Modeling of Infectious Diseases
Analyzing the SIR model

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Abstract

Predicting the spreading of infectious diseases is of growing importance. Diseases like malaria, SARS and measles can become very harmful for populations and can spread easily with air traffic and other kinds of human transport. When the spreading of these kind of diseases can be predicted, precautions can be taken in order to reduce the spread of diseases. One of the tools to help predicting these kind of diseases is to make models of them and compare these models with existing data. In this research an attempt has been made to model the spreading of infectious diseases in order possibly to predict the spreading of infectious diseases in the future. Several versions of the SIR model, the SEIR model and the SIS model are analyzed with different parameters to see how the spreading of infectious diseases acts within different populations. Although these models are a simplified version of real world situations they are still very useful in specific cases of infectious diseases. More parameters can be added to the models discussed in this research to adapt the models to more real world situations and datasets.

Contents

1 Introduction

The prediction of infectious diseases is important in a world were the population grows and individuals can travel all over the world. An example of an epidemic spread of an infectious disease is the outbreak of SARS in Guangdong, China, in 2002. The disease spreaded quickly, 792 people contracted the disease and the disease became fatal for 32 people [1]. From China, the disease was spreading to a lot of other countries as well, such as Vietnam, Canada and also in Europe. Other examples of the outbreak of harmful diseases are malaria, AIDS, and measles. To limit the spread of these kind of diseases precautions have to be taken. But these precautions have to be carefully examined before applying them.

There are different types of precautions that could be taken to tackle infectious diseases. In some cases it is possible to vaccinate a (large) part of the population in order to make this fraction of the population immune for the disease. The disease then cannot spread enough to become epidemic dies out. Interventions do not have to be medical, the spread of diseases could also be limited by school closure or travel restrictions. Modeling the disease can help to predict the outcomes of such interventions and can help with planning and decision making [2]. A model has to be made which can reproduce real data as closely as possible. When a model can predict existing data well, parameters of the model could be altered to see how the disease then acts. Possible precautions could be added to the model to see if they really work or that they will not be helpful.

In this research different versions of the SIR model are presented and as an addition the SIR and SEIR model are analyzed. SIR stands for the three classes in which the population can be divided according to this model: Susceptibles, Infecteds and Recovereds. In section 2 the basic version of the SIR model is presented. To the basic SIR model demography can be added as well, this is discussed in section 3. The SEIR model has an exposed class added to the SIR model, this model is analyzed in section 4. The SIS model is for diseases in which a lifelong immunity does not follows after being infected and is discussed in section 5. Finally, in section 6 a conclusion is provided.

2 Basic SIR model

In this section the basic SIR model will be analyzed. This basic model assumes that the infections are acute, that the pathogen causes illness for a certain time period and after this period a lifelong immunity follows. Kermack and McKendrick were the first ones to study this model in depth [3]. The population can be categorized in three distinct groups: Susceptibles (which never have been exposed to the pathogen), Infecteds (exposed to the pathogen and can infect susceptibles) and Recovereds (the infection is cleared and the hosts become immune to the pathogen). The population is assumed to be of a constant size (there are no births, deaths or migration). The SIR equations can be defined as following [3]:

$$\frac{dS}{dt} = -\beta SI \tag{1}$$

$$\frac{dI}{dt} = \beta SI - \gamma I \tag{2}$$

$$\frac{dR}{dt} = \gamma I \tag{3}$$

These equations describe the change in susceptibles (S), infecteds (I) and recovereds (R). The term β can be described as the product of the contact rates between the individuals and the transmission probability. The term γ describes the force of infection (the per capita rate at which individuals are infected). β and γ can be combined to a formula which represents the basic reproductive ratio (R_0):

$$R_0 = \frac{\beta}{\gamma} \tag{4}$$

The basic reproduction ratio can be defined as the average number of secondary cases of an infection caused by an average primary case [4]. The population is assumed to be entirely susceptible. If $R_0 < 1$ no epidemic occurs, is $R_0 > 1$ an infectious disease can invade the population. This is logical since an infectious disease that cannot infect more than one individual cannot invade the population [5]. In section 2.1 the model will be analyzed for the epidemic and endemic case and more explanation will be provided about the spreading of the disease in both cases.

2.1 Numerical Integration of the Basic Model

The system of ordinary differential equations described in equations (1), (2), and (3) cannot be solved analytically. Therefore, the equations must be solved numerically. In appendix A an overview of the python code that is used to (numerically) solve the differential equations can be found.

When solving the equations we can find two different states of the spreading of the disease, either epidemic or no epidemic. Epidemic means that the disease spreads through the population quickly. After a short time more people will become recovered and gain lifelong immunity, the number of infecteds will then die out quickly again. In figure 1 an example of an epidemic case of the SIR model is provided. We can clearly see that the infectious disease spreads quickly. In three days the fraction of infecteds is at its maximum and the disease dies out after seven days. All the individuals who became infected are in the recovered class after seven days. In figure 2 a phase plot of an epidemic state of the SIR model is provided. In this phase plot we can see the fraction of the population which is susceptible or infected for different initial conditions. The curves do not converge to a single solution and we can observe that the final state of the system (the fraction of susceptibles, infecteds and recovereds when $t \to \infty$) is determined by the initial fractions.

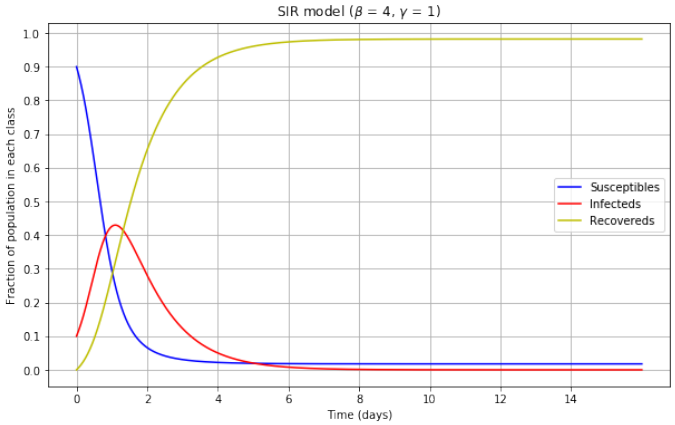

Figure 1: Time evolution of the SIR model in an epidemic state. The initial state of the populations contains a fraction of 0.1 infecteds, the rest of the population at t = 0 is susceptible.

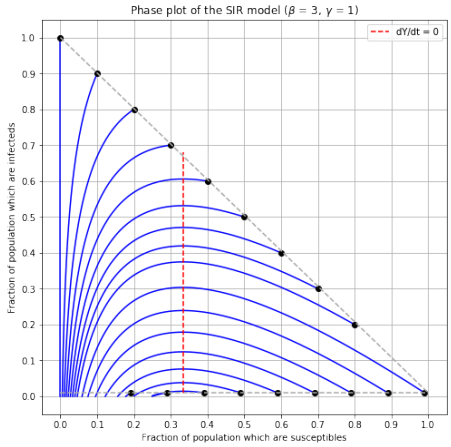

Figure 2: Phase plot of the SIR model in an epidemic state. β and γ are kept constant while the initial conditions are varied. The grey horizontal line shows where I(0) = 0.01, the grey diagonal line shows where S(0) = I (0). The red dotted line shows where the change in infecteds is 0.

