Mathematical Analysis of a Compartment Model

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Abstract. We give a theoretical investigation of a Covid model. This model was successfully used in the context of MPC control to keep the Covid pandemic manageable [1]. We compute especially a next generation basic reproduction number, a Lyapunov function and reveal some peculiarities if demography is skipped. Finally, we look at the model with two age groups.

1 Introduction

Epidemics and infectious diseases are often described using so-called compartment models in order to be able to make the best possible, realistic predictions about the course of the disease in larger population groups. A population is divided into different groups (*"compartments"*) and the flow (inflows an d ou tflows) between these compartments is examined more closely. A classic compartment model is the SIR model according to Kermack and McKendrick.

2 ODE Model

In [1] a detailed Covid model is developed and successfully used in the context of model predictive control (MPC) in order to mitigate the COVID-19 outbreak. The model was used with weekly updates of the parameters. Optimal mass-testing and age-dependent social distancing policies were determined [1].
Here a theoretical investigation of the mathematical properties of an autonomous version of this model is performed. At the beginning the model is simplified to one age class and enhanced with demography. Therefore the following autonomous mathematical compartment model is investigated in this research:

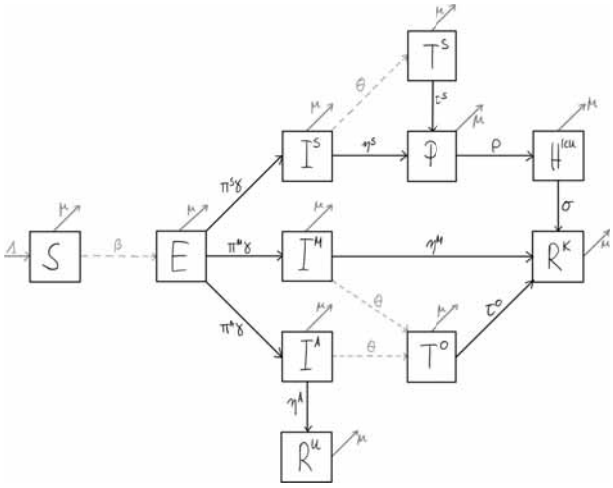

Figure 1: SEIPTHR model with demography.

2..1 ODE System

The associated ODE system with *mass action incidence* is given by

$$\dot{S} = \Lambda - \beta S[I^S + I^M + I^A + T^S + T^O] - \mu S \quad (1a)$$
$$\dot{E} = \beta S[I^S + I^M + I^A + T^S + T^O] - (\gamma + \mu)E \quad (1b)$$
$$\dot{I}^S = \pi^S \gamma E - (\eta^S + \theta + \mu)I^S \quad (1c)$$
$$\dot{I}^M = \pi^M \gamma E - (\eta^M + \theta + \mu)I^M \quad (1d)$$
$$\dot{I}^A = \pi^A \gamma E - (\eta^A + \theta + \mu)I^A \quad (1e)$$
$$\dot{T}^S = \theta I^S - (\tau^S + \mu)T^S \quad (1f)$$
$$\dot{T}^O = \theta[I^M + I^A] - (\tau^O + \mu)T^O \quad (1g)$$
$$\dot{P} = \eta^S I^S + \tau^S T^S - (\rho + \mu)P \quad (1h)$$
$$\dot{H}^{ICU} = \rho P - (\sigma + \mu)H^{ICU} \quad (1i)$$
$$\dot{R}^K = \eta^M I^M + \tau^O T^O + \sigma H^{ICU} - \mu R^K \quad (1j)$$
$$\dot{R}^U = \eta^A I^A - \mu R^U \quad (1k)$$

together with non-negative initial values

$$S(0)=S_0, E(0)=E_0, I^S(0)=I_0^S, I^M(0)=I_0^M,$$
$$I^A(0)=I_0^A, T^S(0)=T_0^S, T^O(0)=T_0^O, P(0)=P_0,$$
$$H^{ICU}(0)=H_0^{ICU}, R^K(0)=R_0^K, R^U(0)=R_0^U. \quad (11)$$

2.2 Model Description

The following compartments are introduced in [1]:

- $S(t), E(t)$: Susceptible persons (S) accumulate after infection with the pathogen in a compartment E (exposed), but are not yet infectious themselves.
- $I(t) = I^S(t) + I^M(t) + I^A(t)$: The infectious compartment I is divided into three classes depending on the course of infection. A distinction is made between severe cases I^S, mild cases I^M and asymptomatic cases I^A.
- $T^S(t), T^O(t)$: Infectious persons have the opportunity to be tested, in which we in turn differentiate according to the course of the disease.
- $P(t)$: Seriously ill people will either go directly to a physician (P) and go into quarantine or only after receiving a positive test result.
- $H^{ICU}(t)$: After isolation in P, severely ill persons are transferred to an intensive care unit H^{ICU}.
- $R(t) = R^K(t) + R^U(t)$: The compartment of recovered individuals R is divided into two classes depending on the course of infection: individuals who have actually been identified as infected are collected in R^K (known), the other ones recover in a natural way without having previously been identified as diseased (R^U - unknown).

