BSc report APPLIED MATHEMATICS

"The spread of COVID-19 "

(Dutch title: "De verspreiding van COVID-19 ")

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Preface

Currently we are living in a global pandemic of coronavirus disease 2019 (COVID-19). In this difficult and almost unpredictable time I have had the opportunity to write my final thesis about the spread of this virus. During my bachelor Applied Mathematics I have learned a lot and it was very interesting to apply these mathematical skills to this ongoing worldwide problem. Because there are still many uncertainties about this virus, it was a great challenge to make realistic predictions. If in the future there are more clarities about this virus, the model I have written can be very useful to make us better understand the coronavirus. I hope that this report will help everyone understand the importance of mathematics for worldwide problems.
Special thanks to my supervisor, Mr Vuik, who supported me during this project.

Jurriaan Rutten
Delft, July 2020

Resume

In this report we investigate the spread of the coronavirus 2019 (COVID-19) using mathematical models. We start with a simplified model consisting of a system of three ordinary differential equations and expand it more and more to try to simulate reality. We use Python's **odeint** function to solve these systems numerically. Because a fraction of all infected people will not develop any symptoms, it makes it easy for a virus to spread. Therefore we look at how big the effect asymptomatic people have on spreading the virus. We look at how government measures affect the spread of the virus and thereafter we look at what happens if the government eases the taken measures. We also use MATLAB to analyse the stability of our models and to find solutions to our models using different numerical methods.

"All models are wrong, but some are useful", George Box

Contents

1 Modelling an epidemic

When modelling an epidemic, we use a common technique in Epidemiology: compartmental models[1]. We divide the total population (humans) into a small number of compartments, each containing individuals that are identical in terms of their status of sickness. We analyse and describe the compartmental models for disease transmission. We start with a simplified model.

1.1 The SIR model

The SIR model consist of three compartments:

1. S: Susceptible; Individuals who do not have immunity to the infectious agent (corona in our case), so might become infected when exposed to the virus.
2. I: Infectious; Individuals who are infected and can transmit the virus to susceptible individuals.
3. R: Recovered/Removed; Individuals who are recovered, immune or passed away.

Let us put these compartments in a scheme:

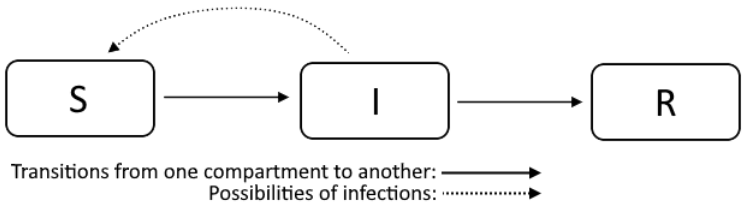


Figure 1

We denote the number of individuals in each compartment at time t with $S(t)$, $I(t)$ and $R(t)$, respectively. The total population size is N, which is equal to $S(t) + I(t) + R(t)$. The amount of individuals in a compartment must be integer but if the total population N is sufficiently large we can treat $S(t)$, $I(t)$ and $R(t)$ as continuous variables. That means we can make a model of differential equations which expresses the dynamics of how each compartment changes over time:

$$\frac{dS}{dt} = -\frac{\beta IS}{N}$$
$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I$$
$$\frac{dR}{dt} = \gamma I$$

[1] Brauer, F. (2008) Compartmental Models in Epidemiology

Now because we do not want to investigate how many individuals there are cumulatively in each compartment, we want each compartment to be a fraction of the total population N. So we make some changes in the variables:

$$S := \frac{S}{N},$$
$$I := \frac{I}{N},$$
$$R := \frac{R}{N}$$

Because N is a constant, we can divide both sides of the equations to obtain the following differential equations:

$$\frac{dS}{dt} = -\beta IS$$
$$\frac{dI}{dt} = \beta IS - \gamma I$$
$$\frac{dR}{dt} = \gamma I$$

In the first equation we can see parameter β. This parameter denotes the transmission rate from compartment S to compartment I: the probability of transmission due to interaction between a person in compartment S and a person in compartment I. In the second equation we see parameter γ which denotes the transmission rate between I and I. This γ has the interpretation that $\frac{1}{\gamma}$ is the average amount of time an individual spends in the infected compartment.
If we add up the differential equations, we find:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

This means that the size of the total population stays the same over time. That is because every individual belongs to a certain compartment and cannot leave the system. With parameters $\beta = 0.35$ and $\gamma = 0.2$, we obtain the following graph:

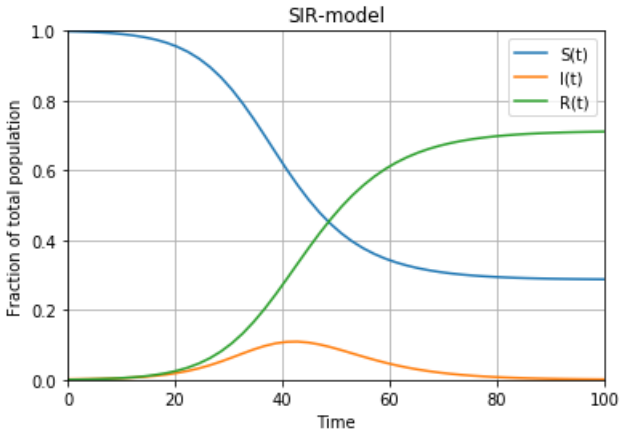


Figure 2: SIR model, with $\beta = 0.35, \gamma = 0.2$

What we can see is that at $t = 0$, $S(0)$ = N and $I(0) = R(0) = 0$. Directly after $t = 0$ an individual gets infected by a virus. That individual infects others and those others infect even more people around them. That is why $S(t)$ is an exponentially decreasing function and $I(t)$ an exponentially increasing function. This implies that the rate of transfer from one compartment to the other is independent of the time spent within the compartment. At $t = 100$ we see that $I(t) \approx 0$ and that $S(t) \approx 0.29$ and $R(t) \approx 0.71$. So again $S(t) + I(t) + R(t) = N$.

1.2 Analysis of the SIR model

Let us have a look at the differential system. If we look at I as a function of S, we can obtain useful results.

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

Now I is only dependent on S. If we integrate the equation we obtain:

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

We can calculate constant C by using the intial values:

$$C = I(0) + S(0) - \frac{\gamma}{\beta} ln(S(0))$$

To find the critical points of function $I(S)$, we set the equation $\frac{dI}{dS}$ equal to zero and find the roots. This is when $S = \frac{\gamma}{\beta}$. Now we want to find out whether this critical point is a maximum, minimum or a saddle point, so we use calculate the second derivative of I with respect to S:

$$\frac{d^2I}{dS^2} = -\frac{\gamma}{\beta S^2}$$

We have that $\frac{d^2I}{dS^2} \leq 0$, because $S^2, \gamma, \beta \geq 0$. So the critical point $S = \frac{\gamma}{\beta}$ is a maximum. Now we can find the maximum of I by filling in the formula:

$$\begin{aligned} I_{max} &= \frac{\gamma}{\beta} ln(\frac{\gamma}{\beta}) - \frac{\gamma}{\beta} + I(0) + S(0) - \frac{\gamma}{\beta} ln(S(0)) \\ &= I(0) + S(0) - \frac{\gamma}{\beta} + \frac{\gamma}{\beta} ln(\frac{\gamma}{\beta} S(0)) \end{aligned}$$

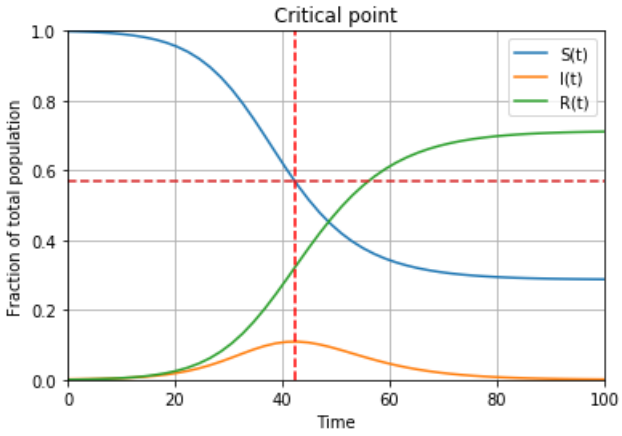


Figure 3: SIR model, with $\beta = 0.35, \gamma = 0.2$

Next we want to determine the stability[2] of the system, so we have to find the equilibrium points. We do this by setting the system of differential equations equal to zero. This means that the 3 compartments do not change over time, hence we will have an equilibrium. If we look at the differential equation we an see that we have an equilibrium point at $I = 0$ and $0 \leq S \leq N$.
Let us rewrite our system of differential equations in a vector form:

$$\frac{d}{d\mathrm{t}}\mathbf{x} = \mathbf{f}(\mathbf{x}), \text{with } \mathbf{x} := \begin{bmatrix} S(t) \\ I(t) \\ R(t) \end{bmatrix}.$$

If $\mathbf{x}^*$ is an equilibrium point then $\mathbf{f}(\mathbf{x}^*) = \mathbf{0}$. We can then take the Taylor expansion of our differential equation:

$$\mathbf{f}(\mathbf{x}) = \mathbf{f}(\mathbf{x}^*) + \mathbf{J}(\mathbf{f}, \mathbf{x}^*)(\mathbf{x} - \mathbf{x}^*) + \cdots,$$

where $\mathbf{J}(\mathbf{f}, \mathbf{x}^*)$ is the Jacobian matrix of partial derivatives, which, in this case, is determined as follows:

$$J(S,I,R) = \begin{bmatrix} \frac{\partial}{\partial S}\frac{dS}{dt} & \frac{\partial}{\partial I}\frac{dS}{dt} & \frac{\partial}{\partial R}\frac{dS}{dt} \\ \frac{\partial}{\partial S}\frac{dI}{dt} & \frac{\partial}{\partial I}\frac{dI}{dt} & \frac{\partial}{\partial R}\frac{dI}{dt} \\ \frac{\partial}{\partial S}\frac{dR}{dt} & \frac{\partial}{\partial I}\frac{dR}{dt} & \frac{\partial}{\partial R}\frac{dR}{dt} \end{bmatrix}.$$

[2]Khasminskii, R (2011) Stochastic Stability of Differential Equations

Our function **f(x)** is now separated into a constant part, a linearized part and the rest terms. We know that the constant part is equal to the zero vector. So now we only have to solve:

$$\frac{d}{d\mathrm{t}}\mathbf{x} = \mathbf{J}(\mathbf{f}, \mathbf{x}^*)(x - x^*),$$

which is a linear differential equation, where the solutions depend on the eigenvalues of the Jacobian. The solutions are a linear combination of separate $e^{\lambda_j t}$'s. So if we have an eigenvalue that is positive, the solutions move away from the equilibrium point and the point is therefore unstable. If all the eigenvalues have negative real parts, then the equilibrium point is stable.
If we look at the Jacobian of our system, we get:

$$J(S,I,R) = \begin{bmatrix} -\beta I & -\beta S & 0 \\ \beta I & \beta S - \gamma & 0 \\ 0 & \gamma & 0 \end{bmatrix}.$$

By substituting the values of our equilibrium point we obtain

$$J(S_0,0,R) = \begin{bmatrix} 0 & -\beta S & 0 \\ 0 & \beta S - \gamma & 0 \\ 0 & \gamma & 0 \end{bmatrix},$$

where the determinant of the matrix $(J(S,0,R) - \lambda I)$ is

$$\det(J(S,0,R) - \lambda I) = -\lambda(-\lambda(\beta S - \gamma - \lambda)) = \lambda^2(\beta S - \gamma - \lambda).$$

Setting the equation equal to zero gives us:

$$\lambda^2(\beta S - \gamma - \lambda) = 0,$$

so $\lambda_{1,2} = 0$ or $\lambda_3 = \beta S - \gamma$. We notice that we have three eigenvalues that are all real. The third eigenvalue λ_3 is positive if $\beta S > \gamma$ and negative if $\beta S < \gamma$. We know now that if an epidemic occurs, then $\frac{dI}{dt}$ is greater than zero only if $S > \frac{\gamma}{\beta}$. From this we can determine that λ_3 is positive and the equilibrium point is unstable.