No epidemic means that the disease does not spread in the population and dies out immediately. The basic reproductive ratio is smaller than 1 and the pathogen cannot invade the population. In figure 3 an example of the no epidemic case for the SIR model is provided. The initial fraction of infecteds in the population is 0.1. We can see that the infectious disease does not spread to the rest of the population, the disease dies out after 7 days and the maximum fraction of infecteds is 0.1. There is not an epidemic curve visible as in figure 1. In figure 4 we can see a phase plot for an endemic case. Like in figure 2 the fraction of the population which is susceptible or infectious can be seen for different initial conditions. We can observe that the final state of the system is even more determined by the initial conditions than in figure 2. We can also observe that less individuals get infected when there is a no epidemic state.

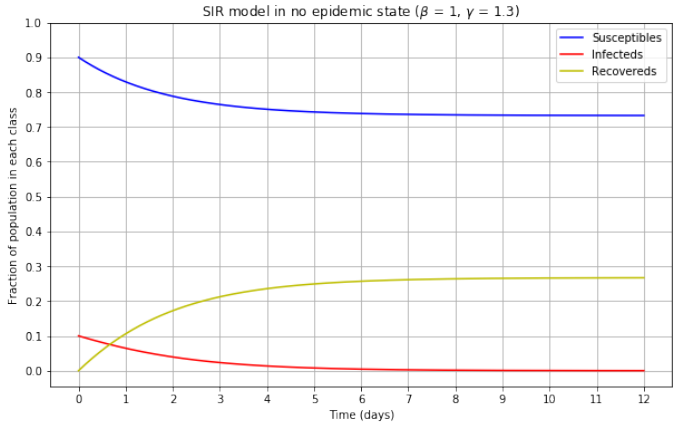

Figure 3: Time evolution of the SIR model in a no epidemic state. The initial state of the populations contains a fraction of 0.1 infecteds, the rest of the population at t = 0 is susceptible.

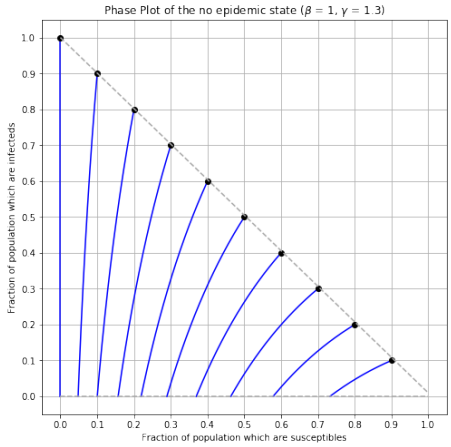

Figure 4: Phase plot of the SIR model in a no epidemic state. β and γ are kept constant while the initial conditions are varied. The grey horizontal line shows where I(0) = 0.01, the grey diagonal line shows where S(0) = I (0).

2.2 Influenza Outbreak in School

The SIR model can be used to predict the spread of a disease in the real world. To make predictions with the SIR model we first need to know how well the model performs. To see how the model performs the model can be compared to a dataset which includes data about the spreading of a disease in a population. It is important that this data contains information about the spreading of the disease in a closed population and that the whole population is monitored. In the SIR model natural mortality, birth and infection induced mortality are not taken into account. Therefore, we can only simulate infectious diseases with a short infectious period which is not fatal. An example of such a disease is influenza.

An interesting example of a dataset about the outbreak of influenza is that of an epidemic in a British boarding school in early 1978 [3]. There were 763 boys in the school of which a large fraction became infected with influenza. At t = 1 day we can observe that only 3 boys had signs of influenza. Five days 291 boys contracted the infection and after two weeks the disease extinguished.

In figure 5 we can see a graph which includes the data and the SIR epidemic curve which is fitted to the data. We can see a typical epidemic curve after six days. The fitting is done using a least squares method is used. An overview of the code used to fit the SIR model to the data can be found in appendix A. The parameters for the curve fit obtained using the least squares method are $\beta = 1.67$ days and $1/\gamma = 2.2$ days.

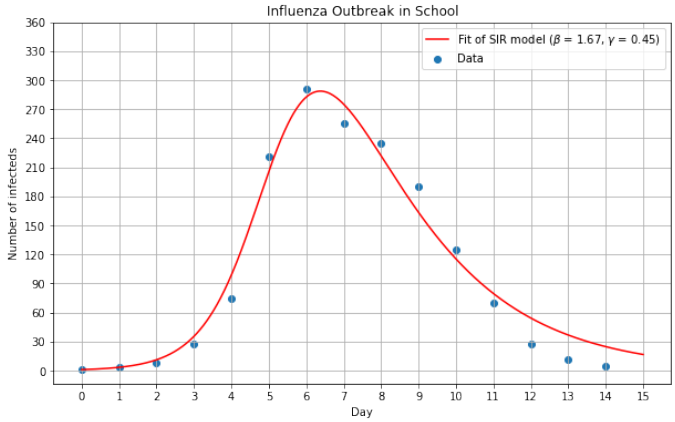

Figure 5: Epidemic for an influenza outbreak in a british school in 1978. The number of infecteds is shown through time. In total there were 763 boys in the school, at t = 0 one of the boys was infected. The SIR model is fitted on the data (blue dots) to obtain the curve shown in red.

To prevent such an epidemic in the future, vaccinations might help. By vaccinating the boys they will move from the susceptible class to the recovered class (the class in which they have lifelong immunity). Not all of the boys in the boarding school have to be vaccinated in order to prevent an epidemic state of the disease. In figure 6 a time evolution of the SIR model is provided in which 590 boys (77% of the population) are vaccinated and therefore start in the recovered class at t = 0. There is no epidemic curve visible and the disease does not spread through a large part of the population. The fraction of susceptibles stays at an almost constant value, meaning that even the boys which are not vaccinated will benefit from the vaccination plan.

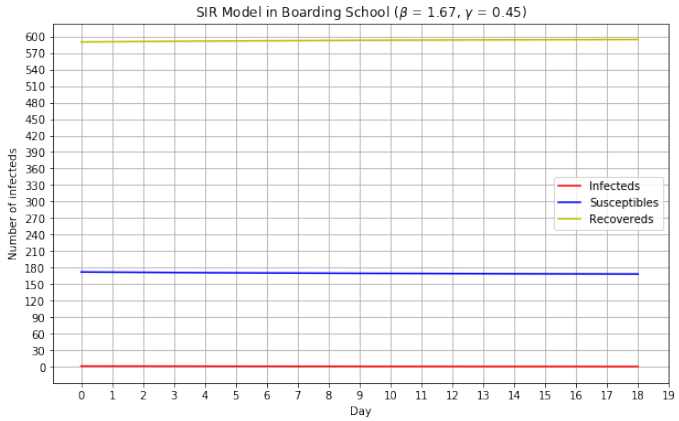

Figure 6: Time evolution of the SIR model with initial conditions S(0) = 172, I(0) = 1 and R(0) = 590. There is no epidemic state of the infectious disease visible.

