Modelling the spread of infectious diseases

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1 Introduction

Almost all people get infected at least once by an infectious disease during their life. Almost all children have to deal with the chicken-pox and which adult can say that it never got the flu? The outbreaks of these various diseases can be modelled thanks to various work on mathematical models that can make accurate representations of the outbreaks of various infectious diseases. These models can be used in order to prevent future outbreaks of infectious diseases by proposing vaccination plans.

In this report we present the findings of our research concerning various models simulating the spread of infectious diseases amongst humans.

2 Theoretical background

We use different models to represent real world situations. Depending on the dynamics of population we are trying to model we must choose a model in such a way that it has the most accurate representation of the infectious disease among a population.

2.1 SIR model without demography

The least complex model is the so called "simple" SIR model, in which demography is not taking into account. In this model there are three different classes in which the population N is divided.

1. The susceptible fraction S
2. The infected fraction I
3. The recovered fraction R

In this simple variant of the SIR model we assume that the population stays closed, e.g. no babies are being born and people are not dying. With these assumptions we can schematically represent the model, like in figure 1.

We translate these dynamics into a system of ordinary differential equations (ODEs):

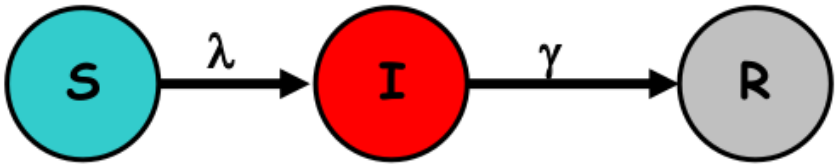


Figure 1: SIR model without demography

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

With S being the fraction of the people who are susceptible for an infectious disease, I the fraction of infected people and R the fraction of the recovered people. Since we assume the population is closed we say $S + I + R = 1$.

The basic reproductive ratio R_0 is the ratio between β and γ:

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

In order for a disease to spread: $R_0 > 1$, which means the rate of infection β must be higher than the rate of recovery γ.

Another important factor that determines if a disease can spread is the fraction of the susceptible people S. When we rewrite the formula for our I class this becomes more clear:

$$\frac{dI}{dt} = I(\beta S - \gamma)$$

This shows us when $S_{(0)} < \gamma/\beta$ the infection will die out, since this will make $dI/dt < 0$.

2.2 SIR with demography

For long-term disease we must take into account that babies are being born and people die by natural cause, so we introduce a natural mortality rate μ, see figure 2.

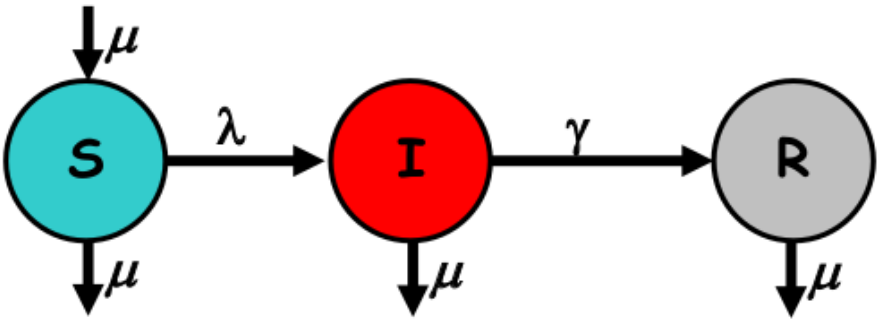


Figure 2: SIR model with demography

Babies being born will go into the susceptible class, assuming that babies are always being born as susceptible. Natural death however has effect on all the classes. These new assumptions are changing our system of ODEs:

$$\begin{aligned}\frac{dS}{dt} &= \mu - \beta SI - \mu S \\ \frac{dI}{dt} &= \beta SI - \gamma I - \mu I \\ \frac{dR}{dt} &= \gamma I - \mu R\end{aligned}$$

This also changes R_0, because the I class now decreases with γ and μ:

$$R_0 = \frac{\beta}{\gamma + \mu}$$

When solving this system of ODEs, the result will show us oscillatory behaviour. This is due to the fact that the dominant eigenvalues are complex conjugates [3], which can be demonstrated using the formula for the dominant eigenvalues derived by Keeling and Rohani [3]:

$$\Lambda_{2,3} \approx -\frac{\mu R_0}{2} \pm \frac{\sqrt{(\mu R_0) - \frac{4}{AG}}}{2}$$

This becomes complex because we assume $(\mu R_0)^2 << \frac{4}{AG}$. This introduces the term $\sqrt{-1}$ which is solved by turning it into a complex number, which results in the oscillatory behaviour. On the other hand, when $(\mu R_0)^2 > \frac{4}{AG}$, no complex number is needed and therefore there will not appear oscillatory behaviour.