1.3 The contact rate

When modelling an infectious disease, the extent to which people have contact with each other is a very important aspect to include in your model. At meetings, supermarkets or sport-events a virus can easily spread among people. Therefore the government must take action to prevent the virus from spreading. An average contact rate[3] under normal circumstances in a country is around $c_0 = 14$. Now we can make β smaller and $c_0 \cdot \beta$ becomes the effective contact rate: There is interaction between 2 individuals, and one infects the other.
When an epidemic is emerging, all the governments around the world will take health measures: People who have the virus, or have symptoms go into quarantine; stay at

[3] Mixing Patterns Between Age Groups Using Social Networks, Research Gate, 2006

home as much as possible, or eventually a lock down. Because of these health measures, the contact rate will decrease and will not be constant anymore. Let $c(0) = c_0$ be the contact rate at initial time and $\lim_{t\to\infty} c(t) = c_b$ be the minimum contact rate. Let r_1 be the exponential decreasing rate of the contact rate. Then we can make the following formula for the contact rate[4]:

$$c(t) = (c_0 - c_b)e^{-r_1 t} + c_b$$

We add the contact rate to our system of differential equations, so our SIR model will look like this:

$$\begin{aligned}
\frac{dS}{dt} &= -\beta c(t) IS \\
\frac{dI}{dt} &= \beta IS c(t) - \gamma I \\
\frac{dR}{dt} &= \gamma I
\end{aligned}$$

Now we make two new plots: The SIR-model with constant contact rate, and the SIR-model with a continuous decreasing contact rate:

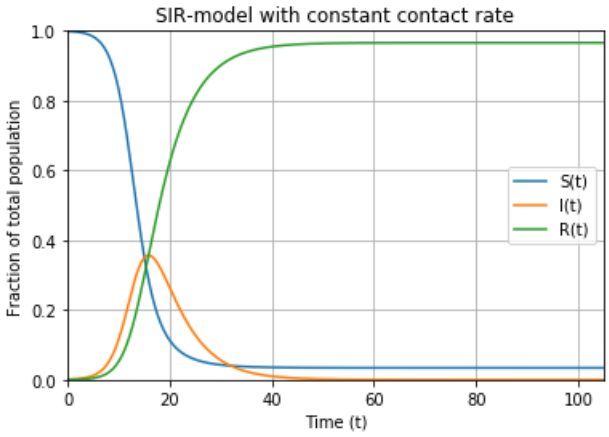


Figure 4: $\beta = 0.35, \gamma = 0.2$

[4] An updated estimation of the risk of transmission of the novel coronavirus (2019-nCov), 2020

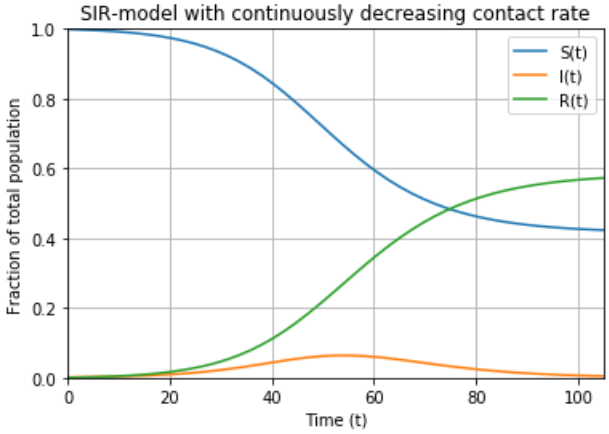


Figure 5: $\beta = 0.35, \gamma = 0.2$

We can see in figure 4 that if the government does not take any measures, so that the contact rate remains constant, almost the whole population would get infected. This can be seen from the fraction of the population that end up in the recovered compartment, R. When the government does take measures, we can see in figure 5 that a much smaller fraction of the population will end up in the recovered compartment. So far fewer people would get infected.

1.4 Basic reproduction number

When we want to predict the spread of a virus, we want to find the basic reproduction number[5]. This is the number of new infections induced by a single infected individual during his/her infectious period per day. In the beginning of an epidemic this number is above one: More people get infected than people go to the recovered compartment. This is because there are not taken any measures yet to prevent the virus from spreading. To find the formula for the basic reproduction number we just have to think logically: If the people that are in the infectious compartment infect an average of βc_0 people per unit time, and the time that is spent in the infectious compartment is equal to $\frac{1}{\gamma}$, then basic reproduction number, $\mathscr{R}_0$ is equal to:

$$\mathscr{R}_0 = \left(\frac{\beta c_0}{\gamma}\right) S_0 \tag{1}$$

As mentioned before, at the start of an epidemic the basic reproduction number will be higher than one. So a single person can infect more than one other persons on a single day. Then those newly infected individuals can also infect more people per person. Therefore, of course, the aim is to bring $\mathscr{R}_0$ below one, so that on a single day one person cannot infect more than other person.

[5]Dietz, K. (1993). The estimation of the basic reproduction number for infectious diseases

We can see in formula 1 that if we let the contact rate decrease continuously, $\mathscr{R}_0$ will get smaller and smaller. Now we want to be able to calculate the basic reproduction number at any time t. This is called the effective reproduction number. We use the continuous contact rate, $c(t)$, and the amount of people in compartment S at time t, $S(t)$, to obtain the following formula for the effective reproduction number:

$$\mathscr{R}_t = \left(\frac{\beta c(t)}{\gamma}\right) S(t)$$

We can see in figure 6 that by letting the contact rate decrease, the reproduction rate will fall below 1.

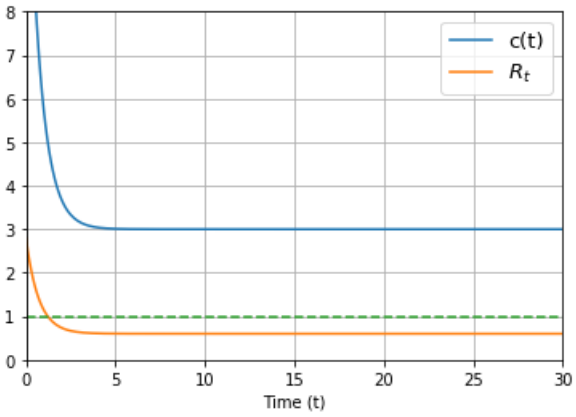


Figure 6: Contact rate vs. basic reproduction number

2 Incubation period and Asymptomatic Individuals

The incubation period is the period after being exposed to the virus and before having symptoms. The individual does not know that he/she has the virus, but a few days before having symptoms he/she is already able to infect others. For the coronavirus the incubation period is 7 days on average[6]. The last 2 days of this period an individual becomes contagious while not knowing he/she is[7]. In these 2 days a person will continue with his daily life. That makes it very easy for the virus to spread.
Another easy way for a virus to spread is via asymptomatic individuals. These individuals are contagious but are not showing symptoms. If we look at the start of the spread of the virus in Noord-Brabant there was only 1 person sick showing symptoms. This person had to stay at home immediately. So only the last 3 days of his incubation period he was able to spread the virus. But after a while the epidemic emerged in Noord-Brabant. In other cities and villages people started showing symptoms. But this went so fast that it is unbelievable that this man was the only cause of the emerge. Probably a few people without symptoms spread the virus without knowing that.
With these 2 easy ways for a virus to spread it is very important to include these in our model. Let us expand our SIR model.

2.1 The SEPIAR model

We introduce three new compartments:

1. E: Exposed, not contagious; People exposed by the virus but not yet contagious.
2. P: Presymptomatic; People that are contagious but not yet showing symptoms.
3. A: Asymptomatic; Infectious people that passed the incubation period but will not show any symptoms

At the next page we show what our compartmental scheme looks like after including the new compartments:

[6]The Incubation Period of Coronavirus Disease 2019 (COVID-19) From Publicly Reported Confirmed Cases, 2020

[7]The Incubation Period of Coronavirus Disease 2019 (COVID-19) From Publicly Reported Confirmed Cases, 2020

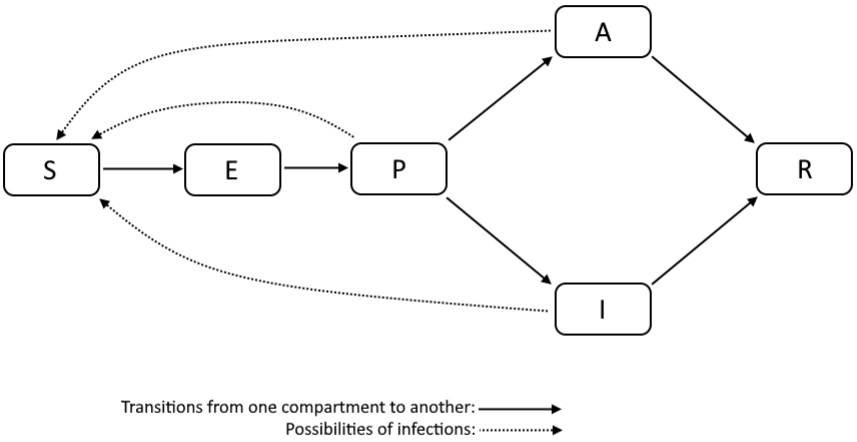


Figure 7

With this scheme we can make the following system of differential equations which expresses the dynamics of how each compartment changes over time:

$$\begin{aligned}
\frac{dS}{dt} &= -\beta c(t) S(I + \theta A + \theta P) \\
\frac{dE}{dt} &= \beta c(t) S(I + \theta A + \theta P) - \varepsilon E \\
\frac{dP}{dt} &= \varepsilon E - \sigma P \\
\frac{dI}{dt} &= \sigma \rho P - \gamma_I I \\
\frac{dA}{dt} &= \sigma (1 - \rho) P - \gamma_A A \\
\frac{dR}{dt} &= \gamma_I I + \gamma_A A
\end{aligned}$$

The sum of these equations is again equal to 0 and as we can see we have a few more parameters. Because people in the compartments A and P do not have the symp-

toms like coughing and sneezing, it is more difficult for them to infect others. So in the first differential equations we multiply A and P with $0 < \theta \leq 1$.
The average time people spend in the E compartment is $\frac{1}{\varepsilon}$ and the average time people spend in the P compartment is $\frac{1}{\sigma}$.
The probability of having symptoms among infected individuals is ρ.
The time spent in the I and A compartments is $\frac{1}{\gamma_I}$ and $\frac{1}{\gamma_A}$ respectively.The parameter γ_A will be smaller than γ_I because people with symptoms will take more rest and live more healthy when they get sick.

2.2 Different initial conditions

We know that how an epidemic proceeds depends on very many things, like all the parameters we have discussed so far: If the probability of getting infected when having contact with somebody is very high, it will definitely be a very dangerous epidemic. But what differences can the initial conditions make? Let us have a look at what happens in our model for different values of E at $t = 0$.
In figures 8 to 11 we see that increasing the fraction of exposed people at $t = 0$ has a noticeable change in the behaviour of the graphs. When $E(0)$ is smaller, the disease will take longer to peak, but also lasts longer than for higher values of $E(0)$. But we can see in figure 11, that higher values for $E(0)$ do not mean that a lot more people get contaminated relatively. With $E(0) = 0.0004$ and $E(0) = 0.04$ differing a factor 100, the fraction of people that end up in the recovered compartment only increases by approximately 1%. But as we can see in figures 9 and 10 is that the pandemic peaks a lot earlier. This means the world has much less time to prepare for the peak and find a vaccine.

