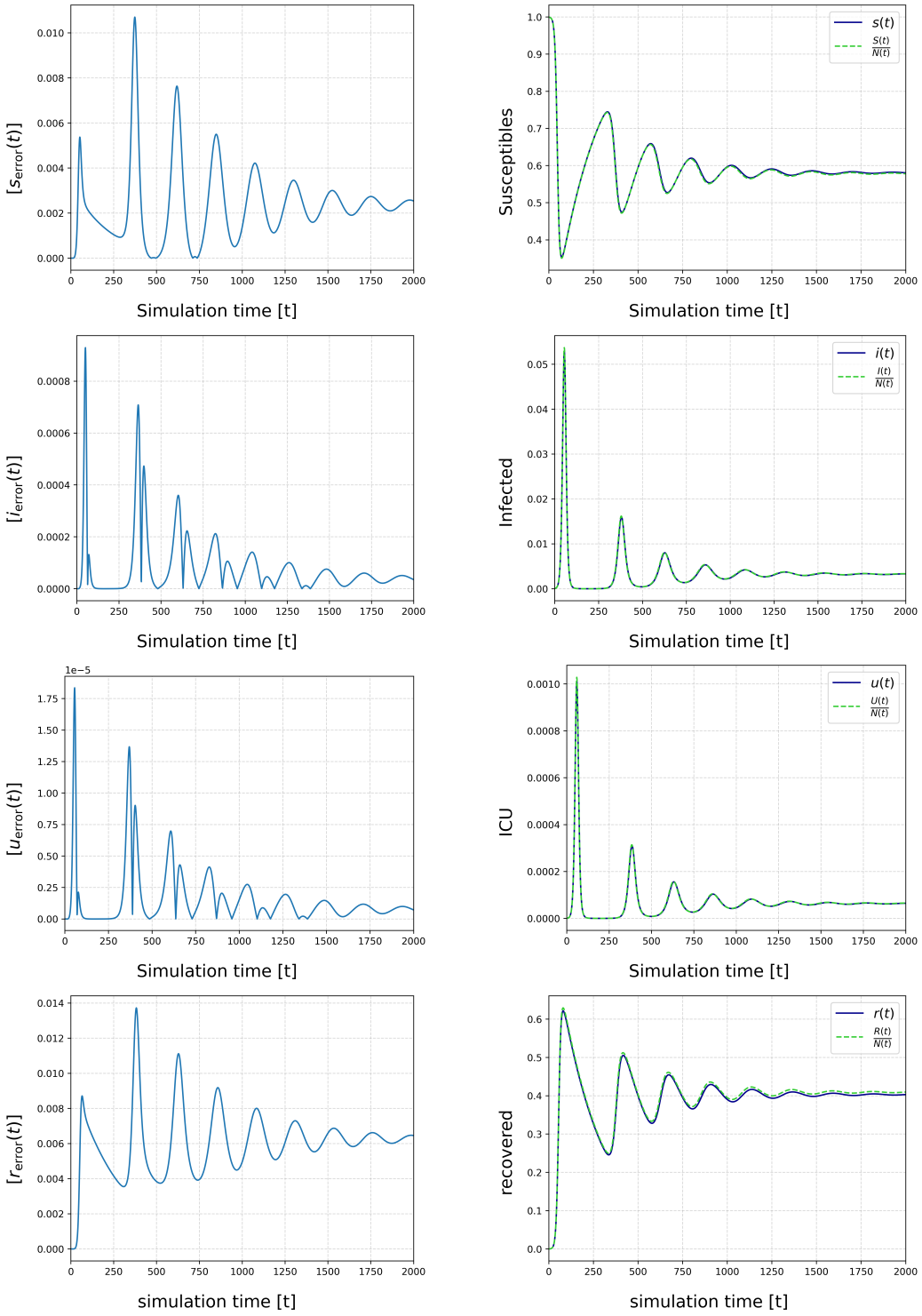


Figure 11: **The comparison of the normalized compartments:** On the left are the plots for the normalization error z_{error} and on the right both normalizations are plotted for each compartment. The plots are made for Scenario 2.