In order to finally understand the interaction between the individual compartments, we need an overview of the parameters modelled in Table 1.
Set $\pi^S + \pi^M + \pi^A = 1$ and $U := S + E + I^S + I^M + I^A + R^U$. All constants in Table 1 are non-negative.

Parameters	Description
$\beta > 0$	infection rate
$\gamma > 0$	average incubation time γ^{-1} in days
$\pi^S > 0$	Proportion of severely ill patients
$\pi^M > 0$	Proportion of mildly ill patients
$\pi^A > 0$	Proportion of asymptomatic patients
$\theta \geq 0$	Test rate (Tests spread in U per day)
$\eta^S > 0$	Recovery rate for severe course
$\eta^M > 0$	Recovery rate for mild course
$\eta^A > 0$	Recovery rate for asymptomatic course
$\tau^S > 0$	Rate at which tested persons recover (severe)
$\tau^O > 0$	Rate at which tested persons recover (others)
$\rho > 0$	average duration of isolation ρ^{-1}
$\sigma > 0$	average length of stay in ICU σ^{-1}

Table 1: Model parameters.

3 Mathematical Analysis

We decompose all compartments into the vector $x = (E, I^S, I^M, I^A, T^S, T^O)$ of infected compartments and the remaining compartments $y = (S, P, H^{ICU}, R^K, R^U)$. All compartments are denoted by $z = (x, y)$.

3.1 Positive Invariance and Existence of Solutions

Starting from our IVP (1), it is important that the biological relevance of the solutions is ensured. This requirement on the mathematical model is fulfilled by the *positive invariance* shown below:

Theorem: The non-negative orthant $\mathbb{R}^{11}_{\geq 0}$ is a positive invariant set.
Proof: The r.h.s. of the ODE is quasipositive. Apply Theorem 4.2.2 in Prüss, Wilke [2], pp. 83–84.

The total population $N(t) := \sum_{i=1}^{11} z_i(t)$ fulfills the initial value problem

$$\dot{N} = \Lambda - \mu N,\ N(0) = N_0,$$

where $N_0 := S_0 + E_0 + I_0^S + I_0^M + I_0^A + T_0^S + T_0^O + P_0 + H_0^{ICU} + R_0^K + R_0^U$.
Its solution $N(t) = \Lambda/\mu + e^{-\mu t}(N_0 - \Lambda/\mu)$ converges monotonically with $t \to \infty$ to $N_\infty := \Lambda/\mu$.
Therefore $N(t) \leq K := \max(N_0, N_\infty)$.

This proves, that the polytop $\Omega := \{z \in \mathbb{R}^{11}_{\geq 0} | N(t) \leq K\}$ is a positive invariant set of the IVP (1).

The next step is to ensure that there is indeed a solution of the IVP:

Theorem: The initial value problem (1) has a unique solution for $t \in [0,\infty[$.
Proof: On the compact set Ω the IVP is globally Lipschitz continuous, due to the polynomial r.h.s. of the ODE. Apply Picard-Lindelöf.

Without loss of generality we set $\Lambda = N_0 \cdot \mu = \mu$ for $N_0 = 1$, this implies $N_\infty = 1$ and $K = 1$. This choice means that the total population at all times is constant equal to 1 and therefore fractions of the population are considered.

3.2 Next-Generation-Approach for the Basic Reproduction Number

Our next goal is to calculate a next-generation basic reproduction number according to [3]. For that we need the existence of a disease-free equilibrium of our ODE, which can be easily seen:
If $\mu > 0$, then there exists a unique disease-free equilibrium $\mathscr{E}_{DFE}$ with compartiment $S = 1 := N$ and all other compartments equal to zero.

Using the decomposition of the compartments the initial value problem

$$\dot{z} = h(z),\ z(0) = z_0$$

is rewritten as

$$\begin{aligned} \dot{x} &= f(x,y) = \mathscr{F}(x,y) - \mathscr{V}(x,y),\ x(0) = x_0, \\ \dot{y} &= g(x,y),\ y(0) = y_0 \end{aligned}$$

with

$$\begin{aligned} \mathscr{F}(x,y) &= \begin{pmatrix} \beta S[I^S + I^M + I^A + T^S + T^O] \\ \mathbf{0} \end{pmatrix} \\ \mathscr{V}(x,y) &= \begin{pmatrix} (\gamma+\mu)E \\ (\eta^S+\theta+\mu)I^S - \pi^S\gamma E \\ (\eta^M+\theta+\mu)I^M - \pi^M\gamma E \\ (\eta^A+\theta+\mu)I^A - \pi^A\gamma E \\ (\tau^S+\mu)T^S - \theta I^S \\ (\tau^O+\mu)T^O - \theta[I^M + I^A] \end{pmatrix}. \end{aligned}$$

Let $F = \frac{\partial \mathscr{F}}{\partial x}$ and $V = \frac{\partial \mathscr{V}}{\partial x}$. We will postpone the evaluation of the Jacobian matrices at the coordinates of the DFE to a later time.

