MATHEMATICAL ANALYSIS OF EPIDEMIC SYSTEMS

COMPARISON OF DIFFERENT MODELS

by

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THESIS

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Abstract

This thesis studies and compares three different ways of modelling epidemic diseases. The simulations are done for a small group over a short time period. In the first chapter an ODE model is presented. This is used to model two different examples of epidemic systems. The second chapter introduces a PDE model, which also takes the geographic position into account. The parameters from the first model are used for the PDE model, to study the spatial effect. Random walk is used as the third model. Here, human behavior has been added to the model to achieve a more realistic result. Throughout the thesis two examples are used, namely an influenza outbreak in an English boarding school and a potential zombiefication based on the TV series *Walking Dead*. The results from these two cases are used to compare the different models.

Acknowledgements

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Contents

Chapter 1

Introduction

Throughout the history great epidemic diseases have spread across the world, leading to catastrophic consequences for human populations. Millions of lives have been taken. The Black Death and Cholera are epidemics that have moved over large distances into Europe Ref.[5, p. 315]. An important aspect in the current spread of diseases is the displacement of human populations. About a million people cross international borders daily. The growth of human population, especially in underdeveloped countries, is another factor that affects the spread. These developments played a key role in the spread of HIV in the 1980's. The World Health Organization has estimated that around 32.6 million people are infected with the HIV virus today Ref.[7]. Knowledge about the spread and severity of epidemic diseases is valuable for the human population in preventing major damages. The current outbreak of Ebola in West Africa in March 2014 Ref.[8], has shown that epidemics will occur repeatedly. Mathematical models can help us understand the severity and prepare the population in the best way possible.

In this thesis three different models will be used to simulate epidemic diseases. The three models that will be used are: the ODE model, the PDE model and Random walk. Each model will be presented and the results will be analyzed and compared throughout the paper. The threshold value for an epidemic disease will be examined in chapter, 2. The chapter 3, focuses on how a travelling wave of infected disperse in an area. The fourth chapter, 4, will look into Monte Carlo methods, which will later be used for the Random walk simulations.

A couple of choices have been made for this thesis. First, the systems will be modeled for a short period of time. The length of the longest simulations is a month, while the fourth chapter only consists of simulations with the length of half an hour. This is done to study variations of human and zombie behavior in a zombiefication. Second, all models are simulated as closed systems. The amount in each simulation never exceeds 763 humans and the time aspect is

short. Therefore the birth and death rate is close to negligible, and are set to zero.

Two different examples will be used for all three models. The first case is based on an influenza outbreak which occurred at an English boarding school in 1978. A basic SIR system will be used to model the epidemic trough 15 days. This example shows the effect of varying the parameter values in the system. This will be done in chapter 2. The maximum concentration of infected humans will be compared, to see if the results between the models differ. The effect from the two spatial models in chapter 3 and chapter 4 will be compared to the ODE model. The second case is based on the TV series *Walking Dead*. Here, a SEIR model will be used to simulate a zombie outbreak. The model is based on the paper *Escaping the Zombie Threat by Mathematics* by Langtangen, Mardal and Røtnes Ref.[3]. The simulations will be done for different phases, and the parameter values in each phase will be changed and studied. Differences in behavior will be used to vary the simulations. Restricted areas will be used in the simulations of the PDE model, while Random walk also adds altered behavior.

The code used for the thesis can be found at `https://github.com/torbjornseland/master`. There will be a link Movie attached to each figure that has a simulation on web. This can be used to study the simulations, especially for the Random walk model.

Chapter 2

ODE models

This chapter will be split into two different parts. The first part is based on the chapter *Dynamic of Infectious Diseases* from Mathematical Biology by J.D Murray Ref.[5]. A basic ODE system will be presented and studied to see how this model can give information about the disease. The section will check if a disease is severe for the human population, and based on this called an epidemic disease. The example from English boarding school will be used. The second part will be based on a scenario where the population faces a zombification, one of the most critical and devastating epidemic diseases that can occur. Here, the TV series *Walking Dead* will be used as reference. The ODE model from the paper *Escaping the Zombie Threat by Mathematics* by Langtangen, Mardal and Røtnes Ref.[3] will be used to model the zombie outbreak.