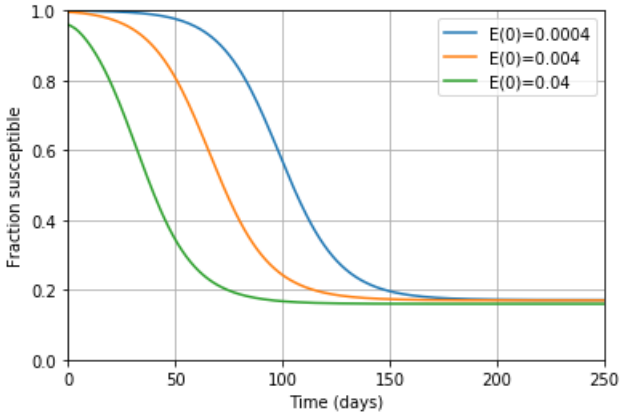


Figure 8

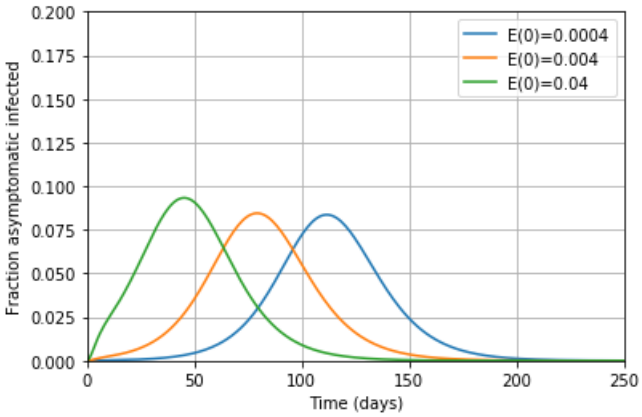


Figure 9

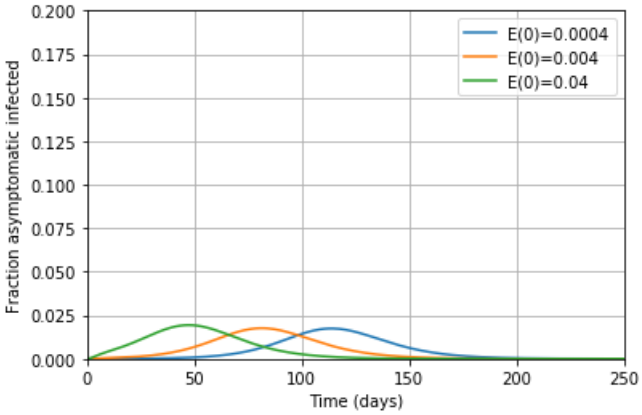


Figure 10

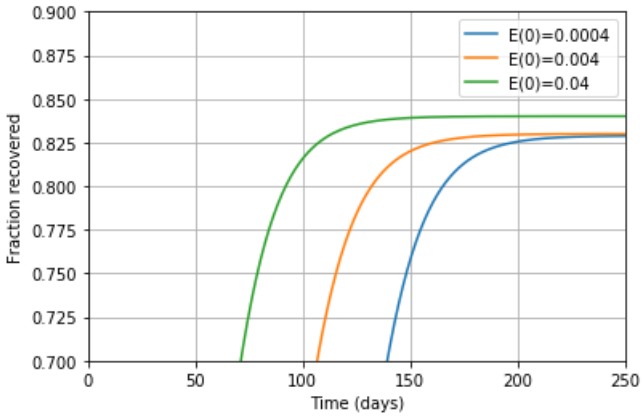


Figure 11

2.3 Infections by A and P

People that are asymptomatic or are in the last days of their incubation period, compartments A and P respectively, can infect others without knowing. This is one of the dangerous aspects of the spread of a virus. If we do not take into account that asymptomatic and presymptomatic people are contagious, we would get a completely wrong picture of how fast the virus is spreading at any moment. Let us look what would happen in Noord-Brabant if include and exclude the possibilities of infections by individuals without symptoms, A and P:

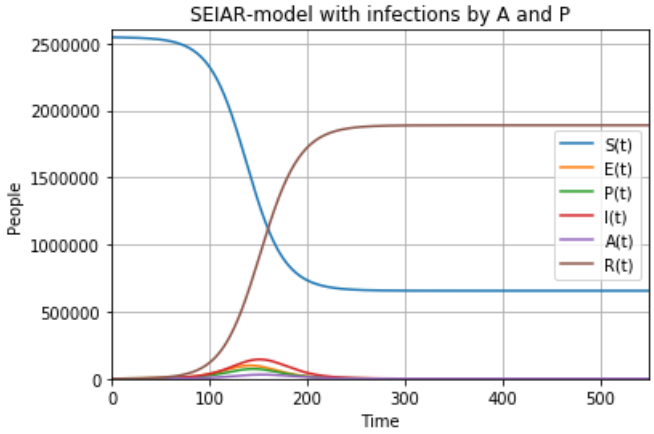


Figure 12

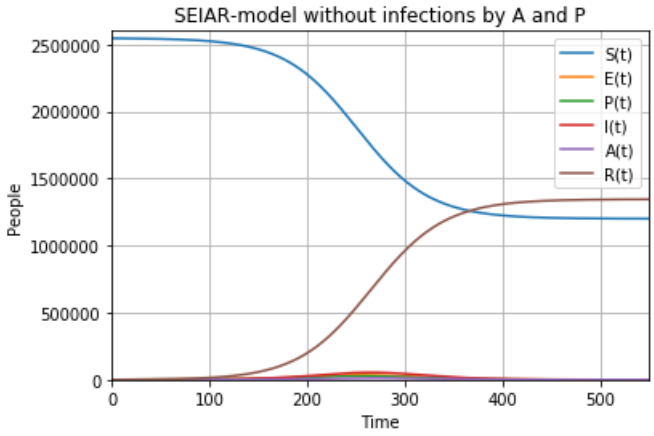


Figure 13

We can see in figure 13 that $\pm$ 0.6 million less individuals end up in the recovered compartment than in figure 12. This means that excluding the fact that people in these two compartments can infect others gives us a very bad estimate of the amount of infected people each day. The only solution to this problem is to test as many people as possible so that we can pick out the people that asymptomatic or presymptomatic and put them into quarantine.

2.4 Equilibrium and stability

Let us have a look at the stability[8] of our model and search for the equilibrium points. Again we have to find the values for the variables for which the system does not change over time, so the values that give: $\frac{dS}{dt} = \frac{dE}{dt} = \frac{dP}{dt} = \frac{dI}{dt} = \frac{dA}{dt} = \frac{dR}{dt} = 0$. We see that there is an equilibrium if we have the following values for S, E, P, I, A and R:

$$\mathbf{x}^* := \begin{bmatrix} S(t) \\ E(t) \\ P(t) \\ I(t) \\ A(t) \\ R(t) \end{bmatrix} = \begin{bmatrix} S \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \tag{2}$$

If we fill in this values in the differential equations we see that $\frac{dS}{dt} = \frac{dE}{dt} = \frac{dP}{dt} = \frac{dI}{dt} = \frac{dA}{dt} = \frac{dR}{dt} = 0$, indeed. This means that $\mathbf{x}^*$ is an equilibrium point. Now we will look at the stability of this point. We do this in the same way as in section 2. We write

[8] Khasminskii, R (2011) Stochastic Stability of Differential Equations

our system of differential equations in a vector form:

$$\frac{d}{dt}\mathbf{x} = \mathbf{f}(t,\mathbf{y}), \text{ with } \mathbf{x} := \begin{bmatrix} S(t) \\ E(t) \\ P(t) \\ I(t) \\ A(t) \\ R(t) \end{bmatrix}$$

Now we take the Taylor-expansion of our system of differential equations, with the Jacobian matrix being:

$$J(S,E,P,I,A,R) = \begin{bmatrix} \frac{\partial}{\partial S}\frac{dS}{dt} & \frac{\partial}{\partial E}\frac{dS}{dt} & \frac{\partial}{\partial P}\frac{dS}{dt} & \frac{\partial}{\partial I}\frac{dS}{dt} & \frac{\partial}{\partial A}\frac{dS}{dt} & \frac{\partial}{\partial R}\frac{dS}{dt} \\ \frac{\partial}{\partial S}\frac{dE}{dt} & \frac{\partial}{\partial E}\frac{dE}{dt} & \frac{\partial}{\partial P}\frac{dE}{dt} & \frac{\partial}{\partial I}\frac{dE}{dt} & \frac{\partial}{\partial A}\frac{dE}{dt} & \frac{\partial}{\partial R}\frac{dE}{dt} \\ \frac{\partial}{\partial S}\frac{dP}{dt} & \frac{\partial}{\partial E}\frac{dP}{dt} & \frac{\partial}{\partial P}\frac{dP}{dt} & \frac{\partial}{\partial I}\frac{dP}{dt} & \frac{\partial}{\partial A}\frac{dP}{dt} & \frac{\partial}{\partial R}\frac{dP}{dt} \\ \frac{\partial}{\partial S}\frac{dI}{dt} & \frac{\partial}{\partial E}\frac{dI}{dt} & \frac{\partial}{\partial P}\frac{dI}{dt} & \frac{\partial}{\partial I}\frac{dI}{dt} & \frac{\partial}{\partial A}\frac{dI}{dt} & \frac{\partial}{\partial R}\frac{dI}{dt} \\ \frac{\partial}{\partial S}\frac{dA}{dt} & \frac{\partial}{\partial E}\frac{dA}{dt} & \frac{\partial}{\partial P}\frac{dA}{dt} & \frac{\partial}{\partial I}\frac{dA}{dt} & \frac{\partial}{\partial A}\frac{dA}{dt} & \frac{\partial}{\partial R}\frac{dA}{dt} \\ \frac{\partial}{\partial S}\frac{dR}{dt} & \frac{\partial}{\partial E}\frac{dR}{dt} & \frac{\partial}{\partial P}\frac{dR}{dt} & \frac{\partial}{\partial I}\frac{dR}{dt} & \frac{\partial}{\partial A}\frac{dR}{dt} & \frac{\partial}{\partial R}\frac{dR}{dt} \end{bmatrix}.$$

If we calculate all partial derivatives and thereafter fill in our values of the variables for our equilibrium point $\mathbf{x}^*$ in the Jacobian matrix, we obtain:

$$J(S,E,P,I,A,R) = \begin{bmatrix} 0 & 0 & -\beta c_0 \theta S & -\beta c_0 S & -\beta c_0 \theta S & 0 \\ 0 & -\varepsilon & \beta c_0 \theta S & \beta c_0 S & \beta c_0 \theta S & 0 \\ 0 & \varepsilon & -\sigma & 0 & 0 & 0 \\ 0 & 0 & \sigma\rho & -\gamma_I & 0 & 0 \\ 0 & 0 & \sigma(1-\rho) & 0 & -\gamma_A & 0 \\ 0 & 0 & 0 & \gamma_I & \gamma_A & 0 \end{bmatrix}$$

If we fill in the values of the parameters we can calculate the eigenvalues of the matrix. We find 6 eigenvalues:

$$\begin{aligned} \lambda_1 &= 0 \\ \lambda_2 &= 0 \\ \lambda_3 &\approx 0.3445 \\ \lambda_4 &\approx -0.5334 + 0.2008\mathbf{i} \\ \lambda_5 &\approx -0.5334 - 0.2008\mathbf{i} \\ \lambda_6 &\approx -0.1038 \end{aligned}$$

We have one positive eigenvalue, λ_3, hence the equilibrium point is unstable.