The Jacobian matrices are given in this application by

$$\begin{aligned} F &= \frac{\partial \mathscr{F}}{\partial x} = \left(\begin{array}{cccccc} 0 & \beta S & \beta S & \beta S & \beta S & \beta S \\ \hline & & & \mathbf{0} & & \end{array}\right) \\ V &= \frac{\partial \mathscr{V}}{\partial x} = \begin{pmatrix} r_1 & 0 & 0 & 0 & 0 & 0 \\ -\pi^S\gamma & r_2 & 0 & 0 & 0 & 0 \\ -\pi^M\gamma & 0 & r_3 & 0 & 0 & 0 \\ -\pi^A\gamma & 0 & 0 & r_4 & 0 & 0 \\ 0 & -\theta & 0 & 0 & r_5 & 0 \\ 0 & 0 & -\theta & -\theta & 0 & r_6 \end{pmatrix} \end{aligned}$$

with $r_1 = \gamma+\mu,\ r_2 = \eta^S+\theta+\mu, r_3 = \eta^M+\theta+\mu,$
$r_4 = \eta^A+\theta+\mu, r_5 = \tau^S+\mu, r_6 = \tau^O+\mu.$

For the next-generation matrix we need

$$V^{-1} = \begin{pmatrix} r_1^{-1} & 0 & 0 & 0 & 0 & 0 \\ m_1 & r_2^{-1} & 0 & 0 & 0 & 0 \\ m_2 & 0 & r_3^{-1} & 0 & 0 & 0 \\ m_3 & 0 & 0 & r_4^{-1} & 0 & 0 \\ m_4 & m_6 & 0 & 0 & r_5^{-1} & 0 \\ m_5 & 0 & m_7 & m_8 & 0 & r_6^{-1} \end{pmatrix}$$

where $m_1 = \frac{\gamma}{\gamma+\mu}\frac{\pi^S}{\eta^S+\theta+\mu}, m_2 = \frac{\gamma}{\gamma+\mu}\frac{\pi^M}{\eta^M+\theta+\mu},$
$m_3 = \frac{\gamma}{\gamma+\mu}\frac{\pi^A}{\eta^A+\theta+\mu}, m_4 = \frac{\gamma}{\gamma+\mu}\frac{\pi^S}{\eta^S+\theta+\mu}\frac{\theta}{\tau^S+\mu},$
$m_5 = \frac{\gamma}{\gamma+\mu}\left(\frac{\pi^M}{\eta^M+\theta+\mu}\frac{\theta}{\tau^O+\mu} + \frac{\pi^A}{\eta^A+\theta+\mu}\frac{\theta}{\tau^O+\mu}\right),$
$m_6 = \frac{\theta}{(\tau^S+\mu)(\eta^S+\theta+\mu)}, m_7 = \frac{\theta}{(\tau^O+\mu)(\eta^M+\theta+\mu)},$
$m_8 = \frac{\theta}{(\tau^O+\mu)(\eta^A+\theta+\mu)}.$

The next-generation-matrix is computed as

$$K = FV^{-1} = \beta S \left(\begin{array}{cccccc} K_1 & 0 & 0 & 0 & 0 & 0 \\ * & & & \mathbf{0} & & \end{array}\right)^T$$

with

$$\begin{aligned} K_1 = \frac{\gamma}{\gamma+\mu}\cdot\Big(&\frac{\pi^S}{\eta^S+\theta+\mu} + \frac{\pi^M}{\eta^M+\theta+\mu} \\ &+ \frac{\pi^A}{\eta^A+\theta+\mu} + \frac{\pi^S}{\eta^S+\theta+\mu}\frac{\theta}{\tau^S+\mu} + \\ &+ \frac{\pi^M}{\eta^M+\theta+\mu}\frac{\theta}{\tau^O+\mu} + \frac{\pi^A}{\eta^A+\theta+\mu}\frac{\theta}{\tau^O+\mu}\Big). \end{aligned}$$

The spectral radius of K is given by $\rho(K) = \beta S \cdot K_1$, since K is a triangle matrix.

