The Mathematics of 'Flattening the Curve'

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The goal of this document is to explain the basic dynamical behavior of an epidemic, such as the flu, by means of a simple mathematical model. In particular, our aim is to show the importance of drastic measures such as a *lockdown* of the population to reduce the impact of an epidemic, as well as the influence of the limited *capacity for medical care* on the final death toll. The mathematics in this document are kept as elementary as possible. Our interest was peaked by the ongoing Corona pandemic. Although we have made an effort to use reasonable model parameters, we do *not* claim that any of the results in this document should be considered as accurate predictions. We work with limited real data and an overly simplified model, which will nonetheless give insight into the basic dynamics. Furthermore, none of the mathematical or epidemiological results are new. More detailed descriptions of the models we use here and many others can be found, for instance, in [Het00].

1 The SIR-model

We consider a population consisting of N individuals. In our examples we will take $N = 11,000,000 = 11 \cdot 10^6$, which is roughly the number of Belgian citizens. The SIR-model is the most elementary mathematical model for describing the dynamics of an infectious disease which spreads in our population. It is an example of a so-called *compartmental model*, which partitions the population into several *compartments* or *groups*. Each of the compartments contains individuals having the same characteristics related to the disease. The SIR-model uses only three groups, which give the model its name:

1. the group of *susceptible* individuals, which are not infected yet, but may be in the future,
2. the group of *infective* individuals, which are infected by the disease and may infect others,
3. the group of *recovered* individuals, which had been infected at some point, but do no longer carry the disease now. They are assumed to have become immune to the disease.

One can argue that this model allows for individuals to 'die', in the sense that the group of 'recovered' individuals can be partitioned further into a group of *healed* and *deceased* individuals. After all, the deceased individuals no longer carry the disease and are immune to it, satisfying the requirements as described previously to belong to that third group. The word 'recover' must in that case simply be understood as transitioning from having the disease to not having the disease. We will model the deceased individuals explicitly in Section 3.

In this model, the possible transitions between the groups is as follows. Susceptible individuals may become infected, and infected individuals may recover. There is for instance no way for recovered individuals to become susceptible or infected again. Schematically, we denote

$$S \longrightarrow I \longrightarrow R.$$

The result of our computation will be the number of susceptible, infected and recovered individuals *as a function of time*. These quantities are denoted $S(t), I(t)$ and $R(t)$ respectively, where t is our time variable, with time expressed in *days*.

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Example 1. *$S(48)$ is the number of susceptible individuals on day 48.*

Example 2. *At each moment in time, i.e., for each t, we have that $S(t) + I(t) + R(t) = N$.*

In order to compute these functions, some information is needed. First of all, we need to know the number of susceptible, infected and recovered individuals at time $t = 0$. These quantities are denoted by

$$S(0) = S_0, \quad I(0) = I_0, \quad R(0) = R_0.$$

Secondly, we need to know *how fast* the transition between the compartments S and I happens. This is captured by a parameter β, called the *infection rate* of the disease. The number β can be thought of as the number of individuals one infective person infects on average per day, assuming everybody else is susceptible. Finally, we need the speed of the transition from I to R, that is, the *recovery rate*. This is represented by the model parameter γ. The constant γ can be thought of as the fraction of infected people that recover per day, on average. In other words, the inverse $1/\gamma$ is the average duration of the infectious period. That being said, we update the schematic representation of our model to

$$S \xrightarrow{\beta} I \xrightarrow{\gamma} R,$$

keeping in mind that β captures the rate of infection when everybody else is susceptible.

1.1 Model equations

To keep the notation simple, we will sometimes use the short notation S, I and R for the functions $S(t), I(t)$ and $R(t)$. According to the SIR-model, the number of people that get infected each day is proportional to S and to I. Indeed, the larger the group of susceptible individuals S and the larger the group of infected people I, the faster the disease spreads. Recall that the parameter β gives the average number of other people that are exposed to the virus by one infected person in a single day. Since only a fraction $\frac{S}{N}$ of the population is susceptible, this causes an average of $\frac{\beta S}{N}$ people to be infected each day for each person in group I. The rate of infection is thus $\frac{\beta IS}{N}$. The second transition, from I to R, happens for a fraction γ of the individuals in I each day. The rate of recovery is therefore γI. The final schematic representation of the SIR-model can be found in Figure 1 below.