3 SIR Model with Demography

In the previous section a basic version of the SIR model is used to model the spread of infectious diseases. It was assumed that there are no births, deaths or migration in the population. In this section births and natural mortality (mortality which is not caused by the infection) are taken into account as well. Because new susceptibles are born into the population the infection can become endemic. Endemic means that the infection stays present in the population and does not die out when $t \to \infty$. The equation of the SIR model with demography are as following:

$$\frac{dS}{dt} = \mu - \beta SI - \mu S \tag{5}$$

$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I \tag{6}$$

$$\frac{dR}{dt} = \gamma I - \mu R \tag{7}$$

The variables added to the SIR equations in (1), (2) and (3) is the mortality rate μ. This is the rate at which all individuals (in class S, I and R) suffer mortality which is not caused by the disease. The lifespan of an individual can be defined as $\frac{1}{\mu}$. Note that the birth rate in the model is also assumed to be μ, which causes a constant size of the population through time. Because new susceptibles are added into the population the disease can become endemic [3]. In the next section the endemic state of this version of the SIR model is analyzed.

3.1 SIR model with birth and natural mortality

As in section two, the differential equations cannot be solved analytically. Using a numerical algorithm the solutions for different parameters and initial conditions can be determined. Because birth and mortality are added to the population we now can examine an endemic state of an infectious disease. In figure 7 we can see such an endemic state for certain parameters and initial conditions. Note that R_0 still has to be larger than 1 in order to make the disease endemic. If R_0 is smaller than one the disease will still die out.

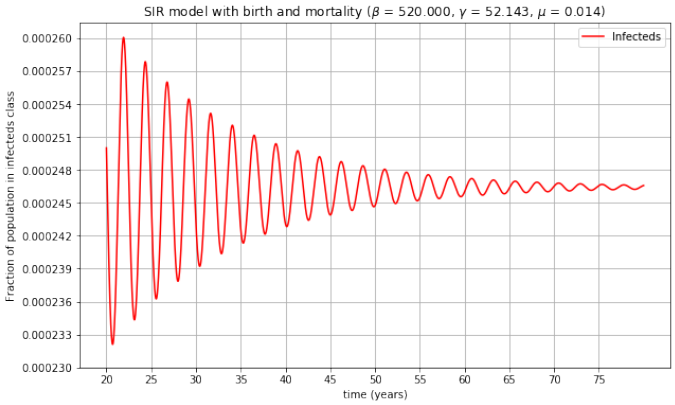

Figure 7: Time evolution of the SIR model in an endemic state with birth and natural mortality taken into account, only the fraction of the population which are infecteds is shown. The initial conditions were $S(0) = 0.1, I(0) = 2.5(10^{-4})$ and $R = 1 - S - I$.

In figure 7 we can see oscillatory behaviour in the fraction of the population which are infecteds. As time goes by the amplitude of the number of infecteds becomes smaller and moves towards an equilibrium. In order to determine the frequency of this oscillatory behaviour we can invoke fourier transformations. In figure 8 we can see what amplitudes and frequencies are of the oscillations in figure 7. It is found that the disease has a period of 2.398 years. The programming code used to calculate the fourier transformations can be found in appendix A.

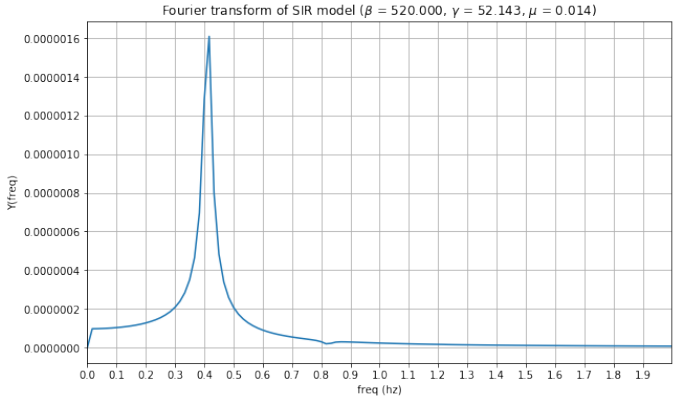

Figure 8: A fast fourier transform is applied to the curve which is shown in figure 6. The amplitudes and frequencies of the curve are obtained in this manner and shown in the graph. A peak can be observed at a frequency of 0.417, meaning that one period of the oscillation takes 2.398 years.

In the phase plots of the version of the SIR model in section 2 the final state of the system depends on the initial state of the differential equations. In figure 9 a phase plot is provided which contains the endemic state of the SIR model. β and γ are kept constant while the initial conditions are varied. It can be observed that the final state of the systems always reaches toward an equilibrium, independent of the initial state of the system.

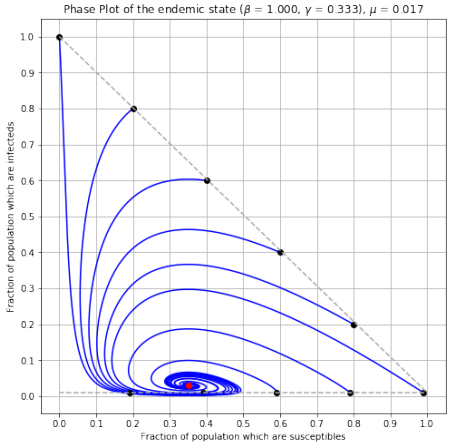

Figure 9: Phase plot of the SIR model in an endemic state. β and γ are kept constant while the initial conditions are varied. The grey horizontal line shows where I(0) = 0.01, the grey diagonal line shows where S(0) = I (0). The red dotted line shows where the change in infecteds is 0.

3.2 SIR model with infection induced mortality

In addition to the SIR model with natural mortality and birth described in equations (5), (6) and (7) we can also add mortality which is induced by the infectious disease. Examples of diseases which can be fatal after a certain infectious period are malaria or measles. Individuals in the infected class can suffer mortality with a probability ρ. Note that ρ can take values ranging from 0 to 1 since it is a probability. This leads to the following equation for dI/dt:

$$\frac{dI}{dt} = \beta SI - \frac{(\gamma + \mu)}{1 - \rho} I \tag{8}$$

The equations for S and R are not changed compared to the previous SIR model with birth and natural mortality and can be found in equations (5) and (7). It is important to note that the size of the population is not constant anymore. In figure 10 a time evolution of the SIR model with the added infection induced mortality is given. We can observe that the total population decreases through time. The spread of infection is less than in the previous diseases due to the mortality

rate in the infecteds class.