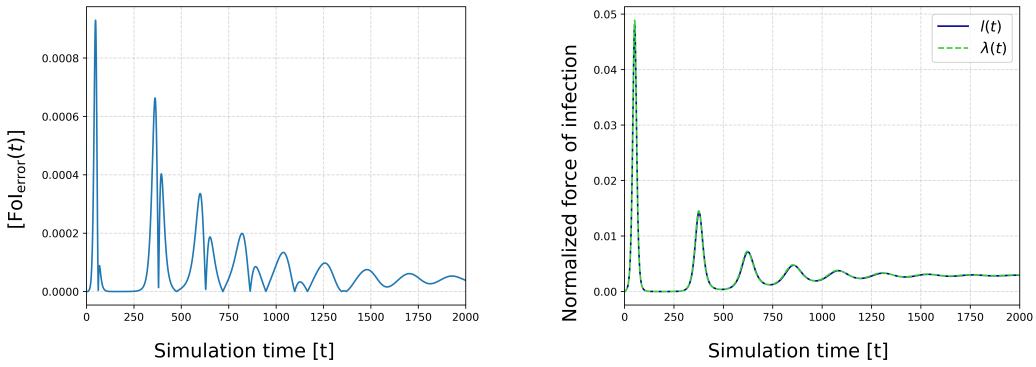
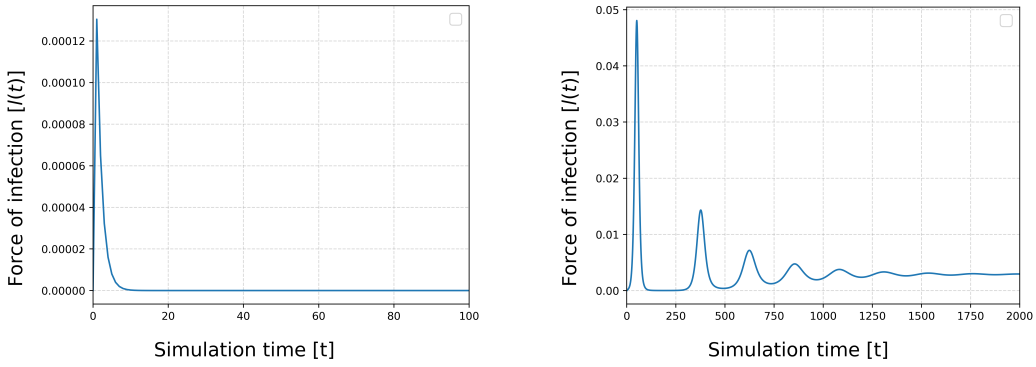
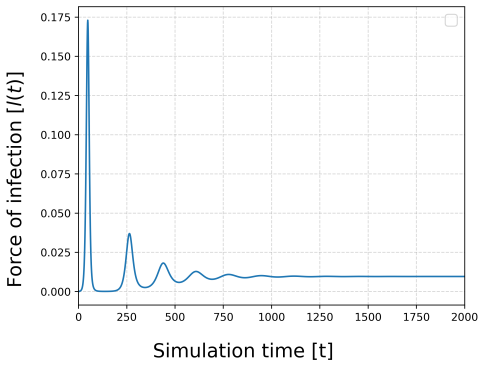


Figure 12: **The comparison of the force of infection term:** On the left are the plots for the error $\mathrm{FoI}_{\mathrm{error}}$ and on the right both force of infection terms $\widehat{\lambda}$ and $\widehat{I}$ are plotted. The plots are made for Scenario 2.



(a) Force of infection for Scenario 1.

(b) Force of infection for Scenario 2.



(c) Force of infection for Scenario 3.

Figure 13: **Plots for the force of infection term I in different scenarios:** for Scenario 1 we have a reproduction number smaller than one. For Scenario 2 and 3 we have reproduction numbers larger than one.