Finally the next generation basic reproduction numberis given by

$$\mathscr{R}_0 = \rho(K)|_{DFE} = \beta N \cdot K_1 \overset{N=1}{=} \beta \cdot K_1.$$

3.3 Stability

In order to analyze the stability of our DFE $(0, y_0)$, it's helpful to write the partitioned linearized ODE as

$$\dot{x} = J_1|_{DFE} \cdot x + J_2|_{DFE} \cdot (y - y_0)$$
$$\dot{y} = J_3|_{DFE} \cdot x + J_4|_{DFE} \cdot (y - y_0).$$

The relevant Jacobian matrices are given by $J_1 = \frac{\partial f}{\partial x}$and $J_4 = \frac{\partial g}{\partial y}$, an easy computation shows $J_2|_{DFE} = \frac{\partial f}{\partial y}|_{DFE} = 0$.

Note that $F \geq 0$ (componentwise) and V is a regular M-matrix, since V^{-1} exists and $V^{-1} \geq 0$ (componentwise). Therefore $-J_1|_{DFE} = (V - F)|_{DFE}$ is a regular splitting due to Varga [4] p. 95, Def. 3.28.

Additionally we know [3, 4]:
If $\mathscr{R}_0 < 1$, then $J_1|_{DFE}$ has only eigenvalues with negative real part.
If $\mathscr{R}_0 > 1$, then $J_1|_{DFE}$ has at least one eigenvalue with positive real part.
The matrix $J_4|_{DFE}$ has eigenvalues with negative real part, a simple calculation gives the eigenvalues $-\mu, -(\rho + \mu)$ and $-(\sigma + \mu)$.

Applyication of the linearization theorem gives the result a). A more complicated argument is required in order to prove b).

Theorem: The considered Covid model has the following properties:

a) If $\mathscr{R}_0 < 1$, then the DFE is locally asymptotically stable.

b) If $\mathscr{R}_0 > 1$, then the DFE is instable.

Following an idea of Shuai/van den Driessche [5] we compute a linear convex Lyapunov function for the case with $\mathscr{R}_0 < 1$ in order to analyze the global stability of our DFE.
According to [5], we have to analyze first when $\tilde{f}(x,y) = (F - V)|_{DFE} \cdot x - \mathscr{F}(x,y) + \mathscr{V}(x,y) \geq 0$ on a positive invariant set. For our model only the first component of $\tilde{f}$ is not equal to zero, more precisely $\tilde{f}_1(x,y) = \beta \cdot (N - S) \cdot [I^S + I^M + I^A + T^S + T^O]$. Thus our positive invariant set is $\bar{\Omega} = \{z \in \mathbb{R}^{11}_{\geq 0} | N(t) \leq N_\infty\} \subset \Omega$.

Next we need a left eigenvector ω^T of the non-negative matrix $V^{-1}F$ to the eigenvalue $\mathscr{R}_0 \geq 0$.
This yields $\omega^T = \begin{pmatrix} 0 & 1 & 1 & 1 & 1 & 1 \end{pmatrix}$, where the E-component takes the value 0. Thus, the linear convex Lyapunov function on $\bar{\Omega}$ is given by

$$Q(x) = \omega^T V^{-1} x = \begin{pmatrix} K_1 & q_1 & q_2 & q_3 & q_4 & q_5 \end{pmatrix} \cdot x,$$

with $q_1 = \frac{1}{\eta^S + \theta + \mu} + \frac{\theta}{(\tau^S + \mu)(\eta^S + \theta + \mu)}, q_2 = \frac{1}{\eta^M + \theta + \mu} + \frac{\theta}{(\tau^O + \mu)(\eta^M + \theta + \mu)}, q_3 = \frac{1}{\eta^A + \theta + \mu} + \frac{\theta}{(\tau^O + \mu)(\eta^A + \theta + \mu)}, q_4 = \frac{1}{\tau^S + \mu}, q_5 = \frac{1}{\tau^O + \mu}$.
One can show, that the DFE is the largest invariant set in the set given by $Q(x) = 0$. Then apply LaSalle [6].

Theorem: The considered Covid model has the following properties:

If $\mathscr{R}_0 < 1$, then the DFE is globally asymptotically stable in$\bar{\Omega}$.

3.4 Numerical Solutions

Finally, we will consider numerical solutions for the ODE system. Two scenarios are investigated: with testing and without testing.
Consider the following IVP:

$$E_0 = 0.01, \;\; S_0 = 1 - E_0 = 0.99, \;\; I_0^S = \ldots = R_0^U = 0$$

The following parameter selection for the age group of 15- to 60-year-olds was taken from [1]:

Parameter	Value
β	0.63
γ	0.19
π^S	$\frac{0.31}{100}$
π^M	$\frac{22.01}{100}$
π^A	$\frac{77.68}{100}$
η^S	0.25
η^M	0.25
η^A	0.17
τ^S	0.75
τ^O	0.92
ρ^{-1}	10.98
σ^{-1}	10.5

Table 2: Parameters for the simulation.

We set $\mu = \frac{1}{365 \cdot 20}$. Unfortunaly, problems occur with the numerical solutions, because the solution curves leave the positive invariant set Ω for a very large t value (see Figure 2).