The arrow labels in Figure 1 govern the speed at which the quantities S, I and R are changing over

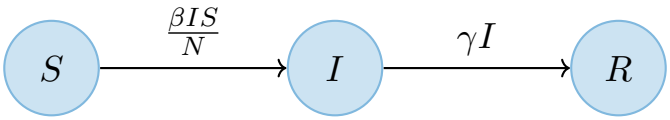

Figure 1: Diagram of the SIR-model.

time. This is captured by a mathematical concept called the *derivative* with respect to time of the functions $S(t), I(t)$ and $R(t)$. For instance, at time t, the number of susceptible individuals *decreases* at a rate of $\frac{\beta I(t)S(t)}{N}$ individuals per day, which results in the derivative

$$\frac{\mathrm{d}S(t)}{\mathrm{d}t} = -\frac{\beta I(t)S(t)}{N}. \tag{1}$$

The minus sign reflects the decrease of $S(t)$ and corresponds to the *outgoing* arrow $S \to I$ in the diagram of Figure 1. The reader who is unfamiliar with derivatives, can read the expression (1)

above as stating that the difference between the number of susceptible individuals at day $t+1$ and day t is approximately

$$S(t+1) - S(t) \approx -\frac{\beta I(t) S(t)}{N}.$$

Writing down analogous expressions for the derivatives of $I(t)$ and $R(t)$ and using the short notation S, I and R we get

$$\begin{aligned} \frac{\mathrm{d}S}{\mathrm{d}t} &= -\frac{\beta IS}{N} \\ \frac{\mathrm{d}I}{\mathrm{d}t} &= \frac{\beta IS}{N} - \gamma I \\ \frac{\mathrm{d}R}{\mathrm{d}t} &= \gamma I. \end{aligned} \tag{2}$$

The system of equations (2) is an example of a *system of ordinary differential equations*. Our approach for understanding the evolution in time of the population subject to the disease will be to solve the following mathematical problem.

Problem 1. *Find functions* $S(t), I(t), R(t)$ *satisfying* (2) *and* $S(0) = S_0, I(0) = I_0, R(0) = R_0$.

Such a problem is called an *initial value problem*. The problem is *nonlinear* since the system contains the product of the unknown functions $I(t)$ and $S(t)$. This system can be solved numerically, i.e., in an approximate way by using computer algorithms designed specifically for this purpose. These methods allow us to show the functions $S(t), I(t), R(t)$ graphically and get a quantitative understanding of the evolution of the three groups over time. The details are outside the scope of this article.

1.2 A first simulation

In order to solve our initial value problem, we need to specify the initial quantities S_0, I_0, R_0 and the parameters β and γ of the model. Let us assume that at time $t = 0$, only one individual is infective and all the others are susceptible. That is,

$$S_0 = 10,999,999, \quad I_0 = 1, \quad R_0 = 0.$$

Moreover, we will assume that the duration of the infectious period of our disease is 14 days on average. Together with the assumption that an infective individual infects 2.5 other people in their infectious period (assuming all other individuals are susceptible), this gives

$$\gamma = \frac{1}{14}, \quad \beta = \frac{2.5}{14}.$$

The result of the numerical simulation over a period of 1 year is shown in Figure 2. We make three observations.

1. Since in our model (2) the 'change' over time of $S(t)$ is always smaller than zero, the number of susceptible individuals can only decrease.

2. Conversely, since $\frac{\mathrm{d}R}{\mathrm{d}t}$ is always positive, the function $R(t)$ can only increase.

3. The derivative of $I(t)$ has two contributing terms. At the beginning of the simulation, when the number of susceptible individuals is high, the term $\frac{\beta IS}{N}$ will dominate over $-\gamma I$ and the derivative will be larger than zero: the number of infected individuals grows. At some point

