University of Amsterdam

Assignment 1: SIR model (ODE)

The SIR model

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Introduction to Computational Science

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5284ITCS6Y

1 Introduction

The SIR model is a compartmental model, first introduced in 1927 by W.O. Kermack and A.G. McKendrick [4]. The SIR model provides a simplified representation of how individuals transition between different health states (susceptible (S), infected (I), recovered/removed (R)). In Figure 1 the flow between the three compartments is illustrated.

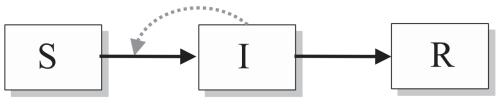


Figure 1: Flow diagram for the SIR model [3].

In this report we will study the SIR model and some of its many variants. In Section 2 we introduce the SIR model equations and its parameters. We show how demography and seasonal effects can be included in the model as well as introduce a variant on the SIR model called the SEIR model. In Section 3 we discuss some of the code and experiments found in the Jupyter Notebook associated with the assignment.

2 Background/Theory

The basic SIR model can be written as a set of first order differential equations

$$\frac{dS}{dt} = -\beta SI, \quad \frac{dI}{dt} = \beta SI - \gamma I, \quad \frac{dR}{dt} = \gamma I,$$

where β is the rate of infection and γ is the rate of recovery. Often we are more interested in $\frac{1}{\gamma}$, which determines the average infectious period. Let us define the **basic reproductive ratio** as

$$R_0 = \frac{\beta}{\gamma}.$$

When $R_0 > 1$, the number of infected individuals grows and the outbreak becomes an epidemic, whereas for $R_0 < 1$ the infection dies out [3].

2.1 The SIR model with demography

The basic SIR framework presented above is suitable for outbreaks in closed populations. Demography can be included in the SIR model as follows

$$\begin{aligned} \frac{dS}{dt} &= \mu - \beta SI - \mu S \\ \frac{dI}{dt} &= \beta SI - \frac{(\gamma + \mu)}{1 - \rho} I \\ \frac{dR}{dt} &= \gamma I - \mu R, \end{aligned} \tag{1}$$

where μ is the birth/death rate and ρ is the probability of dying while infected [3]. By allowing individuals to be born into the susceptible pool it is now possible to observe endemic behaviour. The expression for R_0 in this model is given by

$$R_0 = \frac{(1 - \rho)\beta}{\gamma + \mu}.$$

When $R_0 > 1$, the infection becomes endemic, whereas for $R_0 < 1$ the infection dies out. Note that as ρ approaches 1, infected individuals die almost instantaneously and R_0 drops to 0.

2.2 The SIR model with seasonal effects

For human infectious diseases, seasonality plays an important role [1]. We can include seasonal effects into our model by replacing β by a time varying sinusoidal rate of infection

$$\beta(t) = \beta_0(1 + \beta_1 \sin(\omega t)),$$

where β_0 is the average transmission rate, β_1 is the amplitude of seasonality and ω is the period. The substitution results in the following set of differential equations

$$\begin{aligned} \frac{dS}{dt} &= \mu - \beta(t) SI - \mu S \\ \frac{dI}{dt} &= \beta(t) SI - \frac{(\gamma + \mu)}{1 - \rho} I \\ \frac{dR}{dt} &= \gamma I - \mu R. \end{aligned} \tag{2}$$

2.3 The SEIR model

For many infectious diseases, there is a significant latency period during which individuals have been infected but are not yet infectious, this is called the incubation period. During this period individuals belong to the exposed (E) compartment, see Figure 2

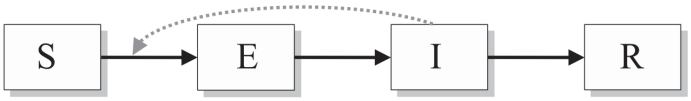


Figure 2: Flow diagram for the SEIR model [3].

The SEIR model can be described by the following set of differential equations

$$\begin{aligned} \frac{dS}{dt} &= \mu - \beta SI - \mu S \\ \frac{dE}{dt} &= \beta SI - \mu E - \sigma E \\ \frac{dI}{dt} &= \sigma E - \frac{(\gamma + \mu)}{1 - \rho} I \\ \frac{dR}{dt} &= \gamma I - \mu R, \end{aligned} \tag{3}$$

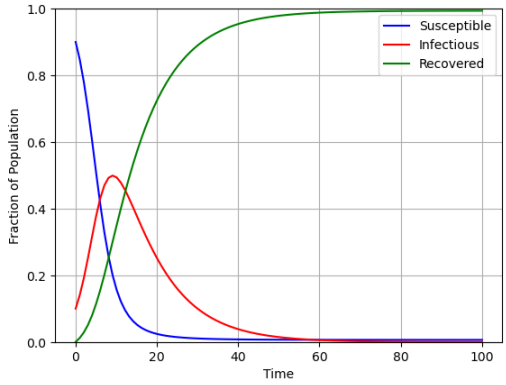
where the new parameter σ is the rate at which individuals transition from E to I.