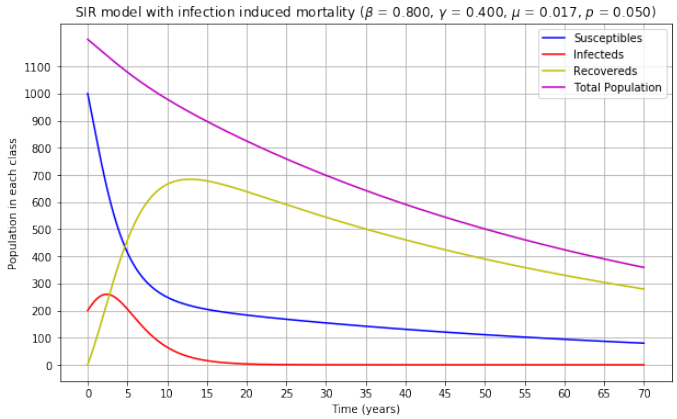

Figure 10: Time evolution of the SIR model with infection induced mortality. The per capita probability of dying from the infection is 0.05. At t = 0 the population has a size of 1200 individuals, of which 200 are infected. The population is not constant in time due to the added mortality.

When the probability of a disease being fatal becomes larger the infection dies out faster. Whereas in figure 10 the disease was in the population for 20 days ($\rho = 0.05$) the disease dies out after only three days when $\rho = 0.8$ (figure 11). This is logical since the fraction of infecteds decreases when more individuals of this class suffer mortality.

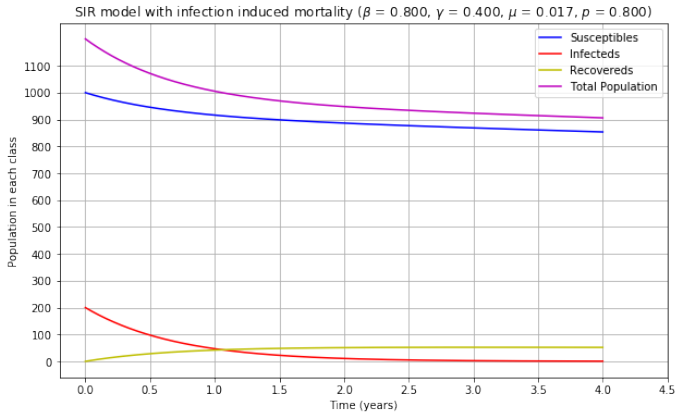

Figure 11: Time evolution of the SIR model with infection induced mortality. The per capita probability of dying from the infection is 0.8. At t = 0 the population has a size of 1200 individuals, of which 200 are infected. The population is not constant in time due to the added mortality.

4 SEIR Model

In the previous versions of the SIR models we assumed that an individual which is exposed to a disease immediately can infect other individuals. This is not the case for most infectious diseases. When an individual is exposed to an infectious disease it takes some time before the pathogen becomes abundant enough to infect other individuals [3]. In the SEIR model the period in which the individual is exposed to a disease but can not yet spread the disease to other individuals is taken into account. The extra class in this model, E, stands for the exposed class. The equations for the SEIR model can be defined as:

$$\frac{dS}{dt} = \mu - (\beta)I + \mu)S \tag{9}$$

$$\frac{dE}{dt} = \beta SI - (\mu + \sigma)E \tag{10}$$

$$\frac{dI}{dt} = \sigma E - (\mu + \gamma)I \tag{11}$$

$$\frac{dR}{dt} = \gamma I - \mu R \tag{12}$$

The average duration of the period in which the individual is exposed is defined as $1/\sigma$. By adding an exposed class into the SIR model the infection has a slower growth rate because susceptibles will first go through the exposed class before going to the infecteds class. In figure 12 a comparison is being made to show the differences with the (demographic) SIR model and the SEIR model. It can indeed be observed that the growth rate of infecteds is smaller in the SEIR model than in the SIR model.

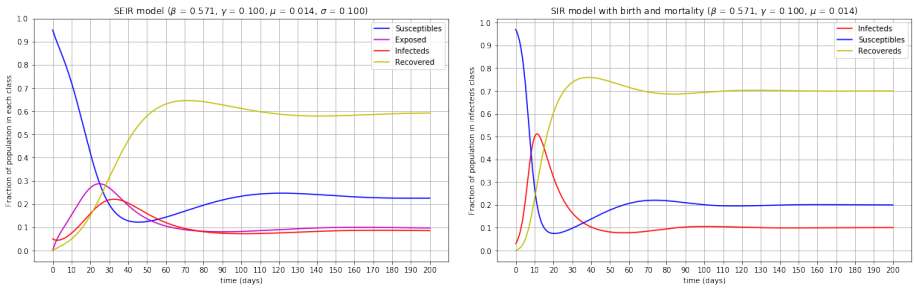

Figure 12: Comparison of SEIR model and SIR model with birth and mortality through time. In both cases at t = 0 the fraction of the population which was infected was 0.03 and the rest of the population was susceptible.

4.1 Addition of Seasonal Effects

Most infectious diseases have proven to have seasonal dynamics. By seasonal effects we mean the effect that some diseases become more prevalent in, for example, certain months within a year. Measles is one of the infectious diseases which shows such seasonal effects. There is a certain periodicity in the epidemics of measles. Data of the number of infecteds with measles of a large population have been investigated and show recurrent epidemics with amplitudes in varying sizes [6]. To add these seasonality into our model we can change the transmission rate, β, into a time dependent transmission rate:

$$\beta(t) = \beta_0(1 + \beta_1 \cos(\omega t)) \tag{13}$$

Here, β_0 represents the average transmission rate, ω is the period of forcing and β_1 is the amplitude of seasonality [3]. By adding this time dependent dependent transmission rate to our SEIR model and solve the model for a certain time period we obtain figure 13. We can indeed observe oscillatory behavior in the model.

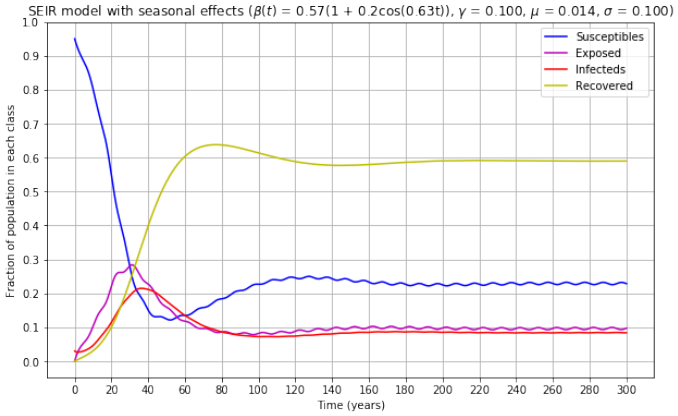

Figure 13: Time evolution of the SEIR model with the addition of seasonal effects, which means that the transmission rate, β, is a function of time now.