2.2.1 Infection induced mortality

For deadly infectious diseases we introduce a probability ρ which represents the infection induced mortality, turning the system of ODEs into:

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \frac{\gamma + \mu}{1 - \rho} I \\ \frac{dR}{dt} &= \gamma I\end{aligned}$$

We see when ρ reaches 1 the fraction will increase, meaning people will almost die immediately.

2.3 SEIR model

Another take on the SIR model is the SEIR model. In this model we add the E class, which consists of people being infected but not yet infectious. Still taking demography into account (but not ρ) our system of ODEs is:

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

With $1/\sigma$ being the average latent period.

2.4 Seasonality

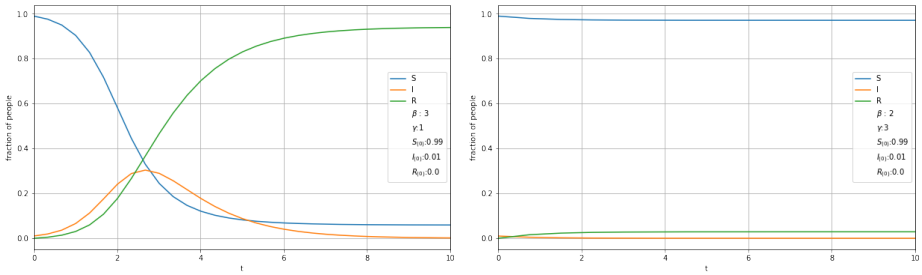
A lot of infectious diseases do not stay constant in their rate of infection β. We see this for example in childhood diseases, which tend to spread faster during school-season in contrast to the school-vacations. To model such diseases we introduce a time dependent β. This time depend β is derived by Bailey [1]:

$$\beta_{(t)} = \beta_0(1 + \beta_1 cos(\omega t))$$

With ω being the period of forcing.

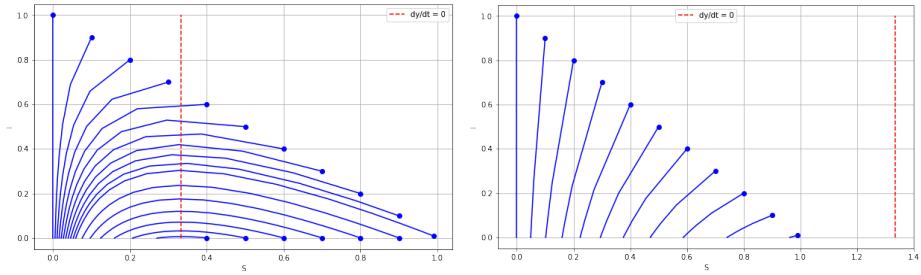
2.5 Fourier transform

All non-linear functions can be deconstructed into multiple different sine-waves. The Fourier transform is an algorithm that makes use of this fact and gives us the frequency of these multiple sine-waves [2].



(a) $R_0 > 1$ (b) $R_0 < 1$

Figure 3: SIR models without demography



(a) $R_0 > 1$ (b) $R_0 < 1$

Figure 4: Phase plots for SIR models without demography

3 Experimental Methods

3.1 SIR model without demography

In order to examine the simple SIR model we numerically integrate our system of ODEs in order to find a solution. We do so for two cases: $R_0 > 1$ and $R_0 < 1$, see figure 3. We see that the infection is spreading in figure 3a, but in figure 3b the infection has no chance of spreading.

To have a closer look at these dynamics, we create a phaseplot of the same situations, see figure. We also plot when $dY/dt = 0$ which is true for $1/R_0$.

4.

In figure 4 we see that the infection is immediately dying out for $R_0 < 1$ (figure 4b) while the infection will spread for $R_0 > 1$ (figure 4a), as long as $S_{(0)} > 1/R_0$.