2.1 Simple epidemic models

Most of the models shown here will have a constant population. The zombie model shown later will have a slight increase considering newborn, but this will be close to negligible. This may differ from the real world, where the population in different areas will vary with population flow. Reasons for doing this are, first of all to simplify the model and second to be able to model a closed system. How the population interacts is another assumption that has to be done. Here this is set to be similar for the whole area that is modeled. To simplify the population can be divided into three different groups.

- *Susceptible* (S), who are humans that are healthy and at risk of becoming infected.
- *Infected* (I), who are humans who have the disease or are carriers of the disease. This group can infect the group *Susceptible*.
- *Removed* (R),who are dead or recovering humans, often people that already have had the disease.

The natural order for a human is,

$$S \to I \to R.$$

This model is called SIR model, but the number of groups can be changed. SI only consists of the two first groups and a $SEIR$ model has added an extra group *Exposed* , E, where the disease is latent. This can be used to model the incubation time.

The transmission of the infection and incubation period are elementary factors in the spread of a disease. These are reflected in the terms of the equations. Since this is a SIR model, the incubation time is negligible. The amount of people in each group can be seen as a function of time, expressed as $S(t), I(t)$ and $R(t)$. The growth of infected caused by susceptible humans, can be viewed as a rate proportional to the number of infected and susceptible humans multiplied by a constant,rSI, where $r > 0$. This constant controls the efficiency of the transmission from S to I. This will appear as a reduction in the function $S(t)$. The rate of removal from infected to removed group can be viewed as the number of infected times a constant, aI, where $a > 0$ controls the time spent in the infected group. The dynamic model will be,

$$\begin{aligned} \frac{dS}{dt} &= -rSI \\ \frac{dI}{dt} &= rSI - aI \\ \frac{dR}{dt} &= aI \end{aligned} \tag{2.1}$$

This model is called the Kermack-McKendrick(1927) model Ref.[5, p. 320]. It is considered that the groups are uniformly mixed and that there is equal probability of contact for all individuals. These assumptions will not be correct for all diseases, especially sexually transmitted diseases. The total number of the population will stay constant, since this is a closed system. This can be seen on the total change.

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \tag{2.2}$$

Therefore the total size of the population, N, will be constant.

$$S(t) + I(t) + R(t) = N \tag{2.3}$$

2.2 Threshold phenomenon

The threshold value is essential when studying an epidemic model. To cause an epidemic situation, the model needs to fulfill $I(t) > I_0$ for some $t > 0$, where I_0 describes the initial condition of the infected group. The initial conditions can be given as,

$$S(0) = S_0 > 0, \qquad I(0) = I_0 > 0, \qquad R(0) = 0. \tag{2.4}$$

These initial conditions given in Eq.(2.4) combined with r and a controls the epidemic situation. These will affect the spread of the infection. From Eq.(2.1) the function for the infected group at initial time is,

$$\left[\frac{dI}{dt}\right]_{t=0} = I_0(rS_0 - a) \tag{2.5}$$

The expression inside the brackets controls the change in I. The function will increase if $S_0 > \frac{a}{r}$, this will therefore be the threshold value for the function. The threshold value will be described by the variable ρ,

$$\rho = \frac{a}{r} \tag{2.6}$$

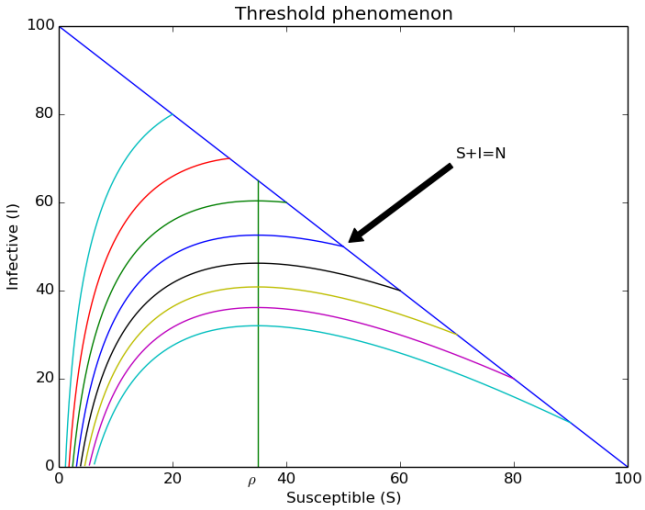

Figure 2.1: Simulations of the SIR model (2.1) with start positions along the blue diagonal line. I increases until S is equal to the threshold value ρ, which is set to 35. Then I is reduced to 0. In the simulations where $S_0 < \rho$, no epidemic situation is achieved.