To see how this seasonal effect can behave in the long term we also added figure 14. Here we look at an endemic case of a disease throughout the years. We can clearly see the seasonal forcing and dramatic peaks in the amplitude of the seasonality. It is interesting to observe that the variety in peaks is not annual but multi annual, there is subharmonic resonance visible.

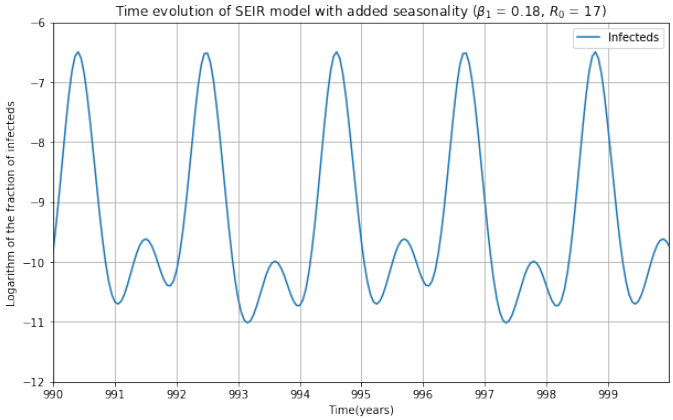

Figure 14: Time evolution of the SEIR model with the addition of seasonal effects. It is clear that there is a different dynamical pattern visible than in figure 12. We assumed that the period of forcing is one year ($\omega = 2\pi$). The initial conditions were $S(0) = 6 \times 10^{-2}$, $E(0) = I(0) = 10^{-3}$ and $R(0) = 1 - S(0) - I(0) - E(0)$. The parameters used were $\mu = 0.02$, $\sigma = 365/8$ and $\gamma = 365/5$ (all in years).

5 The SIS model

There are diseases in which individuals do not gain lifelong immunity after an infectious period. Some sexually transmitted diseases, bacterial infections and rotaviruses do not cause lifelong immunity in individuals [3]. For the modelling of these types of diseases the SIS model can be used. In this model there is no recovered class anymore. Individuals who come out of the infected class will be transferred to the susceptible class. The model can be described by the following equations:

$$\frac{dS}{dt} = \gamma I - \beta IS \tag{14}$$

$$\frac{dI}{dt} = \beta SI - \gamma I \tag{15}$$

When we solve this set differential equations for $R_0 = 4$ years, we obtain a solution as described in figure 15. After 4 years the system reaches an equilibrium with a fraction of 0.37 in the susceptibles class and a fraction of 0.63 in the infecteds class. We can conclude that the disease stays prevalent in the population and does not die out.

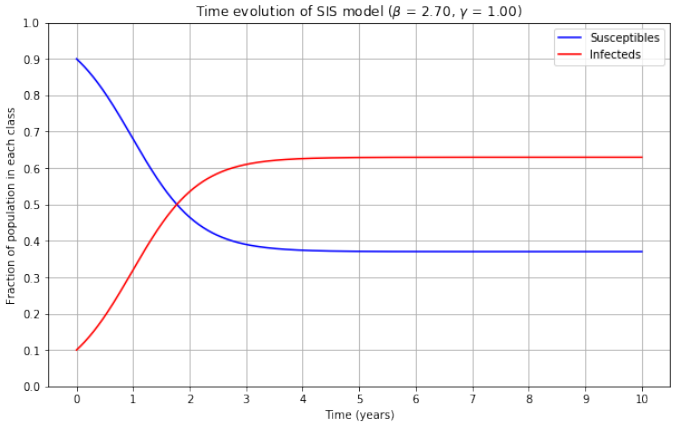

Figure 15: Time evolution of the SIS model. The initial conditions of this figure are I(0) = 0.1 and S(0) = 0.9 (fractions of the population). After 4 years the system reaches its equilibrium.

6 Conclusions

In this report multiple versions of the SIR model, the SEIR model and the SIR have been analyzed. The most simplest version of the SIR model could successfully be fitted on existing data about an influenza outbreak in a british boarding school. For this specific type of epidemic outbreaks the simple SIR models shows to be suitable for the prediction of the development of an infectious disease. By adding demography to the basic SIR model we also analyzed the endemic state of infectious diseases. This endemic state depends on the transmission rate R_0, which depends on the variables β and γ. When the initial conditions are varied the system goes to a certain equilibrium. To observe the oscillatory behaviour in the endemic state we used fourier transformations. In order to extend the model even more infection induced mortality has also been added to the model and analyzed.

For different types of diseases different types of models are needed to describe the diseases. The SIR model has proven to be useful in diseases like influenza and measles. When the disease also has a latent period in it (where an individual is not immediately infected after being exposed to the disease) an extra class can be added. For these types of diseases we can use the SEIR model, which is discussed in section 4. In this section we also adjusted the model by including seasonal behavior. By including seasonal forcing the model became better at predicting diseases with seasonal dynamics as is the case in measles. For diseases in which a lifelong immunity after the infection is not prevalent, the SIS model can be used. Sexual transmitted diseases are one example of diseases which can be used in the SIS model, which is discussed in section 5.

In all of the models discussed in this model we assumed a homogeneous mixed population in which all the individuals had the same probability of contracting the infectious disease. Age is for example not taken into account. We also did not describe the population with discrete variables. We treated the number of individuals in the different classes in a continuous manner. To make the model predict more types of real world situations regarding to the spreading of infectious diseases, the above notes could be taken into account as well.

References

[1] J. Peiris, S. Lai, L. Poon, Y. Guan, L. Yam, W. Lim, J. Nicholls, W. Yee, W. Yan, M. Cheung, *et al.*, "Coronavirus as a possible cause of severe acute respiratory syndrome," *The Lancet*, vol. 361, no. 9366, pp. 1319–1325, 2003.

[2] C. Fraser, S. Riley, R. M. Anderson, and N. M. Ferguson, "Factors that make an infectious disease outbreak controllable," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 101, no. 16, pp. 6146–6151, 2004.

[3] M. J. Keeling and P. Rohani, *Modeling infectious diseases in humans and animals*. Princeton University Press, 2008.

[4] O. Diekmann and J. A. P. Heesterbeek, *Mathematical epidemiology of infectious diseases: model building, analysis and interpretation*, vol. 5. John Wiley & Sons, 2000.

[5] R. M. Anderson and R. May, "Coevolution of hosts and parasites," *Parasitology*, vol. 85, no. 2, pp. 411–426, 1982.

[6] H. Soper, "The interpretation of periodicity in disease prevalence," *Journal of the Royal Statistical Society*, vol. 92, no. 1, pp. 34–73, 1929.