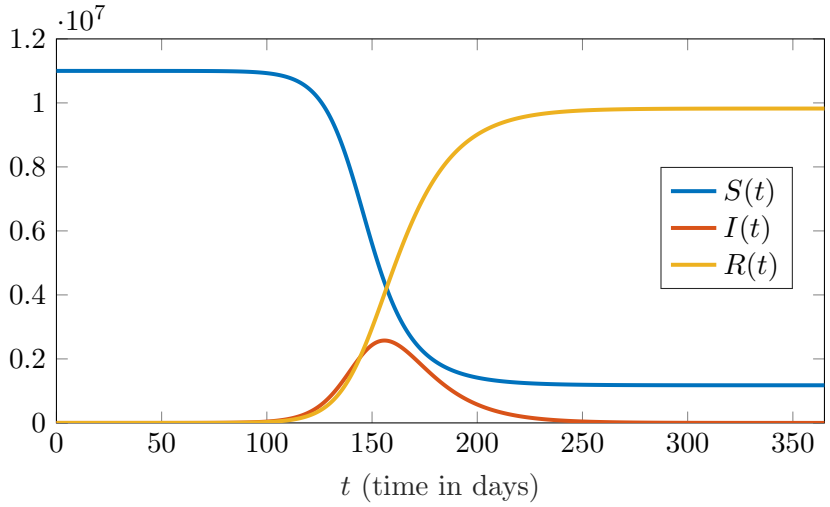

Figure 2: Result of our first simulation with $\beta = 2.5/14$, $\gamma = 1/14$.

(after about 160 days in this example) the disease has infected so many people that too few susceptible individuals are left. The term $-\gamma I$ now dominates the derivative of $I(t)$: the function starts decreasing. From

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \left(\frac{\beta S}{N} - \gamma\right) I$$

we see that $I(t)$ reaches its maximum exactly when the number of susceptible individuals equals $\frac{\gamma N}{\beta}$. On Figure 2, this corresponds to the fact that I reaches its maximum where S reaches the value

$$\frac{\gamma N}{\beta} = \frac{2}{5} \cdot 11,000,000 = 4,400,000.$$

2 Lockdown

In order to reduce the number of simultaneously infected individuals, the population can be urged to practice *social distancing*. In its most extreme form, this comes down to a complete *lockdown* of the population, which prohibits infected individuals (to a certain extent) from infecting more susceptibles. In this section, we show by means of the SIR model what the effects of such drastic measures may be. It is reasonable to assume that the model parameter that is influenced by a lockdown is the infection rate β. As a first experiment, we compare the outcome of two different simulations of the SIR model. For the first simulation, we use the same parameters as in Subsection 1.2. We index the model parameters and outcomes with a '1' to emphasize that they correspond to the first simulation:

$$\gamma_1 = \frac{1}{14} \quad \text{and} \quad \beta_1 = \frac{2.5}{14} \quad \text{give } S_1(t), I_1(t), R_1(t) \text{ as in Subsection 1.2.}$$

For the second simulation, we assume that some sort of lockdown measure has caused the infection rate β_2 to be only $1.5/14$. That is

$$\gamma_2 = \frac{1}{14} \quad \text{and} \quad \beta_2 = \frac{1.5}{14} \quad \text{give } S_2(t), I_2(t), R_2(t).$$

The curves $I_1(t)$ and $I_2(t)$ are shown in Figure 3. We conclude that the effect of decreasing the

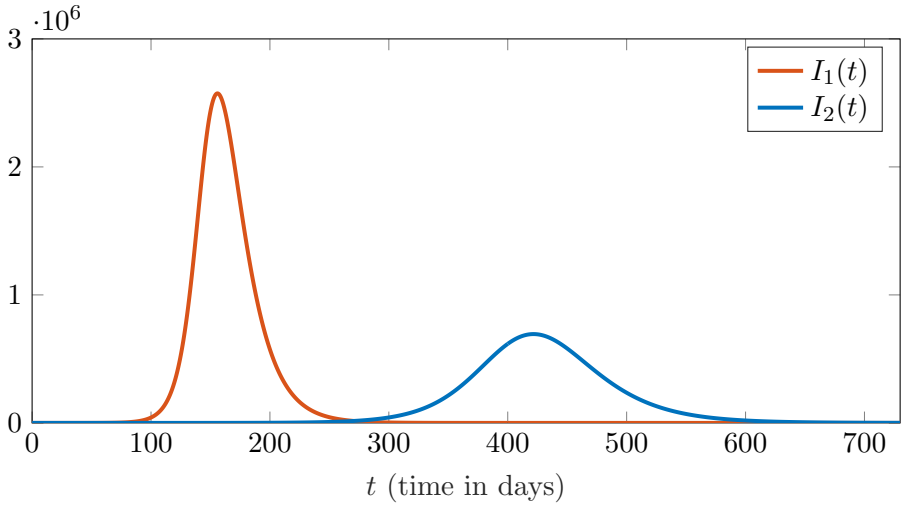

Figure 3: Number of infective individuals as a function of time for $\beta_1 = 2.5/14$ and $\beta_2 = 1.5/14$.

infection rate is to *delay, lower and widen* the peak of infection.