This can be shown with some phase trajectories of the infected and susceptible humans in Fig.(2.1). The simulation shows that I is based on the relation between S and ρ. This can be described with a reproduction rate,

$$R_0 = \frac{rS_0}{a} \tag{2.7}$$

It will cause an epidemic reaction if $R_0 > 1$. This parameter is crucial in the understanding of the work with the disease. To prevent a dispersion, the value of R_0 has to be under 1. An effective way to get control is by global

vaccination programs. Smallpox is an example on a disease that nearly has been eradicated around the world. This is due to a reduction of susceptible humans. However there is always a small chance of side effects when using vaccination, and therefore some people choose to skip it. This is quite critical for the fight of total eradication. Not only is it a big risk for the specific person, but it also increases the number of susceptible humans. An epidemic situation can quickly grow again if the reproduction rate reaches the threshold. Some analytical studies can be done on the model in Eq.(2.1).

$$\frac{dI}{dS} = -\frac{(rS-a)I}{rSI} = -1 + \frac{\rho}{S}, \qquad \rho = \frac{a}{r}, (I \neq 0). \tag{2.8}$$

The singularities will all lie on the I=0 axis. This equation can be integrated and will then give phase plane trajectories in the (I,S) plane. This can be seen in Fig.(2.1).

$$I + S - \rho \ln S = \text{constant} = I_0 + S_0 - \rho \ln S_0 \tag{2.9}$$

All initial values satisfy $I_0 + S_0 = N$ since $R(0) = 0$. This will change when $t > 0$. If a disease appears it would be important to know the severity of the disease and the chance of developing to an epidemic disease. Therefore it is crucial to know the maximum value $I_{\max}$ which occurs when $S = \rho$. At this point, $\frac{dI}{dt} = 0$. This can be found by using (2.9)

$$\begin{aligned} I + S - \rho \ln S &= I_0 + S_0 - \rho \ln S_0 \\ I_{\max} + \rho - \rho \ln \rho &= I_0 + S_0 - \rho \ln S_0 \\ I_{\max} &= -\rho + \rho \ln \rho + I_0 + S_0 - \rho \ln S_0 \\ I_{\max} &= N - \rho + \rho \ln \frac{\rho}{S_0} \end{aligned} \tag{2.10}$$

The different trajectories in Fig.(2.1) shows the difference between $S_0 > \rho$ and $S_0 < \rho$. An increasing of the infected group will occur in the cases where S_0 is higher. While a decreasing will happen when S_0 is lower. An example can be shown. The ρ in the simulation in Fig.(2.1) is set to 35, while $N = 100$ for all trajectories. A calculation can be done on the lowest trajectory which has the initial conditions $S_0 = 90$ and $I_0 = 10$

$$\begin{aligned} I_{\max} &= N - \rho + \rho \ln \frac{\rho}{S_0} \\ I_{\max} &= 100 - 35 + 35 \ln \frac{35}{90} \\ I_{\max} &= 31.94 \end{aligned}$$

This situation causes an epidemic situation since $I_{\max}$ is much higher than the initial condition I_0. The Fig.(2.1) shows that the trajectory of this function starts decreasing after this point. In the two upper trajectories where $S_0 < \rho$, the infected group starts decreasing from the initial condition. The infected group will decrease towards zero as $t \to \infty$.

2.3 English boarding school

The British medical journal published a report from a boarding school in England in 1978. One of the boys had brought with him a disease back to the school. Since this was a boarding school, they were totally isolated from others and had a closed system to model [5, p. 325]. The simulation can be seen in Fig.(2.2)