7 Appendix A

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# coding: utf-8

# Assignment 1
# Introduction to Computational Science
# Marleen Rijksen (10465030)
# 29 September 2017

# necessary packages
get_ipython().magic('pylab inline')
pylab.rcParams['figure.figsize'] = [10, 6]
from scipy.integrate import odeint
from scipy.optimize import curve_fit

# Problem 1.1: basic SIR model

# SIR model function which returns derivative of y
def SIR(y, t, beta, gamma):
    S, I, R = y # y is vector [S, I, R]
    dydt = [-beta * S * I, beta * S * I - gamma * I, gamma * I]
    return dydt

# constants for epidemic case
beta = 4
gamma = 1
y0 = [0.9, 0.1, 0] # initial conditions
t = np.linspace(0, 16, 1000) # time span

# calculate solution
sol = odeint(SIR, y0, t, args=(beta, gamma))

# plot
plt.plot(t, sol[:, 0], 'b', label='Susceptibles')
plt.plot(t, sol[:, 1], 'r', label='Infecteds')
plt.plot(t, sol[:, 2], 'y', label='Recovereds')
plt.legend(loc='best')
plt.xlabel('Time (days)')
plt.ylabel('Fraction of population in each class')
plt.title('SIR model ($\\beta$ = {}, $\\gamma$ = {})'.format(beta, gamma))
plt.xticks(range(0, 16, 2))
plt.yticks(np.arange(0, 1.1, 0.1))
plt.grid()
plt.show()

# Problem 1.1 phase plots epidemic state

# constants
beta = 3
gamma = 1
t = np.linspace(0, 16, 1000) # time span

# iterate over initial conditions
for i in np.arange(0, 0.9, 0.1):
    y0 = [i, 1 - i, 0]
    sol = odeint(SIR, y0, t, args=(beta, gamma))

    # plot for every condition
```

```
        plt.plot(sol[:, 0], sol[:, 1], 'b')

        # draw dot at t = 0
        plt.plot(sol[:, 0][0], sol[:, 1][0], marker='o', color='k')

        # initial conditions when recovereds are not 0
        y0 = [1 - i - 0.01, 0.01, i]
        sol = odeint(SIR, y0, t, args=(beta, gamma))

        # plot
        plt.plot(sol[:, 0], sol[:, 1], 'b')
        plt.plot(sol[:, 0][0], sol[:, 1][0], marker='o', color='k')

# plot some extra lines
plt.plot([0, 1], [1, 0.01], '--', color = 'darkgray')
plt.plot([0, 1], [0.01, 0.01], '--', color = 'darkgray')
plt.plot([gamma / float(beta), gamma / float(beta)], [0.01, 0.68], '--', color = 'r', label='dY/dt = 0')
plt.legend(loc='best')

# show final results
plt.title('Phase plot of the SIR model ($\\beta$ = {}, $\\gamma$ = {})'.format(beta, gamma))
plt.xlabel('Fraction of population which are susceptibles')
plt.ylabel('Fraction of population which are infecteds')
plt.xticks(np.arange(0, 1.1, 0.1))
plt.yticks(np.arange(0, 1.1, 0.1))
plt.grid()
plt.show()

# problem 1.1 no epidemic state

# constants for no epidemic
beta = 1
gamma = 1.3
days = 12
t = np.linspace(0, days, 1000) # time span
y0 = [0.9, 0.1, 0] # initial conditions

# calculate new solution
sol = odeint(SIR, y0, t, args=(beta, gamma))

# plot
plt.plot(t, sol[:, 0], 'b', label='Susceptibles')
plt.plot(t, sol[:, 1], 'r', label='Infecteds')
plt.plot(t, sol[:, 2], 'y', label='Recovereds')
plt.legend(loc='best')
plt.xlabel('Time (days)')
plt.ylabel('Fraction of population in each class')
plt.title('SIR model in no epidemic state ($\\beta$ = {}, $\\gamma$ = {})'.format(beta, gamma))
plt.xticks(range(0, days + 1, 1))
plt.yticks(np.arange(0, 1.1, 0.1))
plt.grid()
plt.show()

# 1.1 phase plot no epidemic state

# constants
beta = 1
gamma = 1.3
```

```
days = 12
t = np.linspace(0, days, 1000) # time span

# iterate over initial conditions
for i in np.arange(0, 1, 0.1):
    y0 = [i, 1 - i, 0]
    sol = odeint(SIR, y0, t, args=(beta,gamma))

    # plot for every condition
    plt.plot(sol[:, 0], sol[:, 1], 'b')

    # draw dot at t = 0
    plt.plot(sol[:, 0][0], sol[:, 1][0], marker='o', color='k')

# plot some extra lines
plt.plot([0, 1], [1, 0.01], '--', color = 'darkgray')
plt.plot([0, 1], [0.0, 0.0], '--', color = 'darkgray')
plt.title('Phase Plot of the no epidemic state ($\\beta$ = {}, $\\gamma$ = {})'.format(beta, gamma))

# show final results
plt.xlabel('Fraction of population which are susceptibles')
plt.ylabel('Fraction of population which are infecteds')
plt.xticks(np.arange(0, 1.1, 0.1))
plt.yticks(np.arange(0, 1.1, 0.1))
plt.grid()
plt.show()

# Problem 1.2: influenza outbreak in school

# data of influenza disease in boarding school
day = [x for x in range(0, 15)]
number_infected = [1, 3, 8, 28, 75, 221, 291, 255, 235, 190, 125, 70, 28, 12, 5]

# initial conditions
y0 = [762, 1, 0]
t = np.linspace(0, 15, 1000)
N = 763

# function which returns derivative of y, not normalized version
def SIR_model_N(y, t, beta, gamma):
    S, I, R = y # y is vector [S, I, R]
    dydt = [- beta * S * I / N, beta * S * I / N - gamma * I, gamma * I]
    return dydt

# function which integrates our ODEs for different beta & gamma
def integrated_SIR(t, beta, gamma):
    sol = odeint(SIR_model_N, y0, t, args=(beta, gamma))
    return sol[:, 1]

# now we have to fit our integrated function on the data
# note that we only change beta and gamma, NOT the initial conditions
# use scipy.optimize.curve_fit to fit our model for different
# beta and gamma to our data points
popt, pcov = curve_fit(integrated_SIR, day, number_infected)
beta = popt[0]
gamma = popt[1]

# plot data and model fit
```

```
plt.scatter(day, number_infected, marker='o', label='Data')
plt.plot(t, integrated_SIR(t, beta, gamma), 'r', label='Fit of SIR model ($\\beta$ = {:.2f}, $\\gamma$
plt.legend(loc='best')
plt.xlabel('Day')
plt.ylabel('Number of infecteds')
plt.xticks(range(0, 16, 1))
plt.yticks(np.arange(0, 370, 30))
plt.grid()
plt.title('Influenza Outbreak in School')
plt.show()

# problem 1.3: vaccination

# change initial conditions, more boys are in the recovereds
# class because of the vaccination
N = 763
I0 = 1
R0 = 590
S0 = N - R0 - I0
y0 = [S0, I0, R0]
t = np.linspace(0, 18, 1000)

# function which returns derivative of y, not normalized version
def SIR_model_N(y, t, beta, gamma):
    S, I, R = y # y is vector [S, I, R]
    dydt = [- beta * S * I / N, beta * S * I / N - gamma * I, gamma * I]
    return dydt