3 Experiment/Method

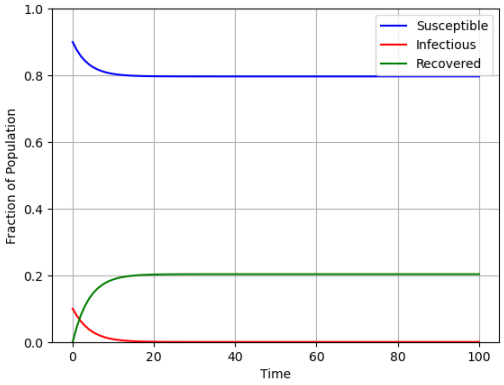
The functions *sir_model*, *seasonal_sir_model* and *seir_model* in the Jupyter Notebook implement the models (1), (2) and (3) respectively. In this section we present some experiments and results using these three models.

3.1 ODE integration

We are interested in the time-evolution of the models parameters S, I and R. As we cannot find an exact solution to the SIR equations, we use a function *solve_sir_model* that employs the *ode_int* function from the SciPy library to obtain numerical solutions for S, I, and R. This now enables us to visualize and analyze disease dynamics under various scenarios.
The Jupyter Notebook contains two functions for visualizing the disease dynamics. The function *plot_sir_model* plots the evolution of S, I and R over time, see Figure 3.



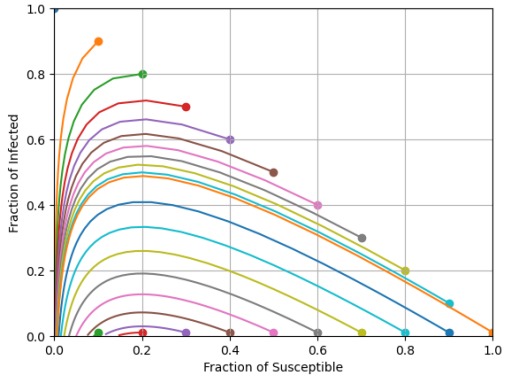
(a) SIR dynamics for $\beta = 0.5$, $\gamma = 0.1$.



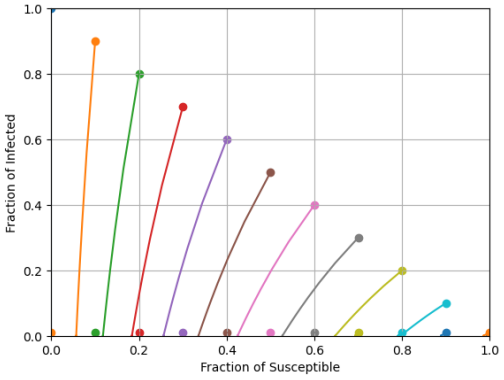
(b) SIR dynamics for $\beta = 0.3$, $\gamma = 0.5$.

Figure 3: SIR dynamics for epidemic ($R_0 > 1$) and no epidemic ($R_0 < 1$) scenario.

The function *phase_space_sir_model* creates a phase space diagram that shows the dynamics of S and I for different initial conditions $S(0)$, $I(0)$ and $R(0)$ indicated by dots, see Figure 11.



(a) Phase space diagram for $\beta = 0.5$, $\gamma = 0.1$.



(b) Phase space diagram for $\beta = 0.3$, $\gamma = 0.5$.

Figure 4: Phase space diagrams for epidemic ($R_0 > 1$) and no epidemic ($R_0 < 1$) scenario.

Note that as the population size is constant ($S + I + R = 1$), we can derive the behaviour of R from the behaviour of S and I.

3.2 Case: Influenza outbreak at boys school

Given in Table 1 is the historical data from a case of an influenza outbreak situation. The outbreak was in a boys school with a total of 763 boys.

Day	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Number	1	3	8	28	75	221	291	255	235	190	125	70	28	12	5

Table 1: Historical data from influenza outbreak at boys school.

3.2.1 Fitting data

We assume that one infected boy started the epidemic and use the *curve_fit* function from the SciPy library that uses the least squares method to fit our SIR model to the data from Table 1. This results in the estimated parameters $\beta \approx 1.66$ and $\gamma \approx 0.44$. With our estimated parameters we can plot the data and the fitted SIR model in one figure, see Figure 5.