In practice, authorities will only enforce a lockdown once it is clear that a disease is spreading problematically. To incorporate this into our model, we allow the infection rate β to change over time. Explicitly denoting all time dependencies, the model becomes

$$\begin{aligned} \frac{\mathrm{d}S(t)}{\mathrm{d}t} &= -\frac{\beta(t)I(t)S(t)}{N} \\ \frac{\mathrm{d}I(t)}{\mathrm{d}t} &= \frac{\beta(t)I(t)S(t)}{N} - \gamma I(t) \\ \frac{\mathrm{d}R(t)}{\mathrm{d}t} &= \gamma I(t). \end{aligned} \tag{3}$$

For the reference model, we will keep using the constant function $\beta_1(t) = 2.5/14$. For the second model, we will now assume that the initial infection rate is $2.5/14$ as well. After 100 days, once a significant number of infections is confirmed, a lockdown brings the infection rate down to $1.5/14$. Mathematically, this is denoted by

$$\beta_3(t) = \begin{cases} 2.5/14 & t \in [0, 100] \\ 1.5/14 & t \in (100, \infty) \end{cases}.$$

The result is shown in Figure 4. Note that the curves $I_1(t)$ and $I_3(t)$ agree up to $t = 100$, which makes sense from the definition of $\beta_3(t)$.

We conclude this section by noting that a timely lockdown can not only cause the number of simultaneously infected individuals to decrease drastically, it also causes less infections overall. The interested reader can see this from the results in the first Appendix. The Matlab code which was used to run the simulations in this section can be found in the second Appendix. As we will see in the next sections, in case of a deadly disease, these effects can decrease the death toll of the epidemic significantly.

3 The SIRD-model

In this section, we explicitly keep track of deaths by introducing a fourth group D of *deceased individuals*. We keep the previous groups S, I, and R from Section 1. The diagram of this model,

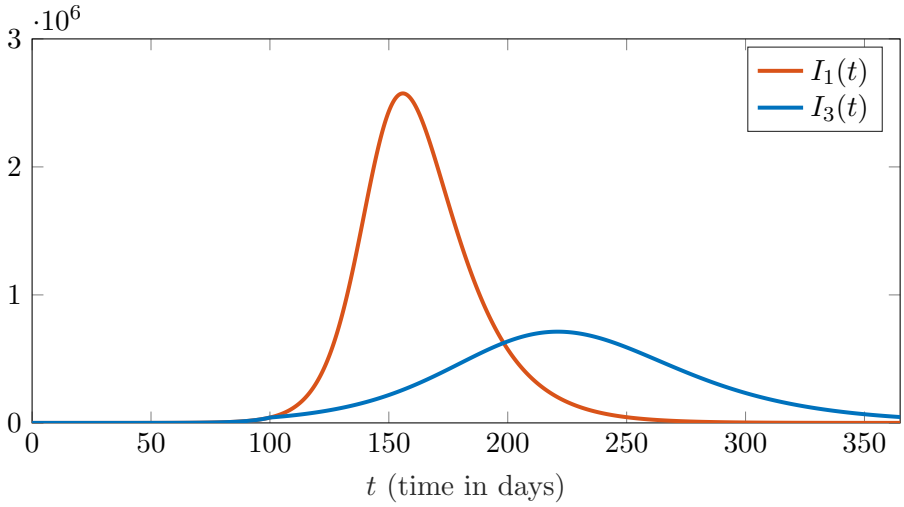

Figure 4: Number of infective individuals as a function of time for $\beta_1(t)$ and $\beta_3(t)$.

called the SIRD-model, is given in Figure 5. The model assumes that infective individuals can either

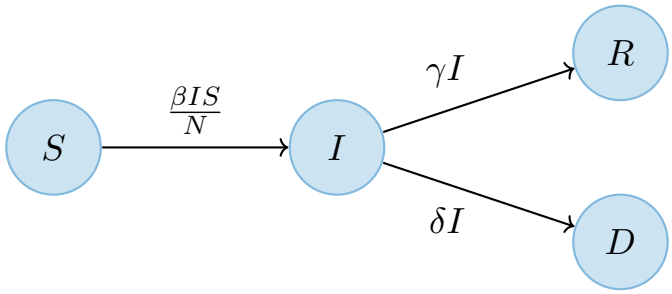

Figure 5: Diagram of the SIRD-model.