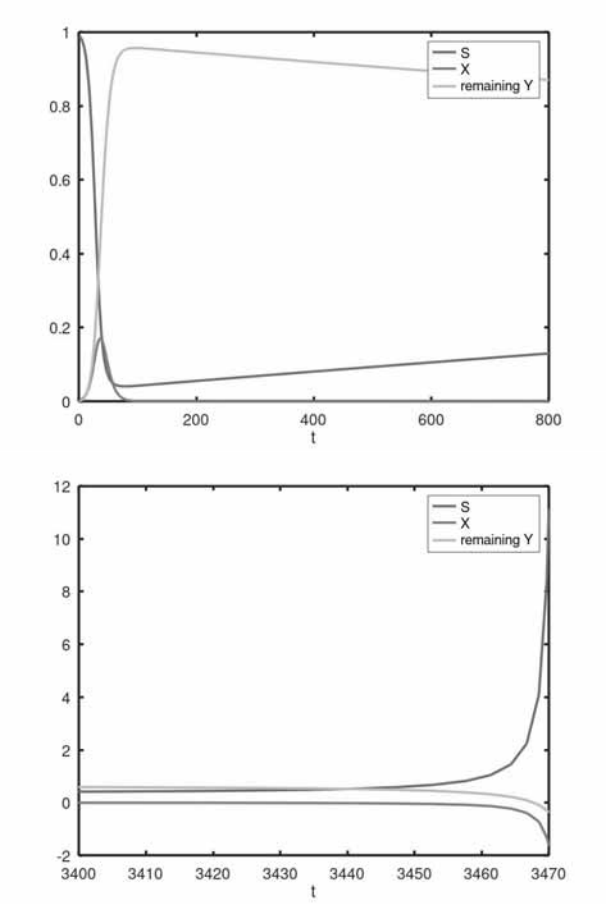

Figure 2: Simulation with demography, without testing.

An implicit stiff integrator can fix this problem (see Figure 3).
For the scenario without testing $\mathscr{R}_0 \approx 3.44$ holds.
Finally, consider test measures with $\theta = 0.4$. The numeric solutions can be seen in Figure 4.
For this scenario we obtain a basic reproduction number of $\mathscr{R}_0 \approx 1.54$

4 Model without Demography

We investigate now our model without demography, we set $\mu = \Lambda = 0$.

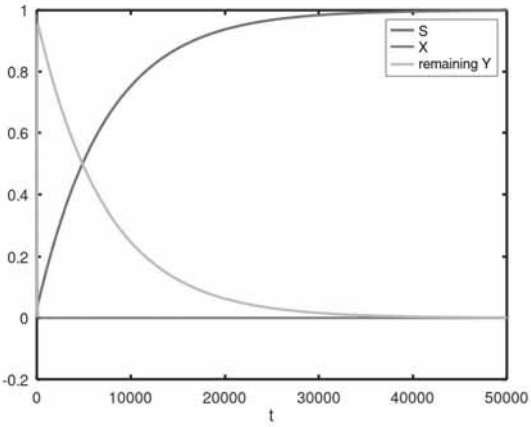

Figure 3: Simulation with demography, without testing, using an implicit stiff integrator.

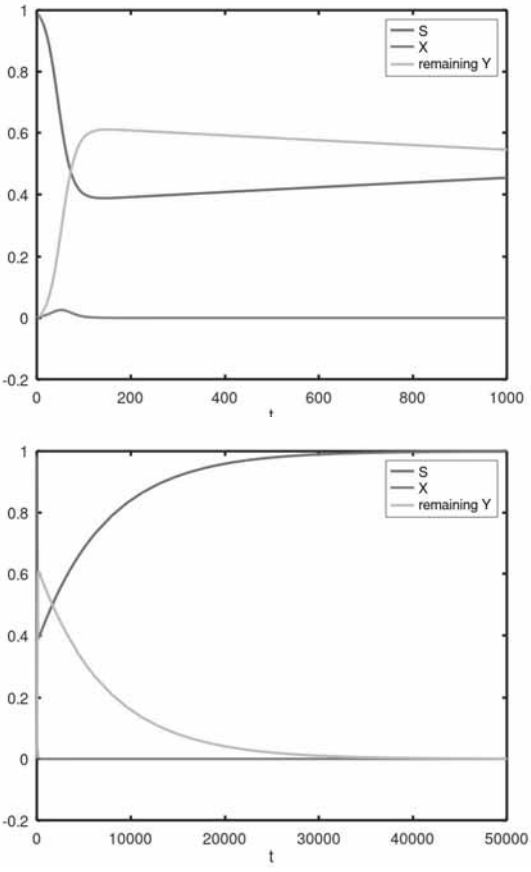

Figure 4: Simulation with demography, with testing, $\theta = 0.4$, using an implicit stiff integrator.