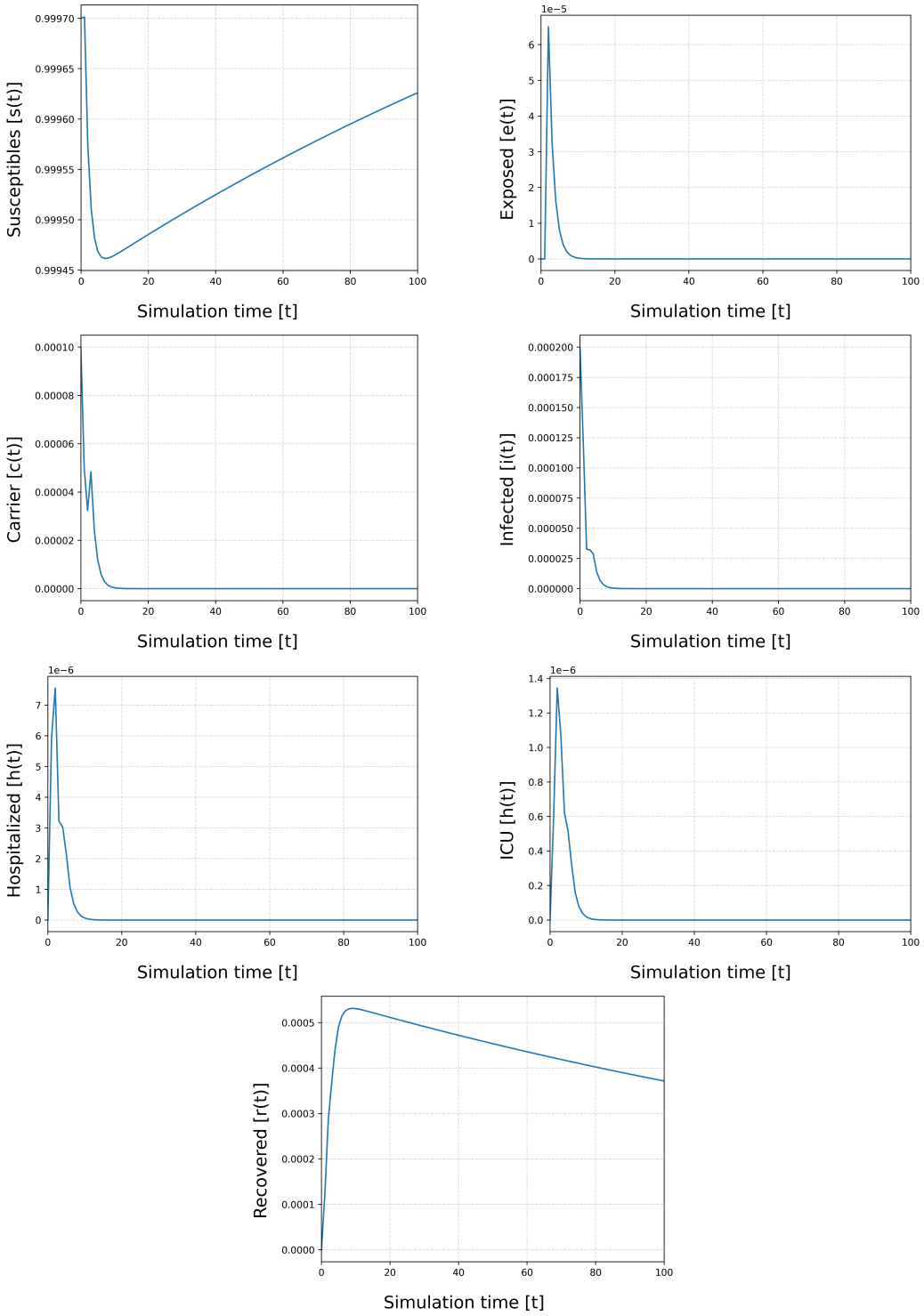


Figure 14: **The normalized compartments in Scenario 1:** where we have a reproduction number smaller than one.