recover ($I \to R$) or die ($I \to D$). The speed of these transitions is given by the model parameters γ for $I \to R$ and δ for $I \to D$. The corresponding system of ordinary differential equations is

$$\begin{aligned} \frac{\mathrm{d}S}{\mathrm{d}t} &= -\frac{\beta IS}{N} \\ \frac{\mathrm{d}I}{\mathrm{d}t} &= \frac{\beta IS}{N} - \gamma I - \delta I \\ \frac{\mathrm{d}R}{\mathrm{d}t} &= \gamma I \\ \frac{\mathrm{d}D}{\mathrm{d}t} &= \delta I. \end{aligned} \tag{4}$$

The initial value problem considered in this section is the following.

Problem 2. *Find functions* $S(t), I(t), R(t)$ *and* $D(t)$ *satisfying* (4) *and* $S(0) = S_0$, $I(0) = I_0$, $R(0) = R_0$ *and* $D(0) = D_0$.

For a first simulation of this model, we use the model parameters

$$\beta = \frac{2.5}{14}, \quad \gamma = \frac{1}{14} \quad \text{and} \quad \delta = 0.003,$$

and the initial conditions

$$S_0 = 10,999,900, \quad I_0 = 100, \quad R_0 = 0, \quad D_0 = 0.$$

The results are shown in Figure 6.

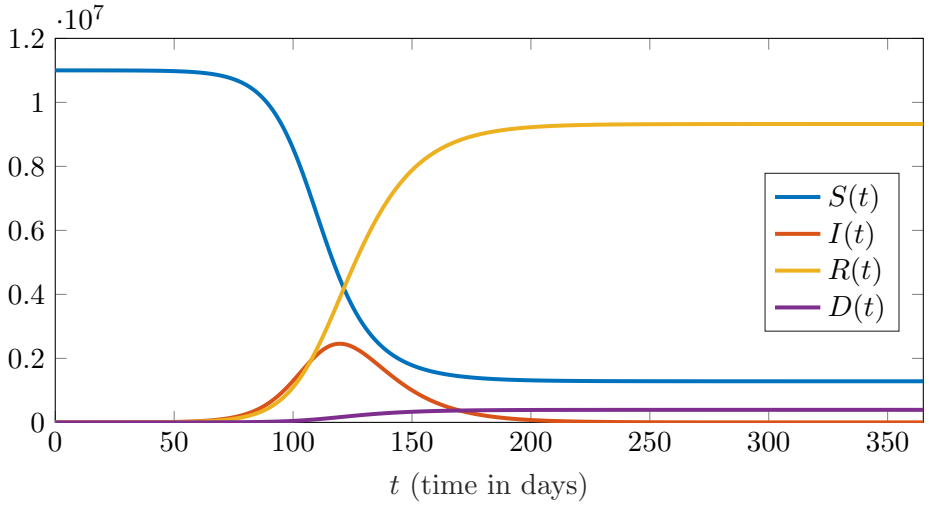

Figure 6: Result of our first SIRD simulation with $\beta = 2.5/14, \gamma = 1/14, \delta = 0.003$.

4 Limited capacity for medical care

A certain proportion of the infective population will experience severe symptoms, being at a higher risk of death. These individuals need additional treatment and fill up the capacity for medical care. The number of individuals that can be treated simultaneously is limited. This limited capacity for medical care causes the death rate δ to depend on the number of patients that is infected. In simple terms, if hospitals are forced to choose which individuals to treat and which not, more people will die.

Let C denote the number of infective individuals that fills up the capacity for medical care. We will call this parameter the *care capacity*. Not all infective individuals need to be hospitalized. If we assume that 10% of infective individuals need care and the maximum number of simultaneous patients is $55,000$ (0.5% of the Belgian population), the care capacity is $C = 55,000/0.10 = 55 \times 10^4$. If the number of infective individuals exceeds this care capacity, not all of the severe cases can be treated.