In contrast to the first model, this time there are peculiarities in the calculations for $\mathscr{R}_0$. Firstly, by analogy with the previous considerations, it can be shown that the non-negative orthant $\mathbb{R}^{11}_{\geq 0}$ and the set $\tilde{\Omega} := \{z \in \mathbb{R}^{11}_{\geq 0} \mid \sum_{i=1}^{11} z_i = 1\}$ are positive invariant for our second ODE.

Next, we need to ensure the existence of a DFE: the difference to the first model is that this equilibrium point is *no longer unique*. Simple calculations together with the positive invariance provide that all disease-free-equlibria fulfill the equation $\tilde{S} + \tilde{R^K} + \tilde{R^U} = 1$. Therefore, there will be no unique basic reproduction number. The calculation of $\mathscr{R}_0$ is similar to that of the first model: We get the same formulas as before, only with $\Lambda = \mu = 0$.

We obtain the next-generation-matrix

$$K = FV^{-1} = \beta S \begin{pmatrix} K_2 & 0 & 0 & 0 & 0 & 0 \\ * & & & \mathbf{0} & & \end{pmatrix}^T$$

with

$$K_2 = \frac{\pi^S}{\eta^S + \theta} + \frac{\pi^M}{\eta^M + \theta} + \frac{\pi^A}{\eta^A + \theta} + \frac{\pi^S}{\eta^S + \theta}\frac{\theta}{\tau^S} + \frac{\pi^M}{\eta^M + \theta}\frac{\theta}{\tau^O} + \frac{\pi^A}{\eta^A + \theta}\frac{\theta}{\tau^O}.$$

The spectral radius of K is given by $\rho(K) = \beta S \cdot K_2$.

Finally, the next generation basic reproduction number is given by $\mathscr{R}_0 = \rho(K)|_{DFE} = \beta \tilde{S} \cdot K_2$.

Depending on the initial values of the unknown DFE-components, we calculate the limit value of S and choose it as $\tilde{S}$.

Another observation is that for $\tilde{S} = 1 = N$ and $\mu \to 0$ the basic reproduction numbers of both models coincide, which can be seen approximately for $\mu = \frac{1}{365 \cdot 20}$ in the following table:

In contrast to the inclusion of demography in the first model, the linearization theorem cannot be used to investigate the local asymptotic stability of the DFE, since the corresponding matrix $J_4|_{DFE}$ has the eigenvalue 0. Instead, we can again calculate a linear convex Lyapunov function for the case with $\mathscr{R}_0 < 1$ of our DFE.

Again we have to analyze when the function $\tilde{f}(x,y) = (F - V)|_{DFE} \cdot x - \mathscr{F}(x,y) + \mathscr{V}(x,y) \geq 0$. For our second model only the first component of $\tilde{f}$ is not equal to zero, more precisely $\tilde{f}_1(x,y) = \beta \cdot (\tilde{S} - S) \cdot [I^S + I^M + I^A + T^S + T^O]$. Thus, we can consider a Lyapunov function on our positive invariant set $\tilde{\Omega}$ only for $S_0 \leq \tilde{S} \leq N_\infty = 1$, since the S-component is monotonically decreasing.

β	$\mathscr{R}_0^{\text{with}}$	$\mathscr{R}_0^{\text{without}}$
0.1	0.545411144346408	0.546221176470588
0.4	2.18164457738563	2.18488470588235
0.8	4.36328915477126	4.36976941176471

Table 3: Basic reproduction numbers with/without demography, without testing.

Once again we get $\omega^T = \begin{pmatrix} 0 & 1 & 1 & 1 & 1 & 1 \end{pmatrix}$, where the E-component takes the value 0. Thus, the linear convex Lyapunov function is given by

$$Q(x) = \omega^T V^{-1} x = \begin{pmatrix} K_2 & q_1 & q_2 & q_3 & q_4 & q_5 \end{pmatrix} \cdot x,$$

where q_1, q_2, q_3, q_4, q_5 are given by the same formulas as before with $\mu = 0$.

Finally, we will consider again a numerical solution with the same parameter selection as in the previous simulations. We implement no testing ($\theta = 0$) and set $\tilde{S} = \lim_{t \to \infty} S(t) \approx 0.0358718761871864$. The numeric solutions can bee seen in Figure 5:

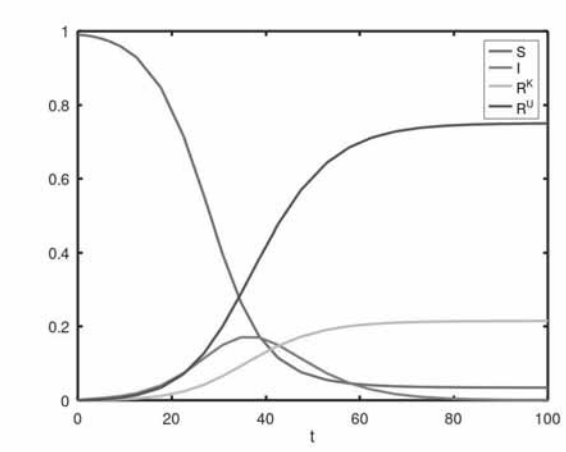

Figure 5: Simulation without demography, without testing.