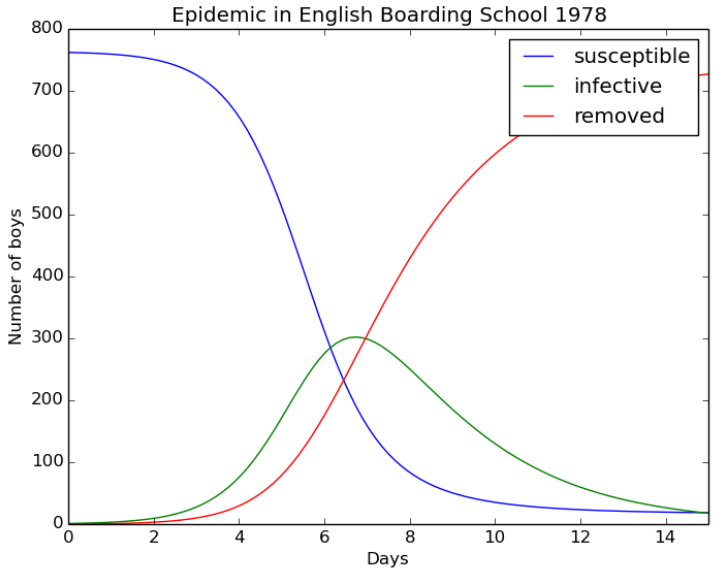

Figure 2.2: An English boarding school is modeled for 15 days with the following parameters: $N = 763$, $S_0 = 762$, $I_0 = 1$, $R_0 = 0$, $\rho = 202$ and $r = 2.18x10^{-3}$. An increase in the infected group can be seen since $S_0 > \rho$.

2.3.1 Maximum concentration of infected

The maximum concentration of the infected group can be found from using the threshold value. The result can be compared to the simulation in Fig.(2.2). Maximum of infected can be found by the following equation from Eq.(2.10)

$$I_{\max} = N - \rho + \rho \ln \frac{\rho}{S_0} \tag{2.11}$$

By inserting the parameters from the simulation in Fig.(2.2) in Eq.(2.11), the value of $I_{\max} = 292$. The $I_{\max}$ of the simulation can be found by checking the maximum number of the infected list. This is similar to the calculated $I_{\max}$. This maximum value of the infected group occurs when the susceptible group is 202, and similar to the value of ρ in the simulation.

2.3.2 Variation in parameter value ρ

The parameter value ρ has a major impact on the result. The epidemic disease could turn out quite differently than in the situation in Fig.(2.2), caused by variations in a and r. Fig.(2.3) consists of some examples where ρ varies from 50 to 400.

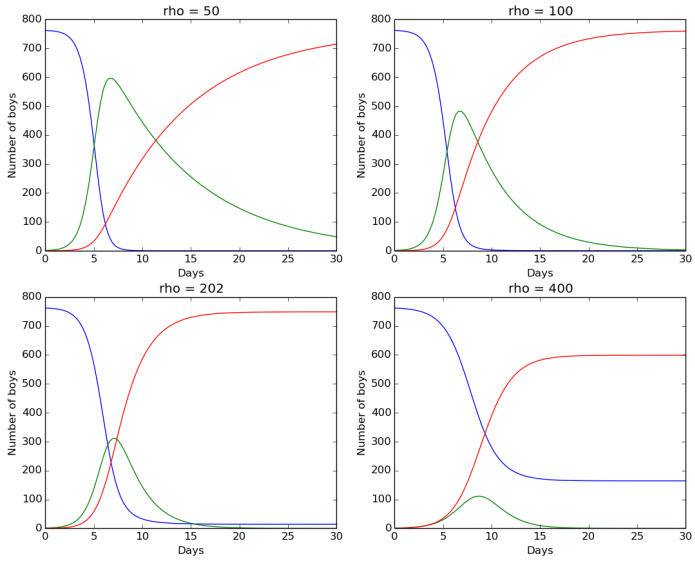

Figure 2.3: English boarding school with four different values of ρ. In the first plot where $\rho = 50$, the infected group will increase until the number of susceptible group falls down to 50. This will result in a majority of infected students. In the last plot where $\rho = 400$, the total number of susceptible humans stays around 170 students and will go towards a steady number as $I(\infty) = 0$.