It has been observed that for the new Corona virus COVID-19, infective individuals with severe symptoms that do not receive the appropriate treatment have a much higher probability of dying. Let us assume that the death rate is $\delta = 0.001$ if $I \leq C$ and that $\delta = 0.005$ for the individuals in I that exceed the capacity C. In the latter case, the proportion of infective people that have access to the available medical care is $\frac{C}{I}$ and the proportion of infective people that do not is $\frac{I-C}{I}$. Hence, one can express δ as a function of I as follows:

$$\delta(I) = \begin{cases} 0.001 & I \leq C \\ 0.001\frac{C}{I} + 0.005\frac{I-C}{I} & I > C \end{cases}. \tag{5}$$

Writing out all dependencies explicitly, the model (4) becomes

$$\begin{aligned}
\frac{\mathrm{d}S(t)}{\mathrm{d}t} &= -\frac{\beta I(t)S(t)}{N} \\
\frac{\mathrm{d}I(t)}{\mathrm{d}t} &= \frac{\beta(t)I(t)S(t)}{N} - \gamma I(t) - \delta(I(t))I(t) \\
\frac{\mathrm{d}R(t)}{\mathrm{d}t} &= \gamma I(t) \\
\frac{\mathrm{d}D(t)}{\mathrm{d}t} &= \delta(I(t))I(t).
\end{aligned}$$

We can now observe the effect of a lockdown as described in Section 2 on the final death toll. Assume that we start our simulation once 100 individuals are infected, i.e., assume

$$S_0 = 10,999,900, \quad I_0 = 100, \quad R_0 = 0, \quad D_0 = 0.$$

The lockdown happens at day 60 and is such that the infection rate β lowers from 2.5/14 to 1.5/14. Furthermore, as before, $\gamma = 1/14$. The results are shown in Figure 7. The number of susceptible,

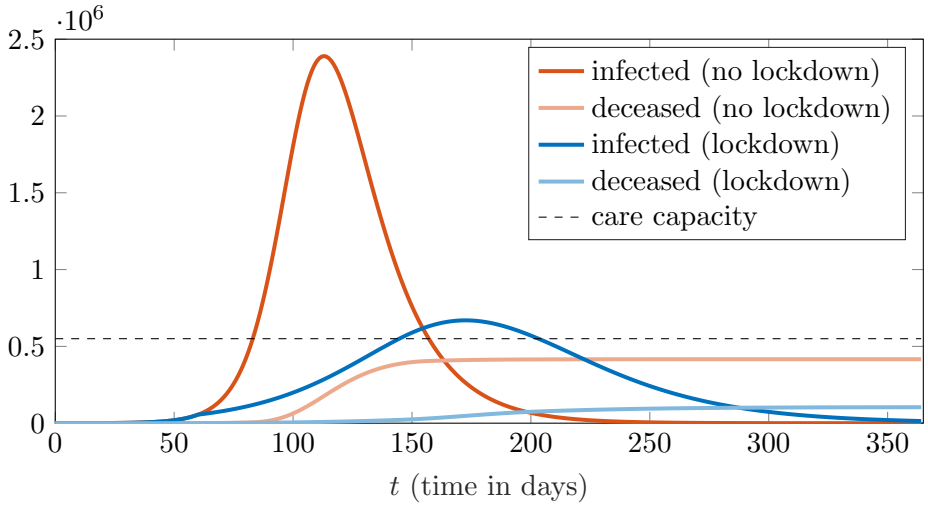

Figure 7: The effect of a lockdown on the number of infective and deceased individuals as a function of time.

infective, recovered and dead people after one year is:

	$S(365)$	$I(365)$	$R(365)$	$D(365)$
no lockdown	12.2%	0.0%	84.0%	3.8%
lockdown	43.2%	0.1%	55.8%	0.9%

(6)

5 Conclusion

Lowering the infection rate $\beta(t)$ over time has the effect of 'flattening the curve' of simultaneously infected people. If the population succeeds at keeping the curve below the care capacity, the final death toll can be reduced significantly.

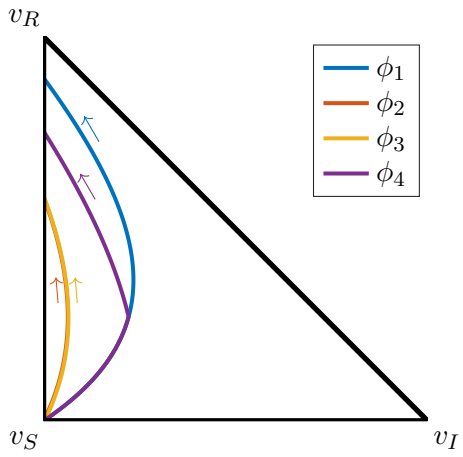

Figure 8: Phase portraits for different choices of the infection rate β.