For this scenario $\mathscr{R}_0 \approx 0.123$ holds.

5 Model without Demography for two Age-groups

Finally, we examine the second model again, which we now expand to include another age group. The respective new infections now no longer depend only on the infected persons of the own age group, but also on those in the other age group, since contacts between population groups are taken into account.

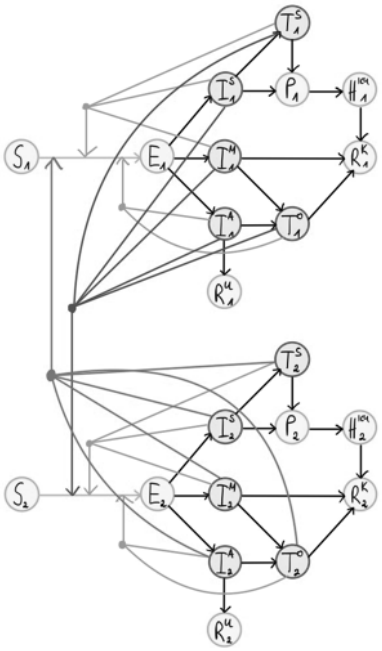

Figure 6: Model with two age groups, without demography.

In Figure 6 we see the mutual influence of the two age groups: The blue and purple arrows describe the influence on the new infections of the other group (orange). The grey arrows indicate the previous influence on the new infections of the own age group.
This extension of the model also changes the differential equation system, which doubles due to the additional compartments of the other age group. The ODE structure is the same for both groups:
We obtain for $i = 1,2$ the ODE system

$$\dot{S}_i = -\sum_{j=1}^{2} \beta_{ij} S_i [I_j^S + I_j^M + I_j^A + T_j^S + T_j^O] \tag{2a}$$

$$\dot{E}_i = \sum_{j=1}^{2} \beta_{ij} S_i [I_j^S + I_j^M + I_j^A + T_j^S + T_j^O] - \gamma E_i \tag{2b}$$

$$\dot{I}_i^S = \pi_i^S \gamma E_i - (\eta^S + \theta_i) I_i^S \tag{2c}$$

$$\dot{I}_i^M = \pi_i^M \gamma E_i - (\eta^M + \theta_i) I_i^M \tag{2d}$$

$$\dot{I}_i^A = \pi_i^A \gamma E_i - (\eta^A + \theta_i) I_i^A \tag{2e}$$

$$\dot{T}_i^S = \theta_i I_i^S - \tau^S T_i^S \tag{2f}$$

$$\dot{T}_i^O = \theta_i [I_i^M + I_i^A] - \tau^O T_i^O \tag{2g}$$

$$\dot{P}_i = \eta^S I_i^S + \tau^S T_i^S - \rho P_i \tag{2h}$$

$$\dot{H}_i^{ICU} = \rho P_i - \sigma H_i^{ICU} \tag{2i}$$

$$\dot{R}_i^K = \eta^M I_i^M + \tau^O T_i^O + \sigma H_i^{ICU} \tag{2j}$$

$$\dot{R}_i^U = \eta^A I_i^A \tag{2k}$$

together with non-negative initial values.
The calculation of the basic reproduction number now becomes a bit more complicated, the structure of the matrices changes a little compared to the second model. As before, due to the missing demography, we have the peculiarity of the non-unique DFE, so again we have to select an arbitrary equilibrium point with $\tilde{S}_1 + \tilde{S}_2 + \tilde{R}_1^K + \tilde{R}_2^K + \tilde{R}_1^U + \tilde{R}_2^U = 1$. In the following calculations, the corresponding placeholders are used again without presenting a detailed calculation option for the missing components as before.
We decompose the x-ODE using

$$\mathscr{F}(x,y) = \begin{pmatrix} \sum_{j=1}^{2} \beta_{1j} S_1 [I_j^S + I_j^M + I_j^A + T_j^S + T_j^O] \\ \sum_{j=1}^{2} \beta_{2j} S_2 [I_j^S + I_j^M + I_j^A + T_j^S + T_j^O] \\ \hline \mathbf{0} \end{pmatrix}$$

and

$$\mathscr{V}(x,y) = \begin{pmatrix} \gamma E_1 \\ \gamma E_2 \\ (\eta^S + \theta_1) I_1^S - \pi_1^S \gamma E_1 \\ (\eta^S + \theta_2) I_2^S - \pi_2^S \gamma E_2 \\ (\eta^M + \theta_1) I_1^M - \pi_1^M \gamma E_1 \\ (\eta^M + \theta_2) I_2^M - \pi_2^M \gamma E_2 \\ (\eta^A + \theta_1) I_1^A - \pi_1^A \gamma E_1 \\ (\eta^A + \theta_2) I_2^A - \pi_2^A \gamma E_2 \\ \tau^S T_1^S - \theta_1 I_1^S \\ \tau^S T_2^S - \theta_2 I_2^S \\ \tau^O T_{1_O}^O - \theta_1 (I_1^M + I_1^A) \\ \tau^O T_2^O - \theta_2 (I_2^M + I_2^A) \end{pmatrix}$$