3.1.1 Application to real world data

We can apply this model to real-world data in order to prevent future outbreaks of similar infectious diseases. To demonstrate this we use a data-set of an

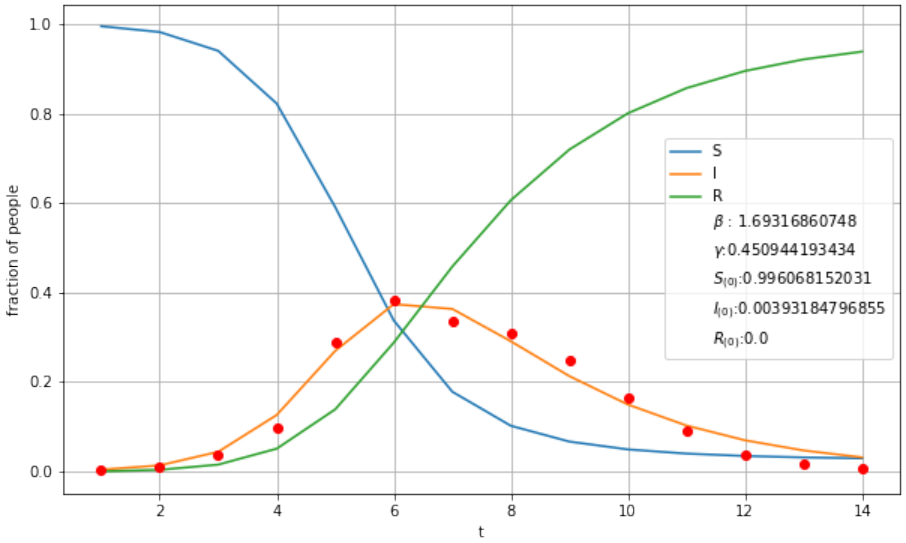


Figure 5: Fitted influenza SIR model

influenza outbreak at a boy-school, of 763 boys in total, of which one boy was initially infected with the flu:

Day	1	2	3	4	5	6	7	8	9	...	14
Infected boys	3	8	28	75	221	291	255	235	190	...	5

We make the assumptions that within this population there is no demography, no death caused by infection and a boy can only become infected once. Therefore our SIR model without demography would be an accurate representation of this population.

Using this model we try to fit the the real world data against the infected class I using the least squares approach. This gives us the estimated values for $\beta = 1.69$ and $\gamma = 0.45$. The fitted result is shown in figure 5.

Since we have an accurate representation of our population over time we can propose a vaccination plan. The vaccination plan consists of bringing down $S_{(0)}$ in such a way that I will always decrease, e.g. $\frac{dI}{dt} < 0$. We know this is true when $S_{(0)} < \gamma/\beta$. So $S_{(0)} < 0.266$ in order for the influenza diseases to never spread.

We confirm our findings by plotting the phaseplot for the influenza model (figure 6) in which we vary $S_{(0)}$ around this value. This clearly shows us that for $S > 0.266$ the I class is first increasing, in contrast to $S < 0.266$ where the disease only decrease.

Therefore a vaccination plan would be to vaccinate 73% of the boys on day 0.

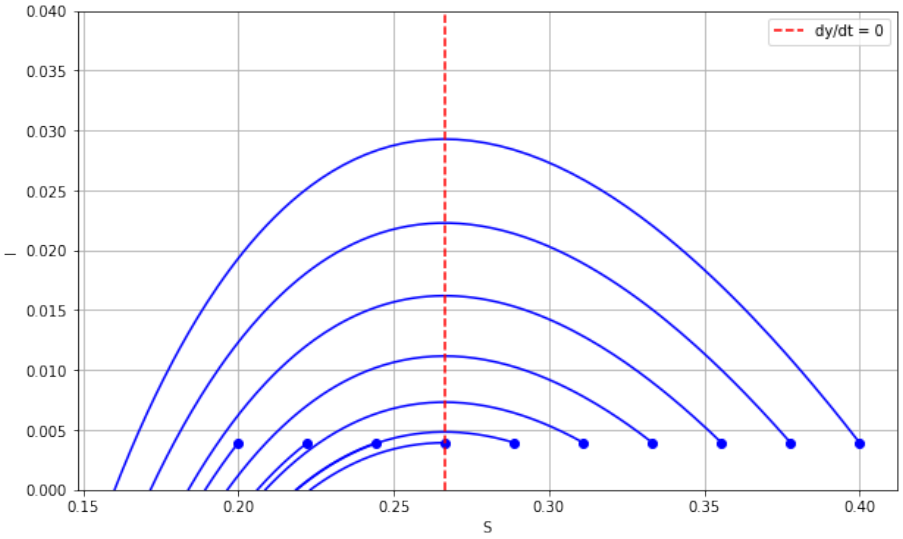


Figure 6: Phase plot for influenza outbreak in boy-school

3.2 SIR model with demography

In the experiments for our SIR model with demography we set our values as follows:

- $\beta = 1$
- $\gamma = 1/3$
- $\mu = 1/60$
- $S_0 = 0.9$
- $I_0 = 0.1$
- $R_0 = 0.0$

In the solution of our system of ODEs we see oscillatory behaviour for all of our classes (figure 7), which we can relate to the addition of μ.