Let us now have a look at the same graph again, but now with each compartment being a fraction of 1:

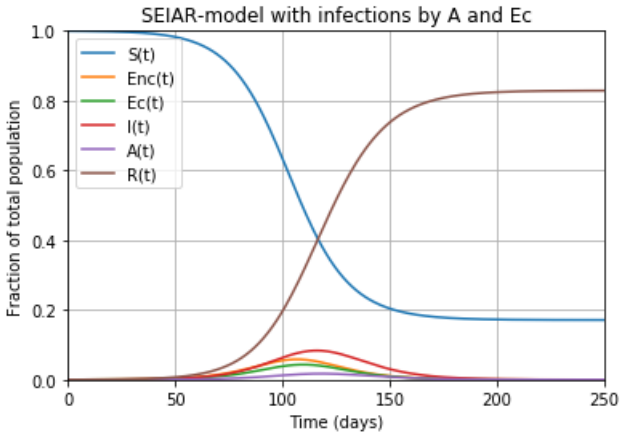


Figure 14: SEIAR model, with $\beta = 0.08$, $\theta = 0.7$, $\gamma_I = \frac{1}{7}$, $\gamma_A = \frac{1}{7}$, $\varepsilon = \frac{1}{4}$, $\sigma = \frac{1}{3}$,$\rho = 0.8$

We can see that from $t = 200$ the fraction of the amount of people in each compartment does not vary much anymore. This means we have another equilibrium point which seems to be stable. But this equilibrium point has other values for the compartments than equilibrium point $\mathbf{x}^*$. We cannot solve this analytically, so we have to approach this point numerically. We can use the function **fsolve** in MATLAB and use an estimate of the equilibrium values for $S(t), E(t), P(t), I(t), A(t)$ and $R(t)$ to calculate the exact values for this equilibrium point. If we look at the figure we estimate the following values for $t = 200$:

$$\mathbf{y}^* = \begin{bmatrix} S(t) \\ E(t) \\ P(t) \\ I(t) \\ A(t) \\ R(t) \end{bmatrix} \approx \begin{bmatrix} 0.17 \\ 0.0005 \\ 0.0005 \\ 0.002 \\ 0.0005 \\ 0.81 \end{bmatrix} \tag{3}$$

The function **fsolve** will search for the closest equilibrium point to our estimate. We find the following values for our equilibrium point $\mathbf{y}^*$:

$$\mathbf{y}^* = \begin{bmatrix} S(t) \\ E(t) \\ P(t) \\ I(t) \\ A(t) \\ R(t) \end{bmatrix} = \begin{bmatrix} 0.1799 \\ 3.90 \cdot 10^{-4} \\ 3.87 \cdot 10^{-4} \\ 0.001 \\ 3.54 \cdot 10^{-4} \\ 0.81 \end{bmatrix} \tag{4}$$

Now we can fill in the values of $\mathbf{y}^*$ in our Jacobian matrix and calculate the eigenvalues to look at the stability of this equilibrium point. We find the following eigenvalues:

$$\lambda_1 = 0$$
$$\lambda_2 \approx -0.3304 + 0.0845\mathbf{i}$$
$$\lambda_3 \approx -0.3304 - 0.0845\mathbf{i}$$
$$\lambda_4 \approx -0.1057$$
$$\lambda_5 \approx -0.0595$$
$$\lambda_6 \approx -0.0006$$

As we can see, the real parts of all the $\lambda_i's$ are ≤ 0 which means this equilibrium point is stable.

2.5 The reproduction number

Let us derive the basic reproduction number[9] from our system of differential equations. To do this, we need to find the so called 'next-generation matrix'. In our system we have got 8 compartments. Five of these compartments are the 'infected' compartments: E,P,I and A. Now let $x_i, i = 1,2,..,4$ be the fraction of the population in the i^{th} infected compartment at time t. We can rewrite the differential equations of these 4 infected compartments as:

$$\frac{dx_i}{dt} = F_i(x) - V_i(x), \text{ where } V_i(x) = \left[V_i^-(x) - V_i^+(x)\right] \tag{5}$$

In these equations $F_i(x)$ represents the rate of appearance of new infections in compartment i. $V_i^+(x)$ represents the rate of transfer of individuals into compartment i by all other means, and $V_i^-(x)$ represents the rate of transfer of individuals out of compartment i. Now we can rewrite equation 5 as:

$$\frac{dx}{dt} = F(x) - V(x),$$

where

$$F(x) = \left(F_1(x), \quad \dots \quad , F_4(x)\right)^T$$

and

$$V(x) = \left(V_1(x), \quad \dots \quad , V_4(x)\right)^T$$

Now F and V are 4×4 matrices, defined as

$$F = \frac{\partial F_i}{\partial x_j}(x_0) \text{ and } V = \frac{\partial V_i}{\partial x_j}(x_0)$$

and FV^{-1} is known as the next-generation matrix. The largest eigenvalue of this matrix is equal to the basic reproduction number of our model.

[9] Jones, J (2007) Notes on R_0

Let us find the next-generation matrix of our model. As mentioned earlier, we only need the following differential equations:

$$\begin{aligned}
\frac{dE}{dt} &= \beta c(t) S(I + \theta A + \theta P) - \varepsilon E \\
\frac{dP}{dt} &= \varepsilon E - \sigma P \\
\frac{dI}{dt} &= \sigma \rho P - \gamma_I I \\
\frac{dA}{dt} &= \sigma(1-\rho) P - \gamma_A A
\end{aligned}$$

First we derive the 4×4 matrix F. We see that new infections only occur in the first equation $\frac{dE}{dt}$. Infections by people that are presymptomatic (P), have symptoms (I) or are asymptomatic (A) happen with a rate of $\beta c(t)\theta$, $\beta c(t)$ and $\beta c(t)\theta$ respectively. We obtain:

$$F = \begin{pmatrix} 0 & \beta c(t)\theta & \beta c(t) & \beta c(t)\theta \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

Second we derive the 4×4 matrix V. When we look at the first equation $\frac{dE}{dt}$, we see that there only is a rate of transfer of individuals going out of compartment E: ε. (Remind that we do not look at new infections now). In the second equation, $\frac{dP}{dt}$ we see that there is a rate of transfer of individuals going into compartment P and going out of compartment P, ε and σ respectively. We do the same for the last 2 differential equations and obtain 4×4 matrix V:

$$V = \begin{pmatrix} \varepsilon & 0 & 0 & 0 \\ -\varepsilon & \sigma & 0 & 0 \\ 0 & -\sigma\rho & \gamma_I & 0 \\ 0 & -\sigma(1-\rho) & 0 & \gamma_A \end{pmatrix}$$

We take the inverse of V and find:

$$V^{-1} = \begin{pmatrix} \frac{1}{\varepsilon} & 0 & 0 & 0 \\ \frac{1}{\sigma} & \frac{1}{\sigma} & 0 & 0 \\ \frac{\rho}{\gamma_I} & \frac{\rho}{\gamma_I} & \frac{1}{\gamma_I} & 0 \\ \frac{1-\rho}{\gamma_A} & \frac{(1-\rho)}{\gamma_A} & 0 & \frac{1}{\gamma_A} \end{pmatrix}$$

We multiply F and V^{-1}:

$$FV^{-1} = \begin{pmatrix} \frac{\beta c(t)\theta(1-\rho)}{\gamma_A} + \frac{\beta c(t)\theta}{\sigma} + \frac{\beta c(t)\rho}{\gamma_I} & \cdots & \cdots & \cdots \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

Now we solve the following equation for the eigenvalues of FV^{-1}

$$det(FV^{-1} - \lambda I) = 0$$

and find that the basic reproduction number of our model, which is equal to the largest eigenvalue λ of FV^{-1}, is

$$\mathscr{R}_t = max\{\lambda_i\} = \frac{\beta c(t)\theta}{\sigma} + \frac{\beta c(t)\rho}{\gamma_I} + \frac{\beta c(t)\theta(1-\rho)}{\gamma_A}$$

2.6 Easing the measures

In the last months, all governments around the world has taken measures to control the spread of the virus. People had to stay at home as much as possible and many activities were cancelled. In the most countries this had a positive effect and the reproduction rate dropped below one. Now many countries are planning to ease the measures in the following months. The Netherlands started taking measures in early March. People were allowed to see a maximum of 3 persons from different households and always had to stay 1.5 meter away from each other. The latter measure still holds but people are now allowed to be in bigger groups, with a maximum of 10 individuals. The government plans to ease the measures a little bit more at the first of June, so that people are allowed to be in groups of maximum 30 individuals. At the first of July, people may be allowed to be in groups of maximum 100 individuals and from then on the government will look at how the progress continues.
But how do we know that there will not be a second wave of infections? And is it not to early to ease the measures?
We already defined the contact rate as the number of contacts per person on a day in an earlier section. We said that this rate was approximately equal to 14 under normal circumstances. We also defined the basic/effective reproduction ratio. This is one of the most important aspects to look at when thinking about easing the measures. We found that in our current model the basic reproduction number is equal to:

$$\mathscr{R}_t = \frac{\beta c(t)\theta}{\sigma} + \frac{\beta c(t)\rho}{\gamma_I} + \frac{\beta c(t)\theta(1-\rho)}{\gamma_A}, \tag{6}$$

with $\beta = 0.032$, $\rho = 0.78$, $\theta = 0.1$, $\gamma_I = \frac{1}{7}$, $\gamma_A = \frac{1}{7}$, $\sigma = \frac{1}{2}$, $S_0 \approx 1$ and c(t) the contact rate at time t.
Let us now have a look at different scenarios about the contact rate. We put the 27'th of February as $t = 0$, the day the Netherlands had her first confirmed case of COVID-19. If we fill in the formula for the basis reproduction ratio, we find that $\mathscr{R}_0 \approx 2.68$. Two weeks later the government announced a lock-down and as a consequence of a very fast growth of people getting infected. All people must stay 1.5 meter away from each other. If everybody strictly adheres to the rules the contact rate will decrease from approximately 14 to approximately 2, which is actually almost impossible. Then the reproduction ratio, with $c(t) \approx 2$, falls below 1 and is approximately equal to 0.683 which means the virus will die out. From the 11th of May, people are allowed to go outside for certain reasons like (no contact) sports and haircuts, the contact rate

increases a bit. From the first of June, after 94 days, the government wants to ease some measures. People are allowed to be in groups of max. 30 people. This means the contact rate will increases. The government has planned to ease it even more from the first of July,to allow people to be in groups of max. 100 people. Again the contact rate will increases. From then on the government will see how it progresses to perhaps ease the measures even more from the first of September.
Let us fix some times at which the government took/takes measures. We know already know the contact rates for t_0 and t_1:

t_0	t=0	$\Delta t = 0$	27 February	c(t) = 14
t_1	t=14	$\Delta t = 14$	11 March	c(t) = 2
t_2	t=74	$\Delta t = 60$	11 May	
t_3	t=94	$\Delta t = 20$	1 June	
t_4	t=124	$\Delta t = 30$	1 July	
t_5	t=184	$\Delta t = 60$	1 September	

With this being set, we can look at different contact rates for different scenarios regarding the number of exposed people.
In the following 6 figures we can see that if the government eases the measures slowly and everyone adheres strictly to the rules that the virus will die out. This makes sense because with contact rate equal 2,3,4 or 5 (at any time) the effective reproduction ratio is ≤ 1:

1. The government does not ease the measures and everybody strictly adheres the rules.

	$t \leq t_1$	$t_1 < t \leq t_2$	$t_2 < t \leq t_3$	$t_3 < t \leq t_4$	$t_4 < t \leq t_5$	$t_5 < t$
c(t)	14	2	2	2	2	2