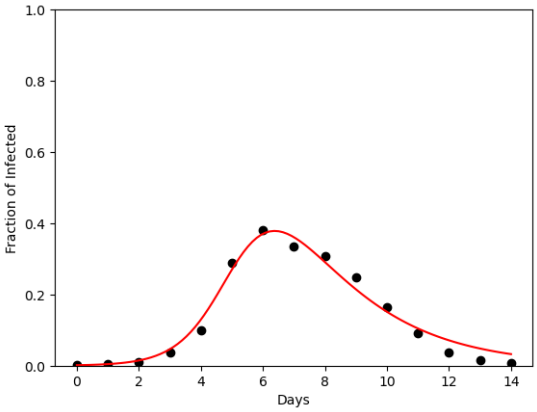
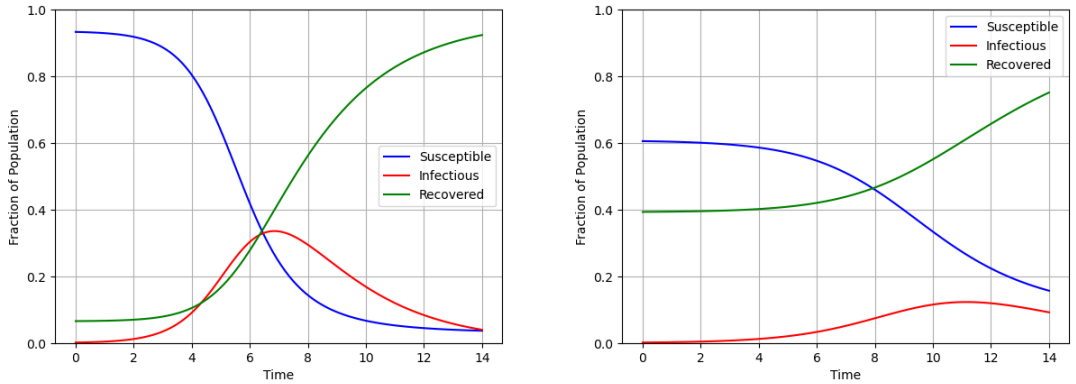


Figure 5: Influenza outbreak at boys school.

3.2.2 Vaccination

We can now study the effects of different vaccination strategies by visualizing the disease dynamics for different initial conditions for R. As we increase the number of vaccinated (removed) individuals we would expect to see less of a peak in infections.



(a) Fitted model with 50 boys vaccinated.

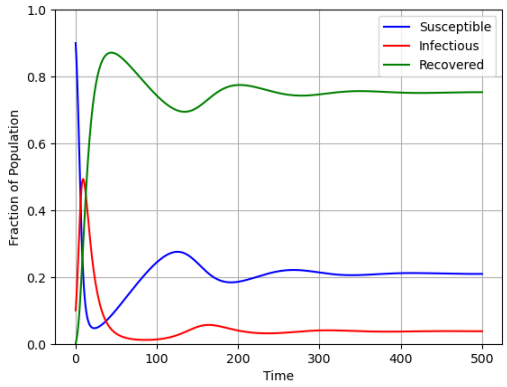
(b) Fitted model with 300 boys vaccinated.

Figure 6: Dynamics of influenza outbreak for different levels of vaccination.

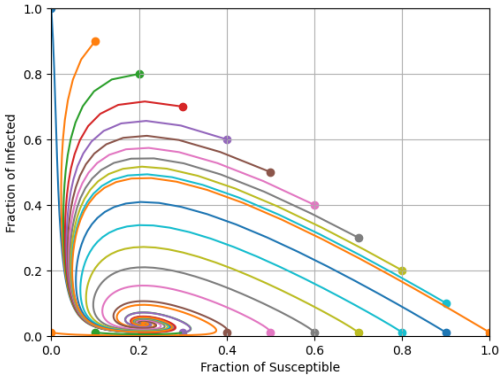
In Figure 6 we see the dynamics of the disease for different numbers of vaccinated students. As we expected, increasing the number of vaccinations indeed seems to "flatten the curve" [2].

3.3 Demography

When we choose the birth/death rate μ to be non-zero and make sure that $R_0 > 1$, we see oscillatory behaviour in the fraction of infected individuals, see Figure 7 for the time-evolution of S, I and R and the corresponding spiral phase space diagram [5].



(a) SIR dynamics for $\beta = 0.5$, $\gamma = 0.1$, $\mu = 0.005$.



(b) Phase space diagram for $\beta = 0.3$, $\gamma = 0.5$, $\mu = 0.005$.

Figure 7: SIR dynamics and corresponding phase space diagram for endemic scenario.