In order to find the frequency of these oscillations we use an analytic approach. We do so by using the formula derived by Keeling and Rohani [3]:

$$T \sim 2\pi\sqrt{AG}$$

With $A = \frac{1}{\mu(R_0-1)}$ and $G = \frac{1}{\mu+\gamma}$.
This tells us $F \sim 0.0166$.

Using the Fourier transform we can find the frequencies in a numerical way as well, see figure 8. In this figure we see the dominant frequency for all the classes, which is the same as our analytic derived frequency. We also see the different classes having the same frequency which is due to the fact that $S_{(0)}$, $I_{(0)}$ and $R_{(0)}$ do not effect the frequency. However, the Fourier transform does

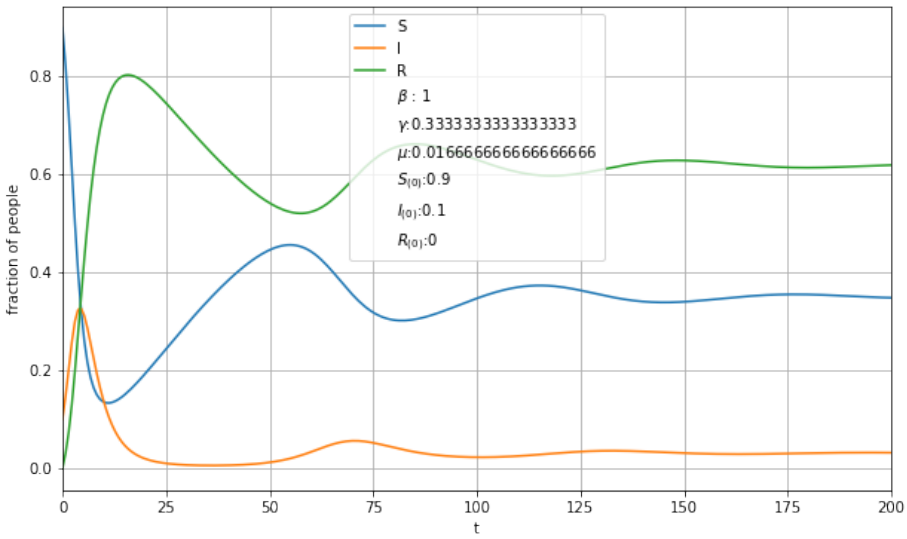


Figure 7: SIR model with demography

tell us that the different initial values produce different amplitudes. Also we can see that other non-dominant frequencies are being represented which relate to the damping of the oscillations over time in our original plots.

3.2.1 Adding infection induced mortality

In order to examine the behaviour of ρ in our model, we plot for four different values of ρ, see figure 9. We can see for $\rho = 0.75$ dies out quickly, after only 50 time-steps. This plot also gives us the illusion that the population is closed, but if we look more close we can see that the addition of the last values of the lines do not count up to 1.

For diseases that have a high probability of dying throughout infection, a more appropriate choice would be to subdivide the infectious period and to only allow mortality in later stages of infection.

3.3 SEIR model

For our experiments on the SEIR model we choose to make β time dependent. Our parameters will be:

- $\beta_0 = 3$
- $\gamma = 1$
- $\mu = 1/60$
- $\sigma = 0.5$
- $\delta = 0.1$
- $\tau = 20$