# calculate solution
sol = odeint(SIR_model_N, y0, t, args=(beta,gamma))

# plot data and model fit
plt.plot(t, sol[:, 1], 'r', label='Infecteds')
plt.plot(t, sol[:, 0], 'b', label='Susceptibles')
plt.plot(t, sol[:, 2], 'y', label = 'Recovereds')
plt.legend(loc='best')
plt.xlabel('Day')
plt.ylabel('Number of infecteds')
plt.xticks(range(0, 20, 1))
plt.yticks(np.arange(0, 620, 30))
plt.grid()
plt.title('SIR Model in Boarding School ($\\beta$ = {:.2f}, $\\gamma$ = {:.2f})'.format(beta, gamma))
plt.show()

# 2.1 include birth and mortality in model

# SIR model function which returns derivative of y for demographic version
def SIR_dem(y, t, beta, gamma, mu):
    S, I, R = y # y is vector [S, I, R]
    dydt = [mu - beta * S * I - mu * S, beta * S * I - gamma * I - mu * I,  gamma * I - mu * R]
    return dydt

# define constants for endemic state
beta = 520
gamma = 1 / 0.019178
mu = 1 / 70.

# define initial conditions
```

```
S0 = 0.1
I0 = 2.5 * (10 ** -4)
y0 = [S0, I0, 1 - S0 - I0]

# define timespan and number of steps
t = np.linspace(20, 80, 5000)

# calculate solution
sol = odeint(SIR_dem, y0, t, args=(beta, gamma, mu))

# plot, this is the endemic case
plt.plot(t, sol[:, 1], 'r', label='Infecteds')
plt.legend(loc='best')
plt.xlabel('time (years)')
plt.ylabel('Fraction of population in infecteds class')
plt.title('SIR model with birth and mortality ($\\beta$ = {:.3f}, $\\gamma$ = {:.3f}, $\\mu$ = {:.3f})'.format(
plt.grid()
plt.xticks(range(20, 80, 5))
plt.yticks(np.arange(0.000230, 0.000261, 0.000003))
plt.show()

# 2.1 fast fourier transform of oscillation
# source: https://plot.ly/matplotlib/fft/

# intervals
Fs = 5000 # sampling rate
Ts = 1.0 / Fs # sampling interval
t = np.arange(20, 80, Ts) # time vector

# calculate solution
y = odeint(SIR_dem, y0, t, args=(beta, gamma, mu))[:, 1]

# substract the mean to correct for line through middle of function
y = y - np.mean(y)

# determine frequency range (one sided)
n = len(y) # length of the signal
k = np.arange(n)
T = n / Fs # signal interval
frq = k / T
frq = frq[range(n // 2)]

# calculate fft and normalize
Y = np.fft.fft(y) / n
Y = Y[range(n // 2)]

# plot
plt.plot(frq, abs(Y))
plt.xlim(0, 2)
plt.xlabel('freq (hz)')
plt.ylabel('Y(freq)')
plt.title('Fourier transform of SIR model ($\\beta$ = {:.3f}, $\\gamma$ = {:.3f}, $\\mu$ = {:.3f})'.format(beta
plt.grid()
plt.xticks(np.arange(0, 2, 0.1))
plt.show()

# find frequency at which Y is maximal
maxi = list(Y).index(max(Y))
```

```
print(frq[maxi])

# 2.1 phase plot of demographic SIR model in endemic state

# define constants
beta = 1
gamma = 1 / 3
mu = 1 / 60.
t = np.linspace(0, 1000, 50000)

# iterate over initial conditions
for i in np.arange(0, 1, 0.2):
    y0 = [i, 1 - i, 0]
    sol = odeint(SIR_dem, y0, t, args=(beta,gamma, mu))

    # plot for every condition
    plt.plot(sol[:, 0], sol[:, 1], 'b')

    # draw dot at t = 0
    plt.plot(sol[:, 0][0], sol[:, 1][0], marker='o', color='k')

    # initial conditions when recovereds are not 0
    y0 = [1 - i - 0.01, 0.01, i]
    sol = odeint(SIR_dem, y0, t, args=(beta, gamma, mu))

    # plot
    plt.plot(sol[:, 0], sol[:, 1], 'b')
    plt.plot(sol[:, 0][0], sol[:, 1][0], marker='o', color='k')

# plot extra lines
plt.plot([0, 1], [1, 0.01], '--', color = 'darkgray')
plt.plot([0, 1], [0.01, 0.01], '--', color = 'darkgray')

# plot dot at final point
plt.plot(sol[:, 0][50000 - 1], sol[:, 1][50000 - 1], marker = 'o', color = 'r')

# show final results
plt.title('Phase Plot of the endemic state ($\\beta$ = {:.3f}, $\\gamma$ = {:.3f}), $\\mu$ = {:.3f}'.format(bet
plt.xlabel('Fraction of population which are susceptibles')
plt.ylabel('Fraction of population which are infecteds')
plt.xticks(np.arange(0, 1.1, 0.1))
plt.yticks(np.arange(0, 1.1, 0.1))
plt.grid()
plt.show()

# problem 2.2: add infection induced mortality

# SIR model function with infection induced mortality
def SIR_dem_mort(y, t, beta, gamma, mu, p):
    S, I, R = y # y is vector [S, I, R]
    dydt = [mu - beta / N * S * I - mu * S, beta * S * I / N - ((gamma + mu) / (1 - p)) * I, gamma * I - mu *
    return dydt

# define constants
beta = 0.8
gamma = 0.4
mu = 1 / 60.
p = 0.05
```

```
years = 70

# define initial conditions
N = 1200
S0 = 1000
I0 = 200
y0 = [S0, I0, N - S0 - I0]

# define timespan and number of steps
t = np.linspace(0, years, 10000)

# calculate solution
sol = odeint(SIR_dem_mort, y0, t, args=(beta, gamma, mu, p))

# plot
plt.plot(t, sol[:, 0], 'b', label='Susceptibles')
plt.plot(t, sol[:, 1], 'r', label='Infecteds')
plt.plot(t, sol[:, 2], 'y', label='Recovereds')
plt.plot(t, sol[:, 0] + sol[:, 2] + sol[:, 1], 'm', label = 'Total Population')
plt.legend(loc='best')
plt.xlabel('Time (years)')
plt.ylabel('Population in each class')
plt.xticks(np.arange(0, years + 5, 5))
plt.yticks(range(0, S0 + 200, 100))
plt.title('SIR model with infection induced mortality ($\\beta$ = {:.3f}, $\\gamma$ = {:.3f}, $\\mu$ = {:.3f}, $p
plt.grid()
plt.show()

# Problem 3: SIS model
# function which returns derivatives of SIS model
def SIS(y, t, beta, gamma):
    S, I = y # y is [S, I]
    dydt = [gamma * I - beta * I * S, beta * S * I - gamma * I]
    return dydt