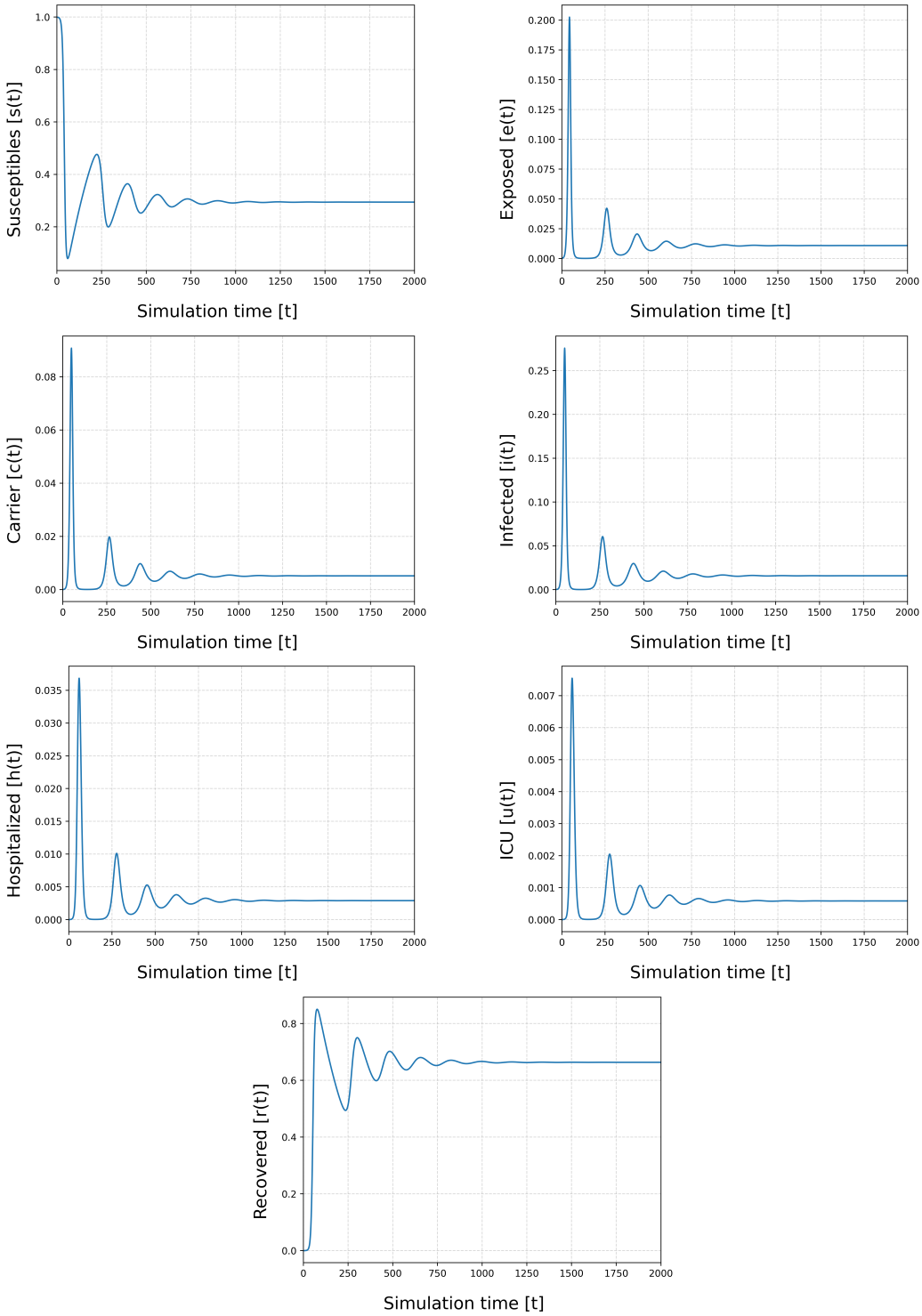


Figure 15: **The normalized compartments in Scenario 3:** where we have a reproduction number larger than one.