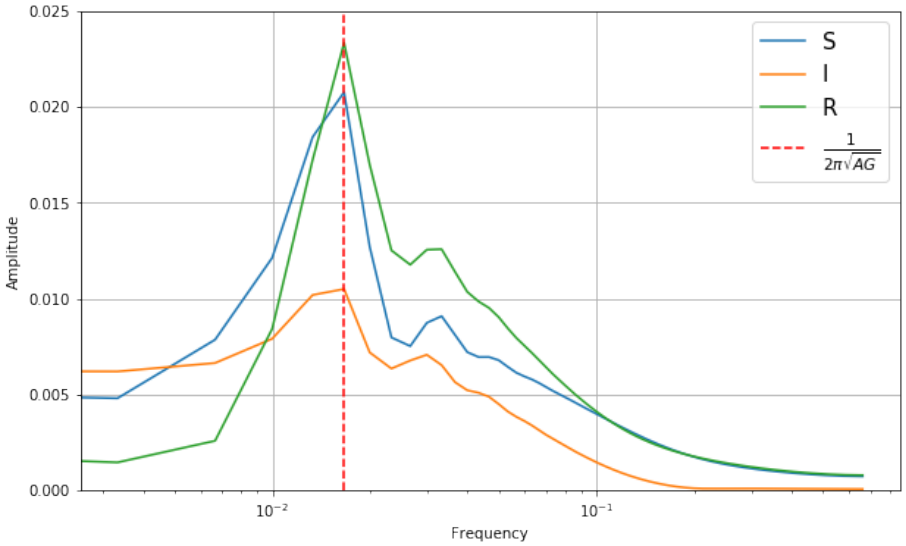
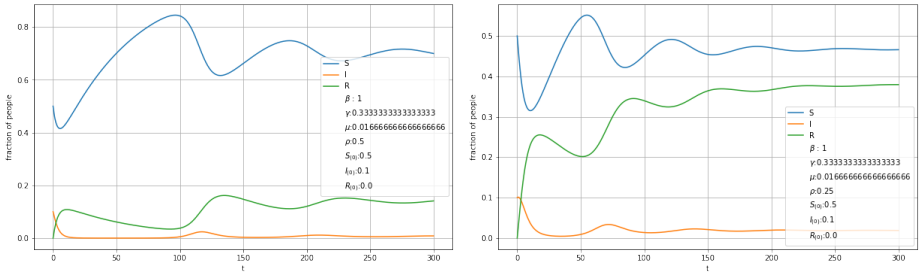
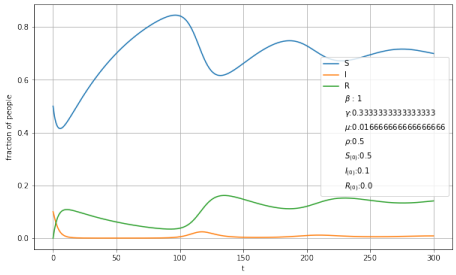


Figure 8: Fourier transform applied to SIR model with demography

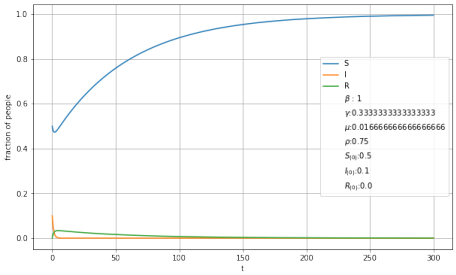


(a) $\rho = 0$

(b) $\rho = 0.25$



(c) $\rho = 0.5$



(d) $\rho = 0.75$

Figure 9: Infection induced mortality for SIR models

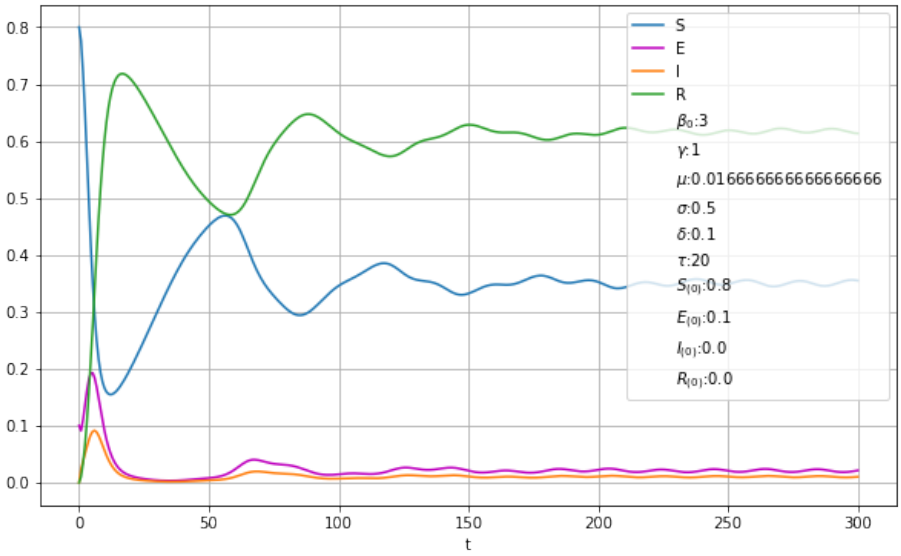


Figure 10: SEIR model over time

The result of numerically integrating the ODEs results in figure 10. Yet again we see oscillatory behaviour for all our classes.