Both functions have values in $\mathbb{R}^{12}$ and their entry struc-ture is identical to that of the base model.
The big Jacobian matrices are not included, since nothing fundamentally changed in the structure.

The next-generation matrix does not require all entries for the spectral radius, it has the following structure:

$$K = FV^{-1} = \left(\begin{array}{cc|c} \mathscr{R}_{11}^{(S_1,\pi_1)} & \mathscr{R}_{12}^{(S_2,\pi_1)} & \\ \mathscr{R}_{12}^{(S_1,\pi_2)} & \mathscr{R}_{22}^{(S_2,\pi_2)} & \mathbf{0} \\ * & * & \end{array}\right),$$

where

$$\mathscr{R}_{ij}^{(S_k,\pi_l)} = \beta_{ij}\tilde{S}_k \cdot \left(\frac{\pi_l^S}{\eta^S+\theta_l} + \frac{\pi_l^M}{\eta^M+\theta_l} + \frac{\pi_l^A}{\eta^A+\theta_l} + \frac{\pi_l^S}{\eta^S+\theta_l}\frac{\theta_l}{\tau^S} + \frac{\pi_l^M}{\eta^M+\theta_l}\frac{\theta_l}{\tau^O} + \frac{\pi_l^A}{\eta^A+\theta_l}\frac{\theta_l}{\tau^O} \right).$$

Next, K is a 12×12 matrix. For the spectral radius one needs the eigenvalues of K, which in this case must be calculated using the characteristic polynomial. The Laplace expansion for determinants provides:

$$\det(K-\lambda I) = \lambda^{10} \cdot \left[\lambda^2 - \lambda\left(\mathscr{R}_{11}^{(S_1,\pi_1)} + \mathscr{R}_{22}^{(S_2,\pi_2)}\right) + \left(\mathscr{R}_{11}^{(S_1,\pi_1)}\mathscr{R}_{22}^{(S_2,\pi_2)} - \mathscr{R}_{12}^{(S_2,\pi_1)}\mathscr{R}_{12}^{(S_1,\pi_2)}\right)\right]$$

Thus, K has ten times the eigenvalue 0 and the two eigenvalues

$$\frac{\mathscr{R}_{11}^{(S_1,\pi_1)} + \mathscr{R}_{22}^{(S_2,\pi_2)} \pm \sqrt{A}}{2},$$

where

$$A = \left(\mathscr{R}_{11}^{(S_1,\pi_1)} + \mathscr{R}_{22}^{(S_2,\pi_2)}\right)^2 - 4\left(\mathscr{R}_{11}^{(S_1,\pi 1)}\mathscr{R}_{22}^{(S_2,\pi_2)} - \mathscr{R}_{12}^{(S_2,\pi_1)}\mathscr{R}_{12}^{(S_1,\pi_2)}\right).$$

Therefore the basic reproduction number is defined by

$$\mathscr{R}_0 := \frac{\mathscr{R}_{11}^{(S_1,\pi_1)} + \mathscr{R}_{22}^{(S_2,\pi_2)} + \sqrt{A}}{2}.$$

If we start again from just one age group, then the following applies:

$$R := \mathscr{R}_{11}^{(S_1,\pi_1)} = \mathscr{R}_{22}^{(S_2,\pi_2)}, \quad 0 = \mathscr{R}_{12}^{(S_2,\pi_1)} = \mathscr{R}_{12}^{(S_1,\pi_2)}$$

and thus the basic reproduction number simplifies to

$$\mathscr{R}_0 = R,$$

which corresponds to the original $\mathscr{R}_0$ of the second model.

Finally, we see that for several age groups our $\mathscr{R}_0$ depends on the contacts within and between the individual groups, which would have made intuitive sense even without the calculations.

6 Conclusion

Enhancing the compartment model with demography simplifies the computation of the basic reproduction number. In this setting the disease free equilibria is unique. In the model predictive control setting of the original approach in [1] demography can be skipped, the solutions of the initial-value problem are only needed for one week, and demography changes the solutions only slightly. The advice is to skip demography in the model predictive control application if the time horizon is short but to use demography for the computation of the basic reproduction number and the Lyapunov function.

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