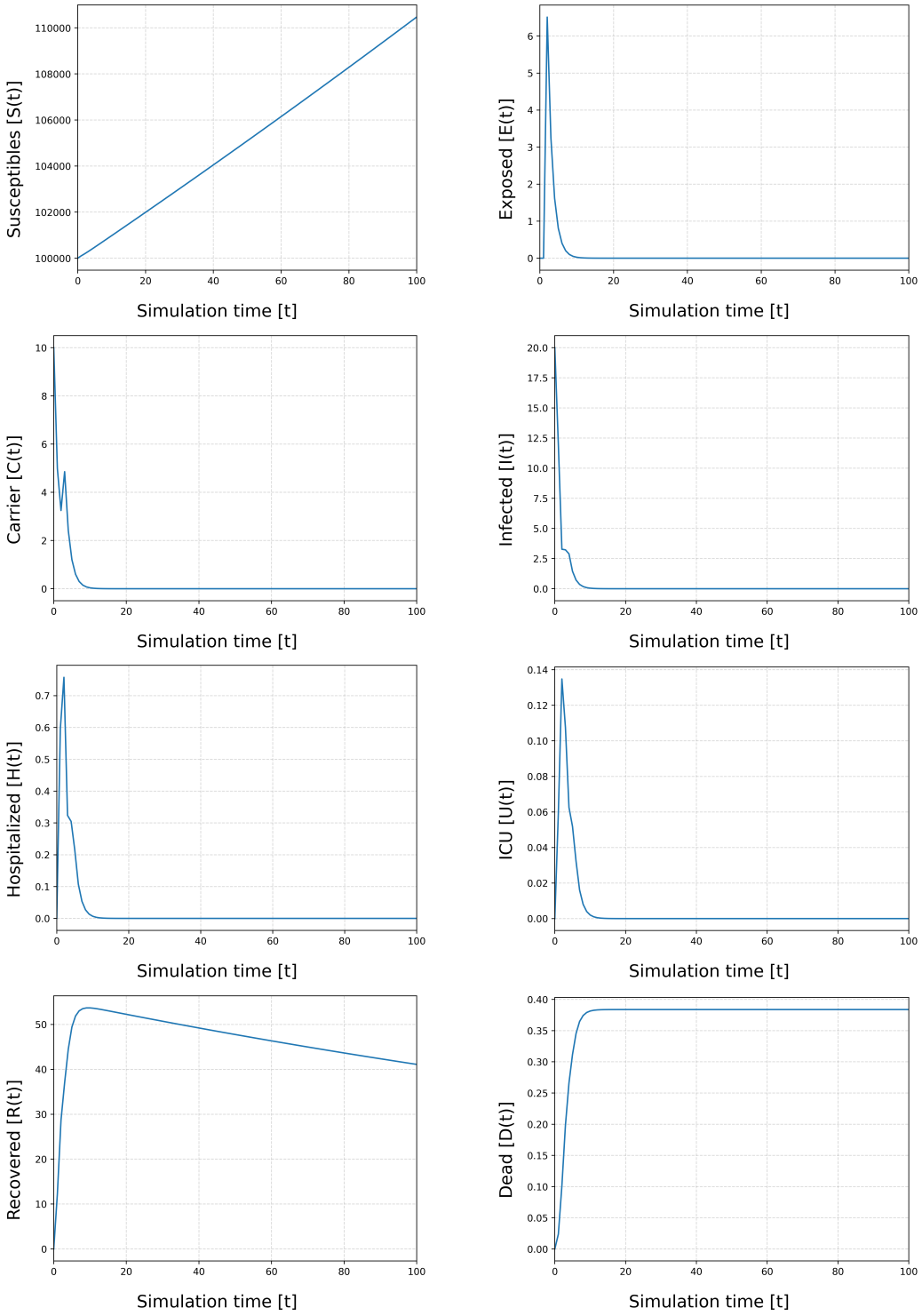


Figure 16: **The non-normalized compartments for Scenario 1:** where we have a reproduction number smaller than one.