2.4 Zombification

One of the worst epidemics that can affect the human population is a zombie attack. This will have a huge impact on the way humans live today. Several movies and series has illustrated this type of situation, but it is time that the scientists also take this threat seriously. There have been written several papers about this. Munz et. al[4] used the SEIR model to simulate a possible upcoming zombiefication, where the latent group(E), is replaced with an infected group(I) and the infected group(I) is replaced with a zombie group(Z). Here it is important to know that the infected group in the $SIZR$ is not the same as in the $SEIR$ model. The following model was used,

$$\begin{aligned}\frac{dS}{dt} &= \Sigma - \beta SZ - \delta S \\ \frac{dI}{dt} &= \beta SZ - \varrho I - \delta I \\ \frac{dZ}{dt} &= \varrho I + \zeta R - \alpha SZ \\ \frac{dR}{dt} &= \delta S + \delta I + \alpha SZ - \zeta R\end{aligned}$$

This is a bit more complicated than the standard $SEIR$ model. A presentation of the parameters;

- Σ describes the birthrate for new susceptible humans. $\frac{dS}{dt}$ is now able to be positive. This will be 0, since the system is closed.
- βSZ describes the numbers of susceptible humans that become infected , based on interactions between zombies and humans. Similar to the case for rSI in the SIR model.
- δ describes the number of natural deaths in the group. This is used in the susceptible and infected groups
- ϱI describes the probability for an infected human to wake up as a zombie.
- ζR describes the number from the group *Removed* that arises in the group *Zombie*.
- αSZ describes the number of zombies killed by susceptible humans in the zombie attacks.

This model was challenged by Langtangen, Mardal and Røtnes [3] now referred to as LMR, where they developed another model. They had three objections to the model from Munz et al. [4]. LMR argue that dead zombies cannot become functioning zombies again. Therefore ζ will be zero, if magic is not introduced. They let the parameters in the model change with time, according to different phases. LMR argue that the behavior will change with time during a zombie attack. The parameters in the model from LMR was based on the movie *The Night of The Living Dead*. This was done to reproduce its scenarios and then predict how a zombie outbreak would appear. There is also added a function $\omega(t)$, which creates a massive attack from the humans. This is controlled by a time variable and give the susceptible humans a chance to fight

back. The system can be seen in Eq.(2.12):

$$\begin{aligned}\frac{dS}{dt} =&\Sigma - \beta SZ - \delta_S S\\ \frac{dI}{dt} =&\beta SZ - \varrho I - \delta_I I\\ \frac{dZ}{dt} =&\varrho I - (\alpha + \omega(t))SZ + \zeta R\\ \frac{dR}{dt} =&\delta_S S + \delta_I I - \zeta R + (\alpha + \omega(t))SZ\end{aligned} \tag{2.12}$$

The main change is the $\omega(t)$. This is a Gaussian curve and can be seen in eq(2.13).

$$\omega(t) = a\sum_{i=0}^{m} \exp\left(\frac{1}{2}\left(\frac{t - T_i}{\sigma}\right)^2\right) \tag{2.13}$$

$\omega(t)$ controls the attacks from the susceptible humans, which will be fired at predefined time steps. These are controlled by the three parameters.

- a here works as a similar parameter as α, but will only be activated when the susceptible group is organized and ready to attack.
- T contains a list of numbers, which controls the time when the attacks will occur.
- σ controls the length of the attack.

This function will be modeled later when it is used in section 2.4.4

2.4.1 Parameters used in the model

The parameter values are essential factors when modelling a zombie attack. Data from the movie *The Night of The Living Dead* was used as basis for the parameters in the ODE system from LMR [3]. This thesis is based on a thorough study of the TV series *Walking Dead* [1]. The data will be based on the first five episodes and are constructed after having watched the episodes carefully. The three phases in a zombie attack will be based on the form used in the paper from LMR, but with an extended version in the *Counter attack phase* .

2.4.2 The Initial phase

The disease is not yet known in this phase and humans try to save the sick ones by taking them to hospitals or getting some kind of treatment. Because of this ignorance related to the disease, the number in the infected group is high. This phase is often quite short and humans soon start to realise that the risk of getting infected by saving others is really high. *Walking Dead* never shows anything from this phase, but the viewer sees the results when the main character sheriff

Rick Grimes wakes up at the local hospital. What he sees is the major damage caused in the *Initial phase*, while the society has moved to the *Hysterical phase*.