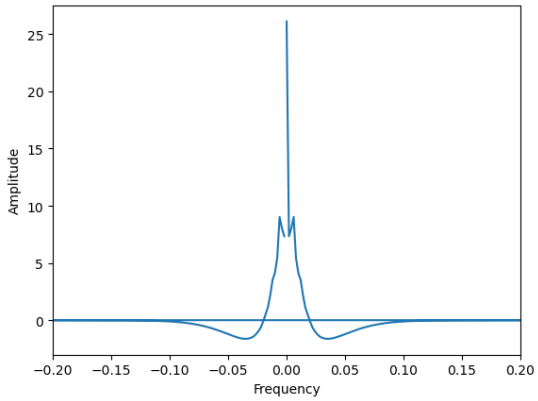


Figure 8

3.3.1 Fourier analysis

We can find the frequency and amplitude of oscillations using Fourier Transform. In the Jupyter Notebook we use the functions *fft* and *fftfreq* from the SciPy library to compute the Fourier Transform, see Figure 8.

3.4 Seasonality

The SIR model with seasonal effects (2) is implemented in the function *seasonal_sir_model*. We can use the same techniques from Section 3.1 to numerically integrate the equations and visualize the disease dynamics, see Figure 9.

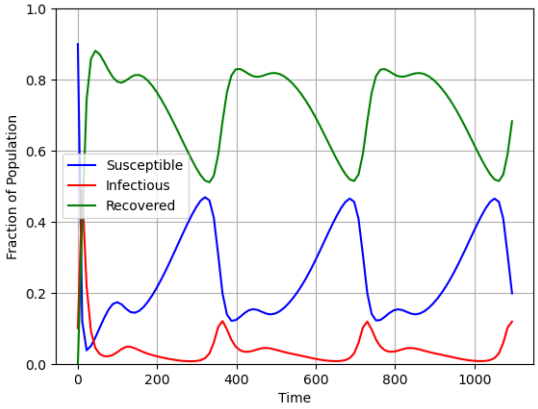


Figure 9: Seasonal SIR dynamics for $\beta_0 = 0.5$, $\beta_1 = 0.5$, $\omega = \frac{2\pi}{365}$, $\gamma = 0.1$, $\mu = 0.005$.

3.5 The SEIR model

The SEIR model (3) is implemented in the function *seir_model*. We can use the same techniques from Section 3.1 to numerically integrate the equations and visualize the disease dynamics, see Figure 10.

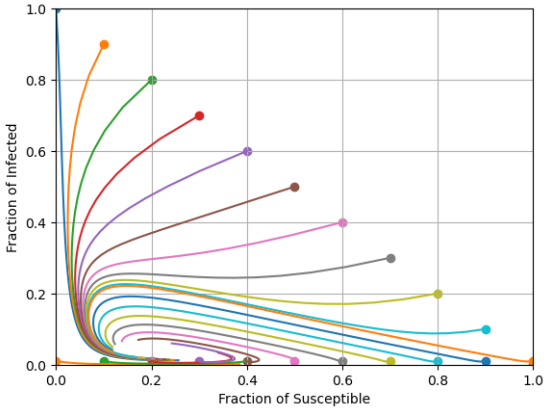


Figure 10: Phase space diagram SEIR for $\beta = 0.5$, $\sigma = 0.1$, $\gamma = 0.1$, $\mu = 0.005$.

If we compare Figure 10 to Figure 7a, we see that the SEIR dynamics are similar to the SIR dynamics only slowed down by the added latent period.

4 Discussion

During this assignment we explored the application of the SIR model in the context of infectious diseases. We adapted the basic SIR framework of differential equations to accommodate for some real world phenomena like demography, seasonality and incubation periods.

There are many more variants of the SIR model not discussed in this report. Some examples include the SIS model, where upon recovery there is no immunity and the SIRS model, where immunity lasts only for a short period of time.

Figure 11: Flow diagrams for SIS and SIRS model [3].

When doing research on a specific disease one should consider its characteristics and pick a model accordingly. There are also situations where stochastic modeling should be considered, this is explained in Chapter 6 of Keeling and Rohani [3].

It is important to emphasize that while epidemiological models like the SIR model are valuable tools for understanding infectious diseases, they should be used with care and considered within their limitations. All models discussed in this report rely on numerous simplifications and assumptions. One should always be careful making predictions using models.

References

[1] Sonia Altizer et al. "Seasonality and the dynamics of infectious diseases". In: *Ecology letters* 9.4 (2006), pp. 467–484.

[2] Marcel Boumans. "Flattening the curve is flattening the complexity of covid-19". In: *History and Philosophy of the Life Sciences* 43.1 (2021), p. 18.

[3] Matt J. Keeling and Pejman Rohani. *Modeling Infectious Diseases in Humans and Animals*. Princeton University Press, 2008.

[4] W.O. Kermack and A.G. McKendrick. "A contribution to the mathematical theory of epidemics". In: (1927).

[5] Steven H. Strogatz. *Nonlinear dynamics and chaos with applications to physics, biology, chemistry, and engineering*. CRC press, 2018.