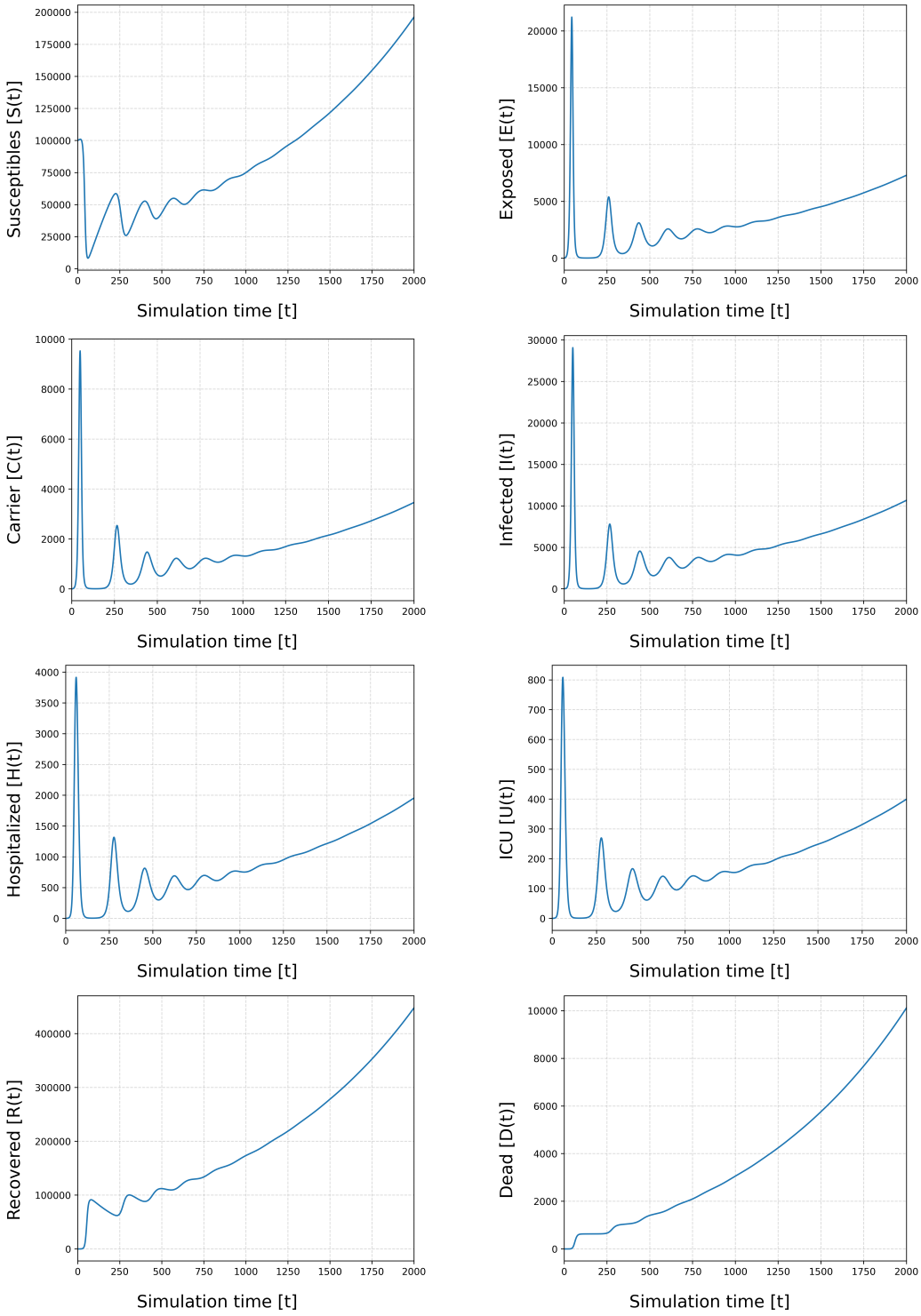


Figure 17: **The non-normalized compartments for Scenario 3:** where we have a reproduction number larger than one.

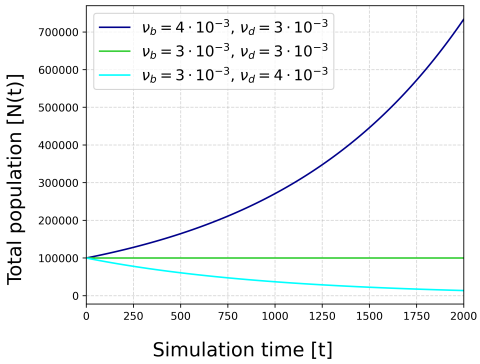


Figure 18: **Total population in a scenario without a disease:** modelled for different birth and death rates. Where we have $\nu_b > \nu_d$, $\nu_b = \nu_d$ and $\nu_b < \nu_d$.