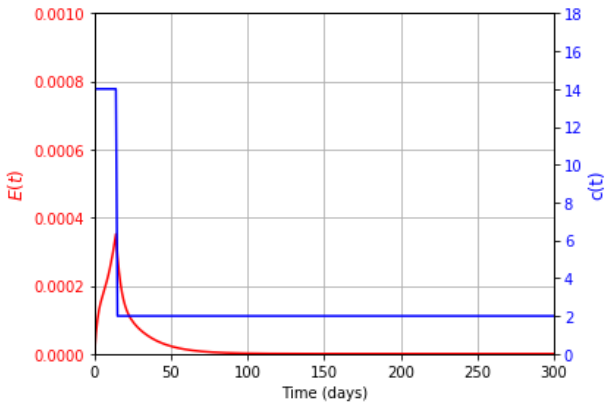


Figure 15

2. The government eases the measures a little bit only at t_2.

	$t \leq t_1$	$t_1 < t \leq t_2$	$t_2 < t \leq t_3$	$t_3 < t \leq t_4$	$t_4 < t \leq t_5$	$t_5 < t$
c(t)	14	2	3	3	3	3

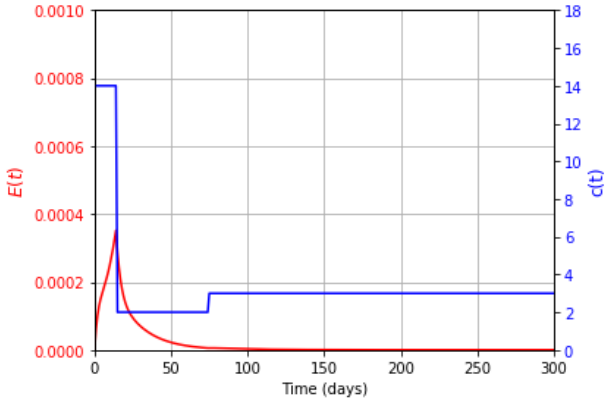


Figure 16

3. The government eases the measures at t_2 and at t_3

	$t \leq t_1$	$t_1 < t \leq t_2$	$t_2 < t \leq t_3$	$t_3 < t \leq t_4$	$t_4 < t \leq t_5$	$t_5 < t$
c(t)	14	2	3	4	4	4

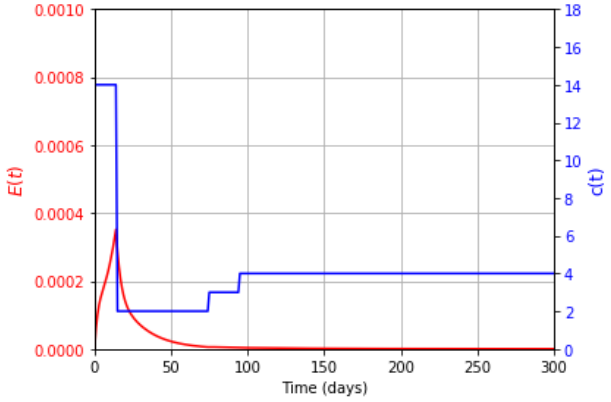


Figure 17

4. The government eases the measures at t_2, t_3 and at t_4

	$t \leq t_1$	$t_1 < t \leq t_2$	$t_2 < t \leq t_3$	$t_3 < t \leq t_4$	$t_4 < t \leq t_5$	$t_5 < t$
c(t)	14	2	3	4	5	5

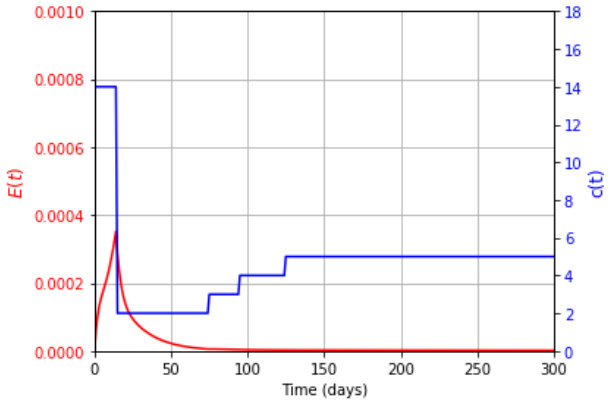


Figure 18

5. The government eases the measures at t_2, t_3, t_4 and at t_5. If we adjust the scale of the y-axis of $E(t)$, we can see that at t_5, when $c(t_5) = 6$, the function $E(t)$ slowly begins to increase again. This is because the effective reproduction ratio for $c(t_5) = 6$ is greater than 1, namely ≈ 1.146.

	$t \leq t_1$	$t_1 < t \leq t_2$	$t_2 < t \leq t_3$	$t_3 < t \leq t_4$	$t_4 < t \leq t_5$	$t_5 < t$
c(t)	14	2	3	4	5	6

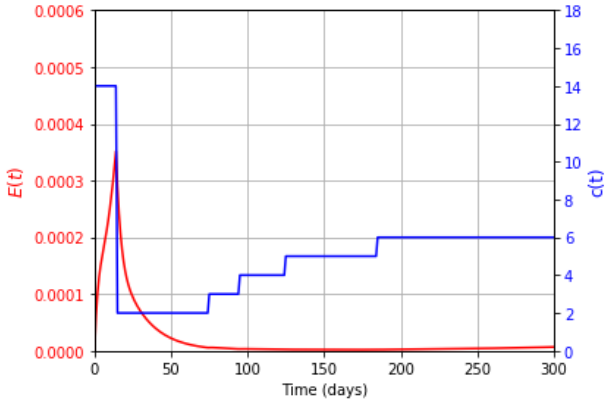


Figure 19

6. In the next figure (18), we can see that if the government waits with easing the measures until t_5 and everybody adheres strictly to the rules that the virus has died out after 150 days. This means people can go back to normal life.

	$t \leq t_1$	$t_1 < t \leq t_2$	$t_2 < t \leq t_3$	$t_3 < t \leq t_4$	$t_4 < t \leq t_5$	$t_5 < t$
c(t)	14	2	2	2	2	14

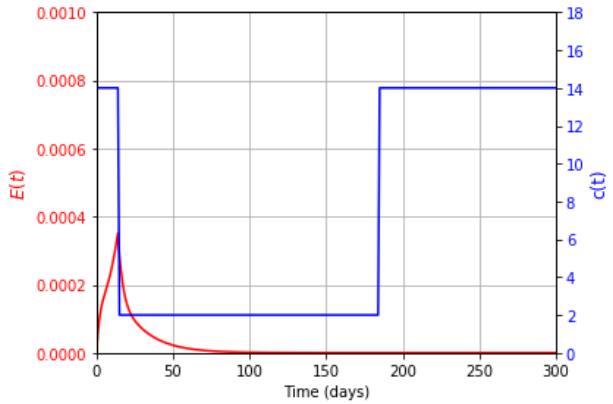


Figure 20

In the last 6 figures we saw what theoretically would have happened if the government would ease the measures and everybody kept 1.5 meter away from each other. In following figures we will see examples of what possibly could go wrong in real life.

7. The government has eased the measures too much at t_2,t_3 and at t_4.

	$t \leq t_1$	$t_1 < t \leq t_2$	$t_2 < t \leq t_3$	$t_3 < t \leq t_4$	$t_4 < t \leq t_5$	$t_5 < t$
c(t)	14	2	4	6	8	8

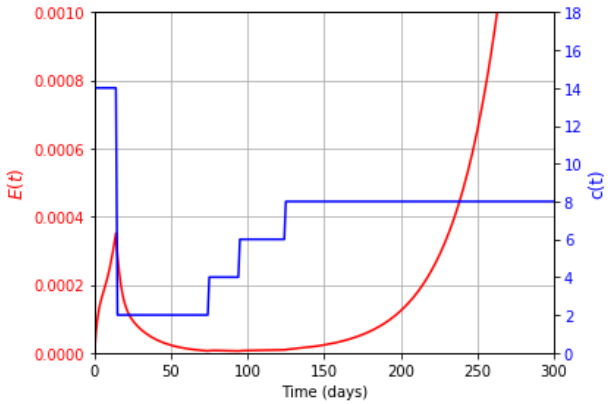


Figure 21

8. The government says that people are allowed to be in groups of 30, but people do not follow the rules of social distancing. After a while, measures are taken and the country goes back into lock-down.

	$t \leq t_1$	$t_1 < t \leq t_2$	$t_2 < t \leq t_3$	$t_3 < t \leq t_4$	$t_4 < t \leq t_5$	$t_5 < t$
c(t)	14	2	6	8	8	2

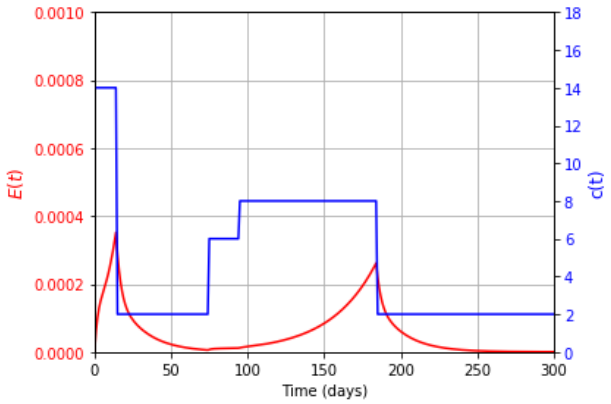


Figure 22

9. People do not follow the rules anymore and again measures are taken and everybody must go back into lock-down.

	$t \leq t_1$	$t_1 < t \leq t_2$	$t_2 < t \leq t_3$	$t_3 < t \leq t_4$	$t_4 < t \leq t_5$	$t_5 < t$
c(t)	14	2	6	10	12	2

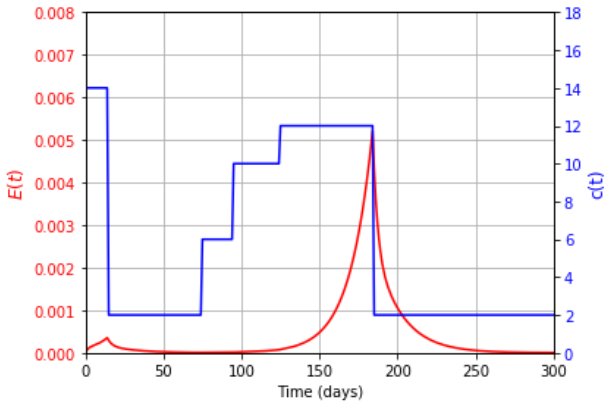


Figure 23

What we can see in figures 15-23, that we are living in a very difficult time: If the country stays in lock-down for a very long time, the coronavirus will eventually die out, but the economy of the Netherlands will get worse and worse. And if the governments decides to ease, there will be a big chance that we will end up in a second wave of the coronavirus.

3 Expanding the model

In the Netherlands, when an individual starts developing symptoms of the coronavirus, he/she has to be quarantined for a minimum of two weeks. When in quarantine, it is very unlikely that this person infects many people. Only his family or roommate(s) have the chance of getting infected. Then we also have people who have very mild symptoms and may not even realise they have the virus. Those people do not go into quarantine and keep going to the supermarkets etc.