To study this behaviour we use the Fourier transform to find their frequencies. This results in figure 11.

In this model the dominant frequency does not depend on the same parameters as in the SIR model. This is probably due to the fact that σ is introduced but also because of β being time dependent.

4 Conclusion

4.1 SIR without demography

From our experiments with the SIR model without demography we conclude that a disease can only spread when $R_0 > 1$ while $S_{(0)} > 1/R_0$. This means we can propose vaccination plans when R_0 is known.

Using the real world example we propose a vaccination plan for influenza outbreaks with similar initial conditions ($S_{(0)}$, $I_{(0)}$, $R_{(0)}$, R_0). The proposed vaccination plan consisted of lower S_0, thus vaccinating the boys on day 0.

4.2 SIR with demography

Adding demography into our SIR model caused oscillations, which is due to the fact that the eigenvalues of the ODEs were complex conjugates. The frequency

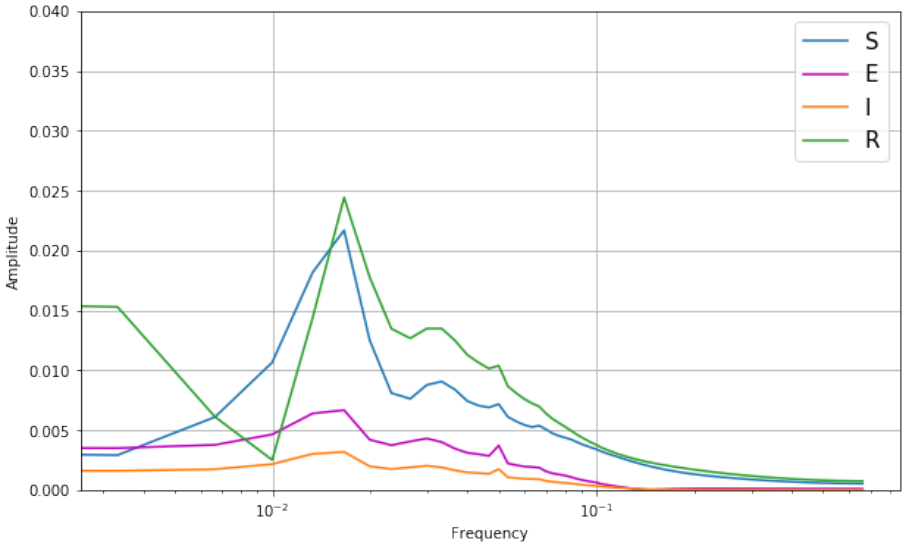


Figure 11: Fourier transform model over time

of these oscillations can be found in an analytic way, but using the numerical Fourier transform gives us more information about the type of oscillations (damped) and the amplitude. We also see that system of ODEs we used to describe infection induced mortality was not an accurate representation for diseases that have a high probability of death. In that case it would be better to use a different approach.

4.3 SEIR model

Applying the Fourier transform to our SEIR model gave us some insight about the frequencies. We found that the frequency is not longer dependent of the same values as in our SIR model but also of σ. Also the fact that β is time dependent will change the analyticall way of find the frequency.

5 Discussion

The appliance of our SIR model without demography for the real world data has some flaws. We assumed that we can vaccinate all boys on day 0 which means that a percentage of the boys should be preventive vaccinated. A better approach would be to introduce a vaccination rate over time for the susceptible class because this would resemble a real world situation more accurately.

Also, in our analysis of the SEIR model we found that the frequency depends on other parameters than in our SIR model. However we did not find the analytic solution for computing the frequency which we could investigate in

future work.

References

[1] Norman TJ Bailey et al. *The mathematical theory of infectious diseases and its applications*. Charles Griffin & Company Ltd, 5a Crendon Street, High Wycombe, Bucks HP13 6LE., 1975.

[2] Ronald Newbold Bracewell and Ronald N Bracewell. *The Fourier transform and its applications*. Vol. 31999. McGraw-Hill New York, 1986.

[3] Matt J Keeling and Pejman Rohani. *Modeling infectious diseases in humans and animals*. Princeton University Press, 2011.