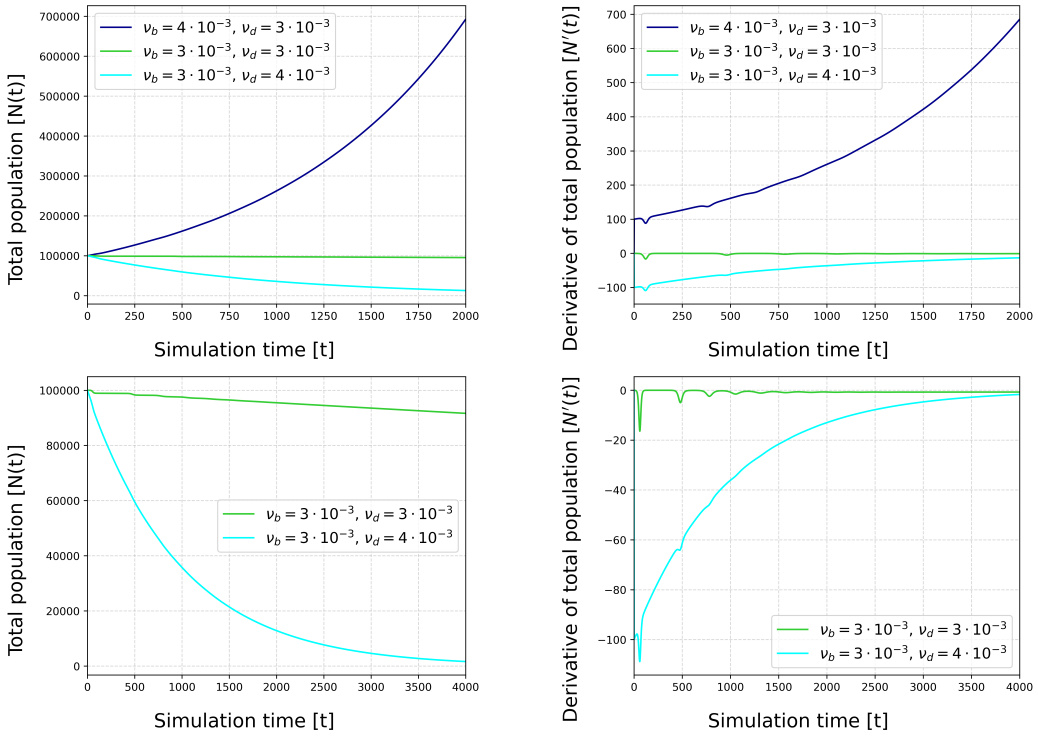


Figure 19: **The total population and its derivative in Scenario 2:** modelled for different birth and death rates. Where we have $\nu_b > \nu_d$, $\nu_b = \nu_d$ and $\nu_b < \nu_d$. In the lower plots we see the same scenario but for a larger time span.

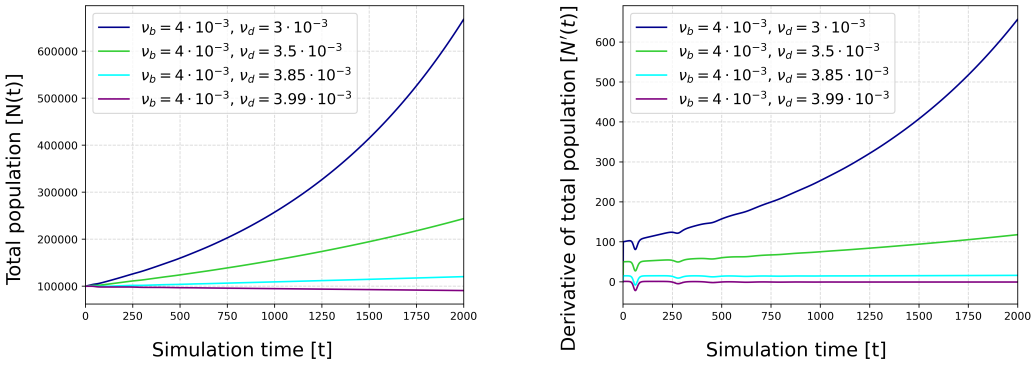


Figure 20: **The total population and its derivative in Scenario 3:** modelled for different birth and death rates. Where always $\nu_b > \nu_d$, but we vary the difference of ν_b and ν_d