3.1 The SEPIMAQR model

When in quarantine, it is very unlikely that this person infects many people. Only his family or roommate(s) have the chance of getting infected. From now on we assume that a person that is quarantined cannot not infect others. These persons go to a new compartment, Q; Quarantined and cannot infect others. Because the symptoms start small, for example with a cough or sneezing a few times, people do not immediately think they have the virus, so keep going out and infect people without knowing that. This means that people will not go into quarantine directly after their incubation period. Let us introduce parameter q with $\frac{1}{q}$ being the average time a person spends in compartment I before going into quarantine. Because people from the infected compartment will not go directly to the recovered compartment anymore, we delete parameter γ_I and add parameter γ_Q to our model so that we can use $\frac{1}{\gamma_Q}$ for the amount of days that is spent in quarantine.
A lot of research has been done on the virus since the start of the pandemic. Researchers recently found that an individual that is in the presymptomatic compartment has the highest amount of infectiousness[10]! So at first we made the probability of getting infected by a presymptomatic person smaller using parameter θ, but now we have to make all the other possible ways of getting infected smaller. This is because after the presymptomatic stage the infectiousness of a person decreases rapidly. To make the model more like reality, we introduce a new compartment, M. This is the compartment individuals go to from the presymptomatic compartment when showing mild symptoms. These individuals probably will not go into quarantine because they may think they are not sick. Because they only have mild symptoms, so cough and sneeze a little bit more, researchers found that they do not infect others at a very high rate. So we multiply the transmission rate βSM with parameter $0.1 < \mu < 0.5$. Researchers found that it is very rare asymptomatic people can infect others. So we multiply the transmission rate βSA with parameter $0 < \alpha < 0.1$. Because people with very severe symptoms can infect others very fast but are not as infectious as in the presymptomatic stage, we multiply the transmission rate βSI with parameter $0.5 < \iota < 1$
New research[11] shows that the chance that an infected person will never show any symptoms is around 15% and around 20% of the people had severe symptoms. From now on we assume the last 65% of people has mild symptoms. All the compartments are listed in the following table:

[10] WHO (2020)

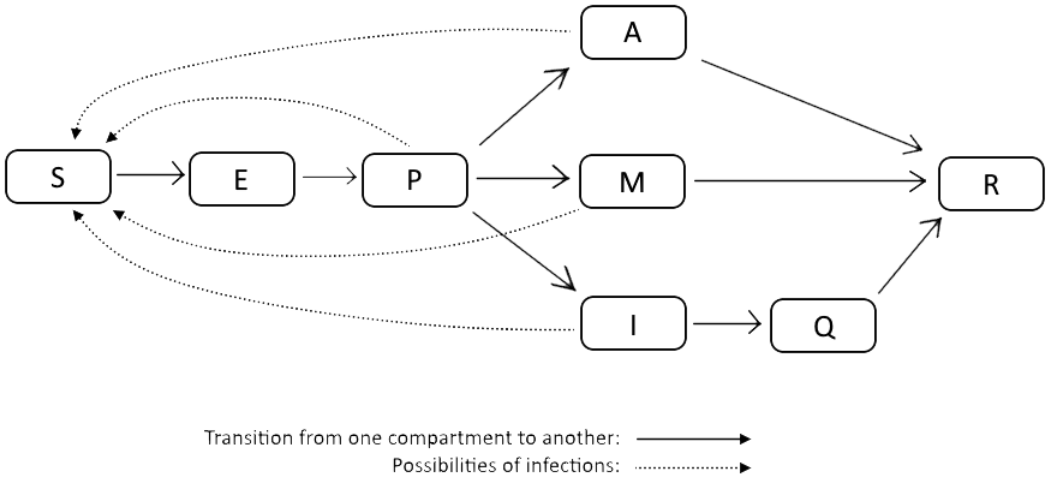
[11] Glasziou, P (2020) Estimating the extent of asymptomatic COVID-19 and its potential for community transmission: systematic review and meta-analysis

Compartments	
S	Susceptible
E	Exposed
P	Presymptomatic
I	People with severe symptoms
M	People with mild symptoms
A	People with no symptoms
Q	People that are quarantined
R	Recovered

Because we have a lot of parameters, we also put them in a table preventing us to get confused:

Parameter	Value	Definition
β	0.04	Probability of transmission per contact
c(t)	3-14	Contact rate
ι	0.75	Probability of transmission per contact with an individual with severe symptoms
α	0.05	Probability of transmission per contact with an individual that is asymptomatic
μ	0.25	Probability of transmission per contact with an individual with mild symptoms
ε	$\frac{1}{4}$	Transition rate of exposed individuals to the presymptomatic compartment
σ	$\frac{1}{2}$	Transition rate of presymptomatic individuals to compartments I, M and A
γ_I	$\frac{1}{2}$	Transition rate of people with severe symptoms to compartment R
γ_M	$\frac{1}{7}$	Transition rate of people with mild symptoms to compartment R
γ_A	$\frac{1}{7}$	Transition rate of asymptomatic people to compartment R
γ_Q	$\frac{1}{14}$	Transition rate of quarantined people to compartment R

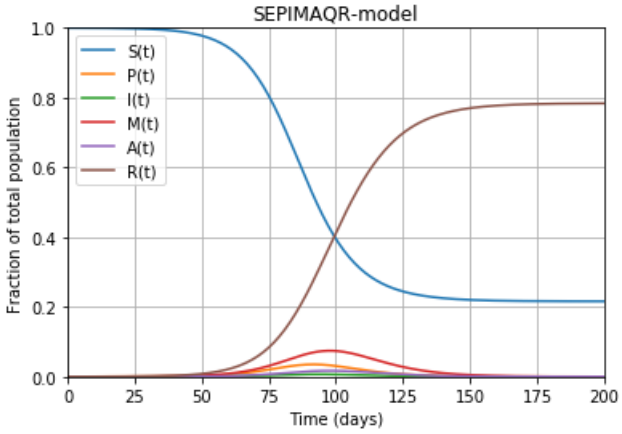
To make the transitions and transmissions between compartments more easy to see, we made the following compartmental scheme:



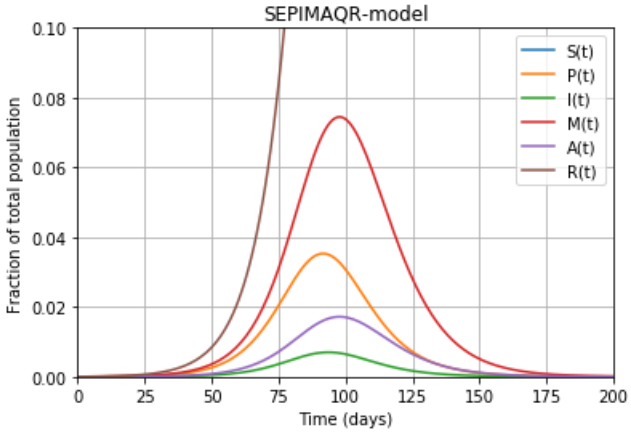
If we add the new compartments and parameters in our old model we obtain the following system of differential equations:

$$
\begin{aligned}
\frac{dS}{dt} &= -\beta c(t) S(P + \iota I + \mu M + \alpha A) \\
\frac{dE}{dt} &= \beta c(t) S(P + \iota I + \mu M + \alpha A) - \varepsilon E \\
\frac{dP}{dt} &= \varepsilon E - \sigma P \\
\frac{dI}{dt} &= 0.2\sigma P - qI \\
\frac{dM}{dt} &= 0.65\sigma P - \gamma_M M \\
\frac{dA}{dt} &= 0.15\sigma P - \gamma_A A \\
\frac{dQ}{dt} &= qI - \gamma_Q Q \\
\frac{dR}{dt} &= \gamma_M M + \gamma_A A + \gamma_Q Q
\end{aligned}
$$

When we take the median of each new parameter, so $\mu = 0.25$, $\alpha = 0.05$ and $\iota = 0.75$, and keep the contact rate constant from $t = 0$: $c(t) = 14$. We obtain the following graph:



Let us zoom in on this graph. We can see that the peak of $M(t)$ is a lot higher than the peak of $P(t)$. This is because $M(t)$ and $P(t)$ are defined as the amount of people in that compartment at time t and the total time people spend in compartment M is a lot longer than that of P.



Because the parameters α, μ and ι are very uncertain, especially μ and ι, we can look at a few different scenarios. Again the contact rate is constant and equal to 14.

1. Best scenario; People with mild symptoms and and severe symptoms are not as contagious as we thought: μ and ι are as small as possible, 0.1 and 0.5 respectively. We obtain the following graph:

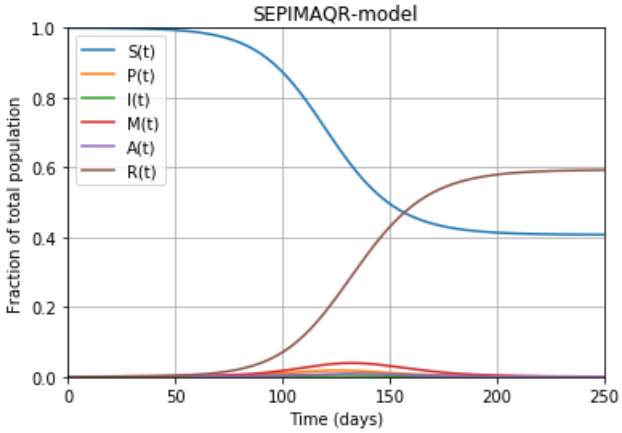


Figure 24: $\mu = 0.1$, $\iota = 0.5$

2. Worst scenario; People with mild symptoms and and severe symptoms are more contagious than we thought: μ and ι are as big as possible, 0.5 and 1 respectively. We obtain the following graph:

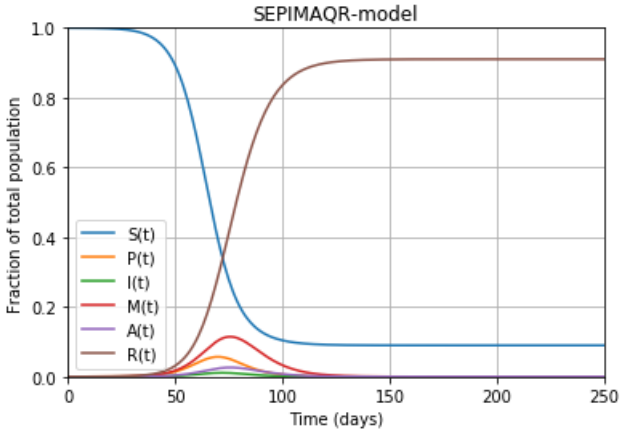


Figure 25: $\mu = 0.5$, $\iota = 1$

If we compare the figures we can see that in the worst scenario the virus is already extinct at $t \approx 150$, while in the best scenario this happens $\pm$ 100 days later. Now that we have expanded the model, it is starting to look a bit more like reality. Let us have a look at the basic reproduction number.