# define constants
beta = 2.7
gamma = 1

# define initial conditions
y0 = [0.9, 0.1]

# define timespan and number of steps
t = np.linspace(0, 10, 1000)

# calculate solution
sol = odeint(SIS, y0, t, args=(beta, gamma))

# calculat equilibrium
print(sol[:, 0][999], sol[:, 1][999])

# plot
plt.plot(t, sol[:, 0], 'b', label='Susceptibles')
plt.plot(t, sol[:, 1], 'r', label='Infecteds')
plt.legend(loc='best')
plt.xlabel('Time (years)')
plt.ylabel('Fraction of population in each class')
plt.xticks(range(11))
```

```
plt.yticks(np.arange(0, 1.1, 0.1))
plt.grid()
plt.title('Time evolution of SIS model ($\\beta$ = {:.2f}, $\\gamma$ = {:.2f})'.format(beta,gamma))
plt.show()

# Problem 3: SEIR model

# function which returns derivatives of SEIR model
def SEIR(y, t, beta, gamma, mu, sigma):
    S, E, I, R = y # y is vector [S, E, I, R]
    dydt = [mu - (beta * I + mu) * S, beta * S * I - (mu + sigma) * E, sigma * E - (mu + gamma) * I, gamma *
    return dydt

# define constants
gamma = (1 / 10)
mu = 1 / 70.
# R0 = 5
beta = R0 * (gamma + mu)
sigma = 0.1
days = 200

# define initial conditions
N = 1000
S0 = 950. / N
E0 = 0. / N
I0 = 50. / N
y0 = [S0, 0, I0, 0]

# define timespan and number of steps
t = np.linspace(0, days, 10000)

# calculate solution
sol = odeint(SEIR, y0, t, args=(beta, gamma, mu, sigma))

# plot
plt.plot(t, sol[:, 0], 'b', label='Susceptibles')
plt.plot(t, sol[:, 1], 'm', label='Exposed')
plt.plot(t, sol[:, 2], 'r', label='Infecteds')
plt.plot(t, sol[:, 3], 'y', label='Recovered')
plt.legend(loc='best')
plt.xlabel('time (days)')
plt.ylabel('Fraction of population in each class')
plt.title('SEIR model ($\\beta$ = {:.3f}, $\\gamma$ = {:.3f}, $\\mu$ = {:.3f}, $\\sigma$ = {:.3f})'.format(beta
plt.yticks(np.arange(0, 1.1, 0.1))
plt.xticks(range(0, 205, 10))
plt.grid()
plt.show()

# problem 2.1: include birth and mortality in SIR model
# function which returns derivative of y for demographic model
def SIR_dem(y, t, beta, gamma, mu):
    S, I, R = y # y is vector [S, I, R]
    dydt = [mu - beta * S * I - mu * S, beta * S * I - gamma * I - mu * I, gamma * I - mu * R]
    return dydt

# define constants
gamma = 1 / 10
mu = 1 / 70.
```

```
R0 = 5
beta = R0 * (gamma + mu)

# define initial conditions
N = 1000
S0 = 970. / N
I0 = 30. / N
y0 = [S0, I0, 0]

# define timespan and number of steps
t = np.linspace(0, 200, 10000)

# calculate solution
sol = odeint(SIR_dem, y0, t, args=(beta, gamma, mu))

# plot, this is the epidemic case
plt.plot(t, sol[:, 1], 'r', label='Infecteds')
plt.plot(t, sol[:, 0], 'b', label='Susceptibles')
plt.plot(t, sol[:, 2], 'y', label='Recovereds')
plt.legend(loc='best')
plt.xlabel('time (days)')
plt.ylabel('Fraction of population in infecteds class')
plt.title('SIR model with birth and mortality ($\\beta$ = {:.3f}, $\\gamma$ = {:.3f}, $\\mu$ = {:.3f})'.format(
plt.yticks(np.arange(0, 1.1, 0.1))
plt.xticks(range(0, 205, 10))
plt.grid()
plt.show()

# problem 3: SEIR model with seasonality
def SEIR_seas(y, t, beta0, beta1, gamma, mu, sigma, omega):
    S, E, I, R = y # y is vector [S, E, I, R]
    dydt = [mu - (beta0 * (1 + beta1 * np.cos(omega * t)) * I + mu) * S, beta0 * (1 + beta1 * np.cos(omega * t))
    return dydt

# define constants
R0 = 5
mu = 1 / 70.
gamma = 1 / 10.
beta0 = R0 * (gamma + mu)
beta1 = 0.2
omega = 0.2 * np.pi
sigma = 0.1
days = 200

# define initial conditions
N = 1000
S0 = 950. / N
E0 = 20. / N
I0 = 30. / N
y0 = [S0, 0, I0, 0]
S = []
E = []
I = []
R = []

# define timespan and number of steps
t = np.linspace(0, 300, 10000)
```

```
# find solution
sol = odeint(SEIR_seas, y0, t, args=(beta0, beta1, gamma, mu, sigma, omega))

# plot
plt.plot(t, sol[:, 0], 'b', label='Susceptibles')
plt.plot(t, sol[:, 1], 'm', label='Exposed')
plt.plot(t, sol[:, 2], 'r', label='Infecteds')
plt.plot(t, sol[:, 3], 'y', label='Recovered')
plt.legend(loc='best')
plt.xlabel('Time (years)')
plt.ylabel('Fraction of population in each class')
plt.title('SEIR model with seasonal effects ($\\beta(t)$ = {:.2f}(1 + {}cos({:.2f}t)), $\\gamma$ = {:.3f}, $\\mu
plt.xticks(range(0, 310, 20))
plt.yticks(np.arange(0, 1.1, 0.1))
plt.grid()
plt.show()
print(odeint(SEIR, y0, 2, args=(beta, gamma, mu, sigma))[0])

# problem 3: SEIR model with seasonality

# initial conditions and constants
I0 = 10 ** -3
E0 = 10 ** -3
S0 = 6 * 10 ** -2
y0 = [S0, E0, I0, 1 - S0 - E0 - I0]
t = np.linspace(0,1100,22001)
beta0 = 1241
beta1 = 0.18
omega = 2 * np.pi #2 * 2 / 2.1 * np.pi
gamma = 365 / 5
mu = 0.02
sigma = 365 / 8

# calculate solution
sol = odeint(SEIR_seas,y0,t,args=(beta0, beta1, gamma, mu, sigma, omega))

# plot!
plt.plot(t, np.log(sol[:, 2]), label='Infecteds')
plt.legend(loc='best')
plt.xlim([990,1000])
plt.ylim([-12,-6])
plt.ylabel('Logarithm of the fraction of infecteds')
plt.xlabel('Time(years)')
plt.xticks(np.arange(990, 1000, 1))
plt.title('Time evolution of SEIR model with added seasonality ($\\beta_1$ = {}, $R_0$ = 17)'.format(beta1))
plt.grid()
plt.show()
```