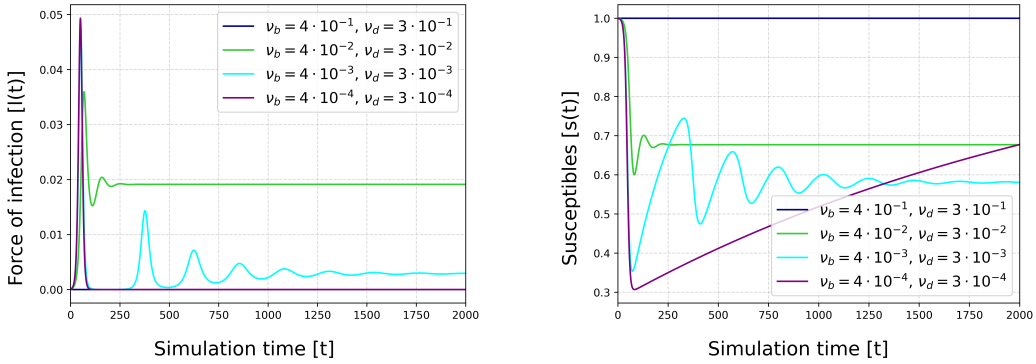


Figure 21: **The force of Infection term l and the normalized susceptibles s in Scenario 2:** modelled for different birth and death rates. Where always $\nu_b > \nu_d$ and we have the same proportion, but we vary the magnitude of the rates.

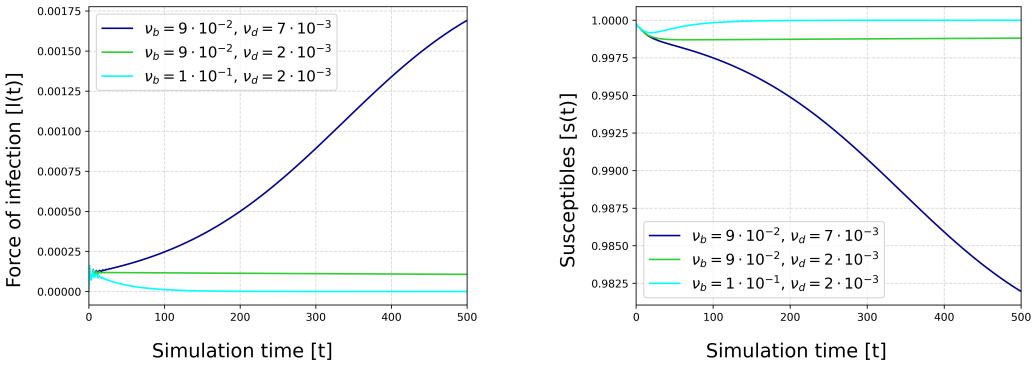


Figure 22: **The force of Infection term l and the normalized susceptibles s in Scenario 2:** modelled for different birth and death rates. Where always $\nu_b > \nu_d$ and we choose them to have a rather large difference.

6 Conclusion

Here we summarize the main results of our thesis and discuss some remaining open questions. In this thesis, we set out to investigate endemic states of a new model for infection dynamics. Our model is based on the SECIR-type IDE model given in [15] and incorporates a birth and a natural death rate. Notably, our model is very general and allows for both population growth and decline. Investigations of endemic states for IDE-based models, in the literature, see [13], are mostly limited to models with constant population size, i.e., models without disease induced death and identical birth and death rates. In these models, the endemic states are precisely the equilibria of the model, and their stability depends simply on the reproduction number R_c.

For scenarios with more general population dynamics, IDE-based models are notably absent from the literature, while many results exist for ODE-based models. Our goal was therefore to adapt the techniques from the ODE-based models to our IDE case. For such models as ours, the long-term analysis is very complex and the notion of an equilibrium is ill-suited. Therefore, we introduced a normalized IDE-based model, which seems to have not yet been investigated in the literature. While our numerical experiments in Section 5.4.3 strongly suggest the validity of our normalized model, its rigorous mathematical derivation from the original model is not yet complete.

We were able to show that the disease-free state is stable if the reproduction number is smaller than one, Theorem 3.3, and is mostly unstable if the reproduction number is larger than one, Theorem 3.6. These results were also replicated for the discretized models numerically in Section 5. The endemic states of our model are much more involved than in previous IDE-based models [13] and ODE-based models [11, 12]. Our analysis showed that the existence of a feasible endemic equilibrium is tightly linked to multiple parameters, besides the reproduction number, which did not play a role in previous results. For quite a wide range of parameters, we showed that no feasible endemic equilibrium exists. However, in the numerical experiments we could see that in cases where no feasible equilibrium exists according to the theoretical analysis, we still see convergence of the model to an endemic state. Our analysis gives rise to new research questions that could be studied in future work. For example, the validity of the normalized model and the existence and stability of an endemic equilibrium.

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