3.2 Reproduction number

Let us derive the basic reproduction number for our expanded model. This time five of the compartments are the 'infected' compartments: E,P,I,M and A. Now let $x_i, i = 1,2,..,5$ be the fraction of the population in the i^{th} infected compartment at time t. We can rewrite the differential equations of these 5 infected compartments as:

$$\frac{dx_i}{dt} = F_i(x) - V_i(x), \text{ where } V_i(x) = \left[V_i^-(x) - V_i^+(x)\right]$$

with $F_i(x)$ and $V_i(x)$ defined in the same way as section 2.5.
Let us find the next-generation matrix of our model. We only need the following differential equations:

$$\begin{aligned}
\frac{dE}{dt} &= \beta c(t) S(P + \iota I + \mu M + \alpha A) - \varepsilon E \\
\frac{dP}{dt} &= \varepsilon E - \sigma P \\
\frac{dI}{dt} &= 0.2\sigma P - qI \\
\frac{dM}{dt} &= 0.65\sigma P - \gamma_M M \\
\frac{dA}{dt} &= 0.15\sigma P - \gamma_A A
\end{aligned}$$

We find that F and V are equal to

$$F = \begin{pmatrix} 0 & \beta c(t) & \beta c(t)\iota & \beta c(t)\mu & \beta c(t)\alpha \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{7}$$

$$V = \begin{pmatrix} \varepsilon & 0 & 0 & 0 & 0 \\ -\varepsilon & \sigma & 0 & 0 & 0 \\ 0 & -0.2\sigma & q & 0 & 0 \\ 0 & -0.65\sigma & 0 & \gamma_M & 0 \\ 0 & -0.15\sigma & 0 & 0 & \gamma_A \end{pmatrix} \tag{8}$$

respectively.
We take the inverse of V and find:

$$V^{-1} = \begin{pmatrix} \frac{1}{\varepsilon} & 0 & 0 & 0 & 0 \\ \frac{1}{\sigma} & \frac{1}{\sigma} & 0 & 0 & 0 \\ \frac{0.2}{q} & \frac{0.2}{q} & \frac{1}{q} & 0 & 0 \\ \frac{0.65}{\gamma_M} & \frac{0.65}{\gamma_M} & 0 & \frac{1}{\gamma_M} & 0 \\ \frac{0.15}{\gamma_A} & \frac{0.15}{\gamma_A} & 0 & 0 & \frac{1}{\gamma_A} \end{pmatrix} \tag{9}$$

We multiply F and V^{-1}:

$$FV^{-1} = \begin{pmatrix} \frac{\beta c(t)}{\sigma} + \frac{0.2\iota\beta c(t)}{q} + \frac{0.65\mu\beta c(t)}{\gamma_M} + \frac{0.15\alpha\beta c(t)}{\gamma_A} & \cdots & \cdots & \cdots & \cdots \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{10}$$

We calculate the eigenvalues of FV^{-1} and find that the basic reproduction number of our model is

$$\mathscr{R}_t = max\{\lambda_i\} = \frac{\beta c(t)}{\sigma} + \frac{0.2\iota\beta c(t)}{q} + \frac{0.65\mu\beta c(t)}{\gamma_M} + \frac{0.15\alpha\beta c(t)}{\gamma_A} \tag{11}$$

3.3 Easing the measures

In the Netherlands the government eased the measures very much. This is possible because the have made rules about wearing face masks at busy places and also the social distancing rule still applies. It seems to be going very well in the Netherlands and people start living as if we the pandemic is over. We would think that the contact rate around 10 again, but with in the previous subsection found formula for the basic

reproduction number

$$\mathscr{R}_t = max\{\lambda_i\} = \frac{\beta c(t)}{\sigma} + \frac{0.2\iota\beta c(t)}{q} + \frac{0.65\mu\beta c(t)}{\gamma_M} + \frac{0.15\alpha\beta c(t)}{\gamma_A} \tag{12}$$

We find that $\mathscr{R}_t \leq 1$ when the contact rate, $c(t)$, is less than 7.2. So actually the contact rate is about factor 1.4 higher when everybody strictly follows the rules about social distancing and wearing face masks. The past months the reproduction number has been below one and after the first peak in the Netherlands, the virus has started to die out. We estimated the past contact rate values and put them into a table:

t_0	t=0	$\Delta t = 0$	27 February	c(t) = 14
t_1	t=14	$\Delta t = 14$	11 March	c(t) = 2
t_2	t=74	$\Delta t = 60$	11 May	c(t) = 4
t_3	t=94	$\Delta t = 20$	1 June	c(t) = 6
t_4	t=124	$\Delta t = 30$	1 July	c(t) = 6
t_5	t=184	$\Delta t = 60$	1 September	

Let us now look at some real scenarios starting at July:

1. People have the feeling that the pandemic and do not follow the rules

	$t \leq t_1$	$t_1 < t \leq t_2$	$t_2 < t \leq t_3$	$t_3 < t \leq t_4$	$t_4 < t \leq t_5$	$t_5 < t$
c(t)	14	2	4	6	6	14

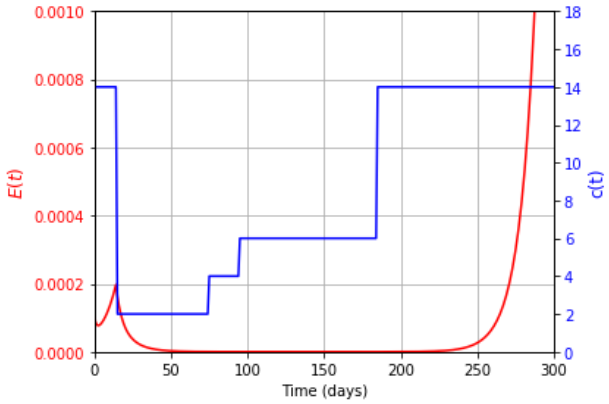


Figure 26

2. The people who go on vacation this summer come in contact with many other tourists and take the virus back to the Netherlands.

	$t \leq t_1$	$t_1 < t \leq t_2$	$t_2 < t \leq t_3$	$t_3 < t \leq t_4$	$t_4 < t \leq t_5$	$t_5 < t$
c(t)	14	2	4	6	14	8

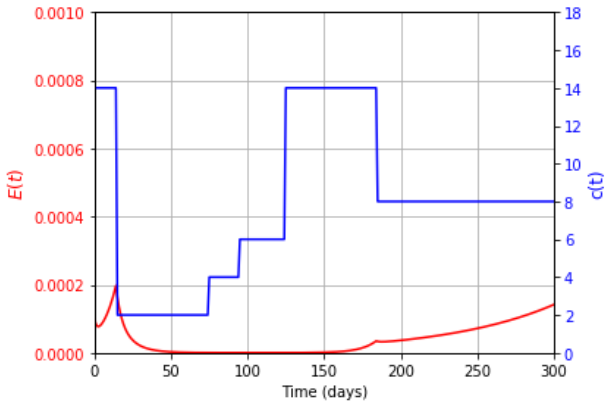


Figure 27

This summer is a very dangerous time for the pandemic. Most of the people are happy because they can go on vacation. Because the weather is nice people go more to to cafes and other activities. This makes it very easy for a virus to spread.

4 Other numerical methods

We have so far determined the solutions of our system by using the **odeint** function in the program Python. This is a numerical method that uses the LSODA algorithm which is a well-known method that uses switching to solve both stiff and non-stiff equations. Because some numerical methods[12] are faster than others and/or make smaller errors, we will look in to some different methods in this section. For this section we fix the following parameters:

Parameter	Value	Definition
β	0.04	Probability of transmission per contact
c	14	Contact rate
ι	0.75	Probability of transmission per contact with an individual with severe symptoms
α	0.05	Probability of transmission per contact with an individual that is asymptomatic
μ	0.25	Probability of transmission per contact with an individual with mild symptoms
ε	$\frac{1}{4}$	Transition rate of exposed individuals to the presymptomatic compartment
σ	$\frac{1}{2}$	Transition rate of presymptomatic individuals to compartments I, M and A
γ_I	$\frac{1}{2}$	Transition rate of people with severe symptoms to compartment R
γ_M	$\frac{1}{7}$	Transition rate of people with mild symptoms to compartment R
γ_A	$\frac{1}{7}$	Transition rate of asymptomatic people to compartment R
γ_Q	$\frac{1}{14}$	Transition rate of quarantined people to compartment R

We fix the following initial values:

Initial values	
S(0)	0.9999
E(0)	0.0001
P(0)	0
I(0)	0
M(0)	0
A(0)	0
Q(0)	0
R(0)	0

Finally, we use $\Delta t = 0.025$ as the size of our time steps. Using the **odeint** function in Python we obtain the following graph:

[12] Vuik, C., Vermolen, F.J., Van Gijzen, M.B., Vuik, M.J., (2015) Numerical Methods for Ordinary Differential Equations

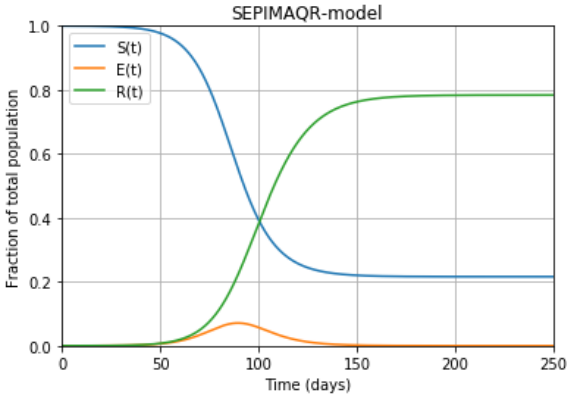


Figure 28

As you can see we only plotted the solutions of $S(t)$, $E(t)$ and $R(t)$ to avoid getting confused by the solutions of the other compartments.

Now let us consider two other numerical methods to solve our system:

1. Forward Euler Method
2. Modified Euler Method

4.1 Forward Euler method

In this subsection we will approximate a solution to our system using the Forward Euler Method. We do this in MATLAB because it is easier in this program. At time t_{n+1} the numerical approximation is given by $\mathbf{w}_{n+1}$, with:

$$\mathbf{w}_{n+1} = \mathbf{w}_n + \Delta t \mathbf{f}(t_n, \mathbf{w}_n).$$

Our system is hereby rewritten to vector form, with $\mathbf{f}(t, \mathbf{y})$ defined as:

$$\frac{d}{dt}\mathbf{y} = \mathbf{f}(\mathrm{t}, \mathbf{y}), \quad \text{met } \mathbf{y} := \begin{bmatrix} S(t) \\ E(t) \\ P(t) \\ I(t) \\ M(t) \\ A(t) \\ Q(t) \\ R(t) \end{bmatrix}.$$

We use the same values for the parameters and initial values. We also take the same size for the time steps, $\Delta t = 0.025$. We plot the solutions of this method and obtain the following figure:

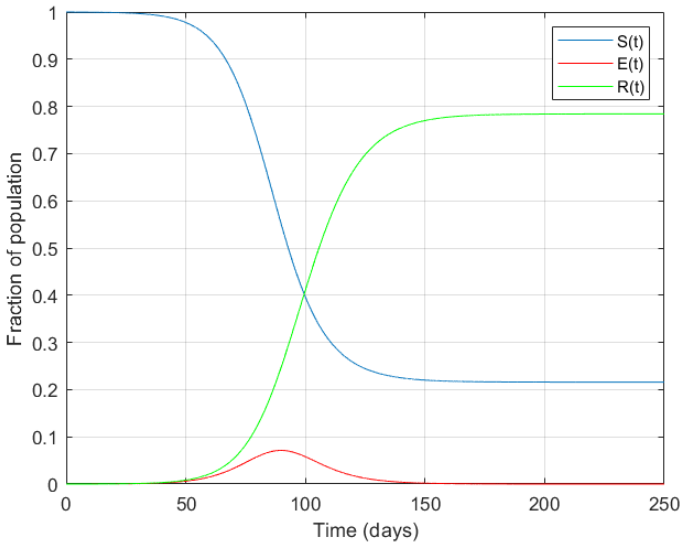


Figure 29: Forward Euler Method

If we compare the two figures, we see that they hardly differ. We calculate the maximum of $E(t)$ for both methods and find $E_{max} \approx 0.07119$ when we use the **odeint** function in Python, and $E_{max} \approx 0.07124$ when we use the Forward Euler Method in MATLAB. If we compare the running time of the **odeint** function and the Forward Euler Method, we find a big difference:
The running times are 0.006 and 0.174 seconds for **odeint** and the Forward Euler Method respectively. The **odeint** function is much faster and there is barely a difference in the solutions.