APPENDIX: Phase plane portraits

Another nice way of representing the outcome of a simulation is by means of a *phase plane portrait*. We consider a triangle Δ whose vertices represent the groups S, I and R. We denote these vertices by v_S, v_I and v_R and we give them coordinates in the plane:

$$v_S = (0,0), \quad v_I = (1,0), \quad v_R = (0,1).$$

As time continues, we keep track of the point

$$\phi(t) = \frac{S(t)}{N} v_S + \frac{I(t)}{N} v_I + \frac{R(t)}{N} v_R.$$

For each moment in time t, $\phi(t)$ is a point in the plane which is a 'linear combination' of the vertices v_S, v_I and v_R. It is even a *convex combination*, which means that $\phi(t)$ is inside the triangle Δ for each t. For the reader to whom it does not make sense to take linear combinations of points in the plane, it is sufficient to know that $\phi(t)$ is closer to the vertex v_S when the number of susceptible individuals is high, and analogously for the other groups in the model. For the different choices $\beta_1(t), \beta_2(t), \beta_3(t)$ from Section 2, we denote the corresponding phase portraits by $\phi_1(t), \phi_2(t)$ and $\phi_3(t)$. The result is shown in Figure 8. Since the difference between $\phi_2(t)$ and $\phi_3(t)$ is nearly invisible, we ran another simulation with an infection rate $\beta_4(t)$, similar to $\beta_3(t)$ but with a lockdown enforced only after 150 days, instead of 100. Note that by looking at where the phase diagram hits the line segment between v_S and v_R, we can deduce how many people have been infected by the disease. At the end of the epidemic, for $\beta_1(t)$ nearly 90 percent of the individuals were infected by the disease. For $\beta_3(t)$, this number has been reduced to almost 60 percent. For $\beta_4(t)$, roughly 75 percent of the population was infected.

APPENDIX: Matlab code

```
function [ S,I,R, tnodes ] = SIR_fwd(S0,I0,R0,beta,gamma,T,dt)
% This solves the system of differential equations of an SIR model for
% the dynamics of an epidemic, such as the flu.

% INPUT:
% ------------------------------------------------
```

```
% S0            initial number of susceptible individuals.
% I0            initial number of infected individuals.
% R0            initial number of recovered/dead (immune) individuals.
% beta          function handle describing the infection rate as a function of time.
% gamma         the recovery/death rate.
% T             the system is solved for the time interval [0,T].
% dt            time step for the discretization of the differential equations.

% OUTPUT:
% ------------------------------------------------
% tnodes        discrete points in time where the solution is computed.
% S             S(t) is the number of susceptible individuals at time tnodes(t).
% I             I(t) is the number of infected individuals at time tnodes(t).
% R             R(t) is the number of recovered/dead individuals at time tnodes(t).

S = [S0]; % susceptible individuals
I = [I0]; % infected individuals
R = [R0]; % recovered/dead individuals
N = S0+I0+R0; % population size
tnodes = linspace(0,T,T/dt);
sol = [S0;I0;R0];

for t = 1:length(tnodes)-1
    tt = tnodes(t);
    v1 = -dt*beta(tt)*S(t)*I(t)/N;
    v2 = dt*(beta(tt)*S(t)*I(t)/N - gamma*I(t));
    v3 = dt*gamma*I(t);
    solnew = sol + [v1;v2;v3];
    S = [S solnew(1)]; I = [I solnew(2)]; R = [R solnew(3)];
    sol = solnew;
end
end
```

Here's an example of a Matlab script to run a simulation.

```
T = 365; % compute a solution up to time T
dt = .1; % time step for discretization
LD = 100; % time of lockdown
dur = 14; % average time an individual is infected

% Model parameters
beta = @(t) (2.5/dur+(t<LD)*1.5/dur); % infection rate
gamma = 1/dur; % recovery rate

% Initial conditions
S0 = 11*1e6 -1 % susceptible individuals
I0 = 1   % infected individuals
R0 = 0   % recovered/dead individuals

[ S,I,R, tnodes ] = SIR_fwd(S0,I0,R0,beta,gamma,T,dt);

figure; hold on;
plot(tnodes,S,'linewidth', 1.5); plot(tnodes,I,'linewidth', 1.5); plot(tnodes,R,'linewidth', 1.5);
legend('susceptible','infected','recovered/dead')
xlabel('time')
```

References

[Het00] Herbert W Hethcote. The mathematics of infectious diseases. *SIAM review*, 42(4):599–653, 2000.