4.2 Modified Euler Method

Now we will have a look at the Modified Euler Method. This is also a very useful numerical method to approximate the solution of our system. At time t_{n+1} the numerical approximation is given by $\mathbf{w}_{n+1}$, with

$$\mathbf{w}^*_{n+1} = \mathbf{w}_n + \Delta t \mathbf{f}(t_n, \mathbf{w}_n),$$
$$\mathbf{w}_{n+1} = \mathbf{w}_n + \frac{\Delta t}{2}(\mathbf{f}(t_n, \mathbf{w}_n) + \mathbf{f}(t_{n+1}, \mathbf{w}^*_{n+1})).$$

Our system is hereby rewritten to vector form, with $\mathbf{f}(t, \mathbf{y})$ the same as in the Forward Euler Method:

$$\frac{d}{d\mathrm{t}}\mathbf{y} = \mathbf{f}(\mathrm{t},\mathbf{y}), \quad \text{met } \mathbf{y} := \begin{bmatrix} S(t) \\ E(t) \\ P(t) \\ I(t) \\ M(t) \\ A(t) \\ Q(t) \\ R(t) \end{bmatrix}.$$

We use the same values for the parameters and initial values but because this is a second order method, we can take a greater Δt. So for the Modified Euler Method we use $\Delta t = 0.05$. We find the following figure:

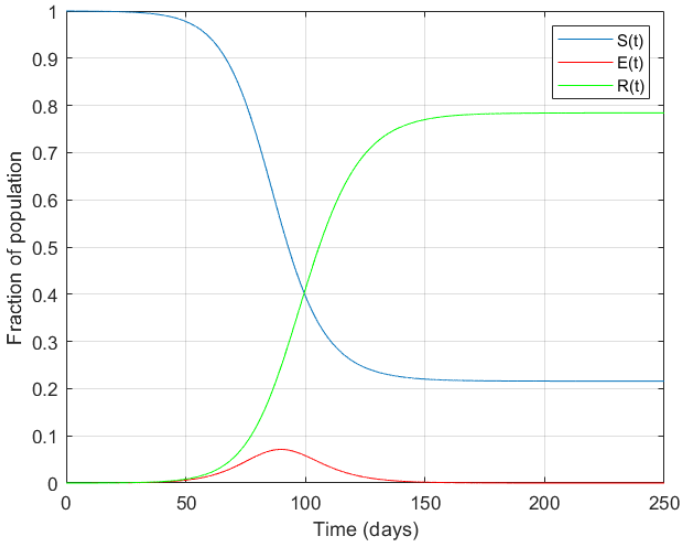


Figure 30: Modified Euler Method

If we compare the figures of the Forward Euler Method and the Modified Euler Method we cannot see any difference. We calculate the maximum of $E(t)$ for the Modified Euler Method and find $E_{max} \approx 0.071203$. This method has a running time of 0.0709 seconds. More than twice as fast as the Forward Euler Method.

5 Conclusion

In this report, we look at the spread of the coronavirus from human to human. We start with a simplified model, the SIR model, and expand this model step by step to make it more and more mimic the real world, to the SEPIMAQR model. For every model we calculate the formula for the basic reproduction number, $\mathscr{R}_0$. We saw that this number is one of the most important aspects to look at when taking measures and eventually easing those measures. We confirm that when a country takes strict measures like going into lock-down, $\mathscr{R}_0$ falls below one and the coronavirus will die out. Thereafter we see that the whole population needs to adhere to these measures and be patient because when a part of a population starts to disobey the taken measures, the contact rate will increase and the reproduction number will rise above 1 again. Because there are still many uncertainties about the behavior of the coronavirus, the parameters we use are also very uncertain and lay in big ranges. We look at different scenarios when assuming different values for the parameters. We saw that the best and worst case scenarios differed very much, what makes it very difficult to make decisions about easing the measures. We saw that going into a lock-down for a very long time is the best and easiest way to fight this virus. But we know that in the real world this is not possible because the world would end up in a economic disaster. This means that certain considerations have to be made by all governments from all over the world.

6 Discussion

In this report we expanded the SIR-model to a model consisting of eight compartments. But in real life there are many more compartments in which people can be at any moment. For example these are compartments that make a distinction between people from different ages, or people that are more susceptible because they have vital professions. Also we did not include the fact that people can die in other ways too and that babies are born during the pandemic. When modelling an epidemic, you also have to deal with a lot of unexpected events, like the 'Black Lives Matter' movement and the protests that came with it. Because the consequences of these unexpected events are so unpredictable, adjusting the model would have taken too much time. We also did not include possible transmission by touching and holding the same things a infectious person did.

Appendix A

```
1  import numpy as np
2  from scipy.integrate import odeint
3  import matplotlib.pyplot as plt
4
5
6
7
8
9
10 beta = 0.04
11 sigma = 1.0/2.0
12 epsilon = 1/4.0
13 gamma_M = 1.0/7
14 gamma_A = 1.0/7
15 gamma_Q = 1.0/2
16 gamma_i = 1.0/2
17 alpha = 0.05
18 mu = 0.25
19 iota = 0.75
20
21 # INITIAL VALUES
22 S0 = 0.9999
23 E0 = 0.0001
24 P0 = 0.0
25 I0 = 0.0
26 M0 = 0.0
27 A0 = 0.0
28 Q0 = 0.0
29 R0 = 0.0
30
31 t = np.arange(0,1000)
32
33
34 # STEPFUNCTION
35 a = np.zeros(len(t))
36 def stepfunction(t):
37     for i in range(len(a)):
38
39         if i <= 14:
40             a[i] = 14
41
42         elif 14 < i <= 74:
43             a[i] = 2
```

```
44          elif 74 < i <= 94:
45              a[i] = 4
46          elif 94 < i <= 124:
47              a[i] =6
48          elif 124 < i <= 184:
49              a[i] =14
50          else:
51              a[i] =8
52      return a
53
54 # time steps
55 t1 = 14
56 t2 = 74
57 t3 = 94  # 1juni
58 t4 = 124 # 1juli
59 t5 = 184 # 1sept
60 # contact at time step
61 t0_t1 = 14.0
62 t1_t2 = 2
63 t2_t3 = 4
64 t3_t4 = 6
65 t4_t5 = 14
66 t5_ = 8
67
68 def SEPIMAQR_model(y,t,beta,epsilon,sigma,gamma_Q,gamma_M
       ,gamma_A,mu,iota,gamma_i,alpha):
69      S, E, P, I, M, A, Q, R = y
70      if t <= t1:
71          u = t0_t1
72      elif t1 < t <= t2:
73          u = t1_t2
74      elif t2 < t <= t3:
75          u = t2_t3
76      elif t3 < t <= t4:
77          u = t3_t4
78      elif t4 < t <= t5:
79          u = t4_t5
80      else:
81          u = t5_
82      dS_dt = beta*u*S*(iota*I + alpha * A+P+mu*M)
83      dE_dt = beta*u*S*(iota*I+ alpha * A+P+mu*M) - epsilon
           *E
84      dP_dt = epsilon*E - sigma*P
85      dI_dt = 0.2*sigma*P  -gamma_i*I
86      dM_dt = 0.65*sigma*P - gamma_M*M
87      dA_dt = 0.15*sigma*P - gamma_A*A
```

```
88      dQ_dt = gamma_i*I - gamma_Q*Q
89      dR_dt = gamma_Q*Q + gamma_A*A + gamma_M*M
90      return([dS_dt, dE_dt, dP_dt, dI_dt,dM_dt, dA_dt,
            dQ_dt ,dR_dt])
91
92 solution = odeint(SEPIMAQR_model,[S0,E0,P0,I0,M0,A0,Q0,R0
       ],t,args=(beta,epsilon,sigma,gamma_Q,gamma_M,gamma_A,
       mu,iota,gamma_i,alpha))
93 solution = np.array(solution)
94
95 ct = 14
96 reproductionrate = ((beta*ct/sigma) + (beta*ct*iota*0.2/
       gamma_i) + (beta*ct*alpha*0.15/gamma_A) + (beta*ct*mu
       *0.65/gamma_M))*1
97 print(reproductionrate)
98
99
100 fig, ax1 = plt.subplots()
101
102 color = 'tab:red'
103 ax1.set_xlabel('Time (days)')
104 ax1.set_ylabel('$E(t)$', color='r', fontsize = '12')
105 ax1.plot(t, solution[:,1], color='r')
106 ax1.tick_params(axis='y', labelcolor='r')
107 ax1.set_ylim([0, 0.001])
108 ax1.grid(axis = 'both')
109
110 ax2 = ax1.twinx()  # instantiate a second axes that
       shares the same x-axis
111
112 color = 'tab:blue'
113 ax2.set_ylabel('c(t)', color='b',fontsize = '12')  # we
       already handled the x-label with ax1
114 ax2.plot(t, stepfunction(t), color='b')
115 ax2.tick_params(axis='y', labelcolor='b')
116 ax2.set_ylim([0, 18])
117 # ax2.grid(axis = 'both')
118
119 fig.tight_layout()  # otherwise the right y-label is
       slightly clipped
120 plt.xlim(0,300)
121 plt.ylim(bottom =0)
122 # plt.grid()
123 plt.show()
```

Appendix B

MATLAB Codes

```
function [f] = FunCorona(x,y);

beta = 0.04;
sigma = 1.0/2.0;
epsilon = 1/4.0;
gamma_M = 1.0/7;
gamma_A = 1.0/7;
gamma_Q = 1.0/2;
gamma_i = 1.0/2;
alpha = 0.05;
mu = 0.25;
iota = 0.75;
c = 14;

%System differential equations
S = -beta*c*y(1)*(iota*y(4) + alpha*y(6)+y(3)+mu*y(5));
E = beta*c*y(1)*(iota*y(4) + alpha*y(6)+y(3)+mu*y(5))-
    epsilon*y(2);
P = epsilon*y(2) -sigma*y(3);
I = 0.2 *sigma * y(3) - gamma_i*y(4);
M = 0.65 *sigma*y(3) - gamma_M*y(5);
A = 0.15 * sigma*y(3) - gamma_A*y(6);
Q = gamma_i*y(4) - gamma_Q*y(7);
R = gamma_Q*y(7) + gamma_A*y(6) + gamma_M*y(5);

f = [S, E, P, I, M, A, Q, R];
end
```

```
clc
clear all
close all

a = 0;            %t0
b = 250;          %t_end
n = 5000;         %steps
h = (b-a)/n;      %stepsize

%Initial values
y1(1,:) = [0.9999, 0.0001, 0, 0, 0, 0, 0, 0];
x(1) = a;
i=0;

%Forward Euler
tic
for j=a:h:b
    i = i+1;
    x(i+1)=x(i) + h;
    y1(i+1,:) = y1(i,:) + h*FunCorona(x(i), y1(i,:));
    xx1(i)=j;
end
toc

%Initial values
y2(1,:) = [0.9999, 0.0001, 0, 0, 0, 0, 0, 0];
i=0;
%Modified Euler
tic
for j=a:h:b
    i = i + 1;
    x(i+1)=x(i) + h;
    we = y2(i,:) + h*FunCorona(x(i), y2(i,:));
    y2(i+1,:) = y2(i,:) + 0.5*h*(FunCorona(x(i),y2(i,:))
        + FunCorona(x(i+1),we));
    xx2(i)=j;
end
toc
figure(1)
plot(xx1, y1(1:n+1,1))
hold on
plot(xx1, y1(1:n+1,2), 'r')
hold on
plot(xx1, y1(1:n+1,8), 'g')
legend('S(t)', 'E(t)', 'R(t)')
ylabel(['Fraction of population'])
```

```
46 xlabel('Time (days)')
47 ylim([0.0, 1.0])
48 xlim([0 250])
49 grid on
50 figure(2)
51 plot(xx1, y1(1:n+1,1))
52 hold on
53 plot(xx1, y1(1:n+1,2), 'r')
54 hold on
55 plot(xx1, y1(1:n+1,8), 'g')
56 hold off
57 legend('S(t)', 'E(t)', 'R(t)')
58 ylabel(['Fraction of population'])
59 xlabel('Time (days)')
60 ylim([0, 1])
61 xlim([0 250])
62 grid on
63 format long g
64 max(y1,[],1);
65 max(y2,[],1);
```

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