To determine the values for each group in each phase, the length of Ricks coma is essential. There are several factors that give an indication of the time aspect. When Rick wakes up at the hospital, he has grown a smooth beard of about 1 cm. This would correspond with 1 month in average for a male of European origin. He also has some flowers that have dried out. These also give the impression that some weeks have gone by. The hospital is running on its emergency generator. This would probably not last for many days with a fully operational hospital, but the hospital is as well as shut down when Rick wakes up and can give the emergency generator a longer lifetime. Dr. Edwin Jenner gives the viewer some information in episode 5 where he tells the videolog that it was 63 days since the epidemic started spreading. By studying the first five episodes in detail, one gets an impression that the time aspect has not been in focus. Therefore the different phases are constructed from the information that has been given. Rick Grimes has probably been in a coma for a month and what he meets the first days will be the basis for the number in each group. The total amount of objects in the model will be based on the number of humans, dead and zombies seen in the first five episodes.

- The number of humans has been estimated to 62. 20 living in the camp with Rick, 40 humans in the old nursing home and the father and son in episode 1.
- The number of dead is estimated to 200. This is based on the amount of dead outside the hospital where Rick woke up.
- The number of zombies are assumed to be 360. These are based on the 30 outside the house of Morgan Jones and his son Duane, 300 zombies in the city Atlanta and 30 zombies attacking the camp.

The total number will be 622, and the time aspect aroud a month, which means that these numbers are for the *Hysterical phase*.Over the three first days when Rick is awake, 1 human and 20 zombies are killed in battles. This can be used to find the final number in the *Initial phase* by calculating backwards. By going nine similar periods backwards, the number of killed zombies is 190. The same can be done for humans, which then results in 9 killed humans in this period. The final number for the *Initial phase* can then be set to 71 humans, 540 zombies/infected and 20 dead. This is the same number as for the initial values for the *Hysterical phase*, since the phases are connected.

Another issue to discuss is the incubation time. Here there are two examples that can be used. The first transformation from human to zombie happens for the character Amy, who was bit in the arm by a zombie. The transformation happens in about 12 hours. The other example is character Jim who has a

slower transformation. This lasts for about two days before the rest of the group leave him alongside the road on their way to CDC(Center for Disease Control). An estimate of the incubation time can be set to 24 hours based on these two transformations.

The ODE system in Eq.(2.12)can be used to model the *Initial phase*. The expected results are $S_0 = 621$ and $Z_0 = 1$ while the two other groups are set to zero. The value of β can be found with the expression $\beta \Delta t SZ$ from the first ODE equation. After three days about 90 percent of the humans are killed.

$$\begin{aligned} \beta \Delta t SZ &= 0.9S \\ 3\beta &= 0.9 \\ \beta &= 0.3 \end{aligned} \tag{2.14}$$

The probability of a human being infected will be set to $\beta = 0.3$. The natural death and the birth number is set to 0, since the simulations are performed over short period and for a small group. $\delta_S = \Sigma = 0$. It is quite hard to find similar realistic data for infected humans, so $\delta_I = \delta_S$. Since this is data for the *Initial phase*, zombies are seen as infeteced humans that can be saved. Therefore $\alpha = 0$. And the two last parameters are also zero, $a = \zeta = 0$. The *Initial phase* is modeled in Fig.(2.4):

The results shows that the human population is eradicated in about a half day. This is not the case, and some adjustments need to be done. There are three parameters that are interesting to study. The first one is β, which describes how many humans that get infected in a human-zombie collision. The second one is ϱ. This parameter controls the incubation time. The last parameter that can affect the number in each group is α. This describes the number of zombies killed in a human-zombie collision. These variables are plotted separately and combined in Fig.(2.5). The idea here is to produce results that fulfill the final number for the groups *Susceptible* and *Removed*, which is 71 and 20. The blue dot in each plot describes this value. A rough estimate has been done for each parameter before using it. This is why they all lie in different regions than the parameter value in Fig.(2.4)

By choosing $\beta = 0.01155$, $\varrho = 1.37$ and $\alpha = 0.00044$, the simulation can be seen in Fig.(2.6). It is possible to argue for the changes done in Fig.(2.6). Increasing ϱ to 1.37 reduces the incubation time. Now the average time will be about 17.5 hours, which is realistic. The probability β is sensitive and has a major effect only by small variations. This is due to the term that it is a part of $\Delta t SZ \beta$. A couple of examples demonstrate this. One hour can be estimated by setting $\Delta t = 1/24$. When using the initial values for the groups $Susceptible$ and $Zombie$ and $\beta = 0.01155$ from Fig.(2.6). A rough estimate of the infected group in the first hour will be $(1/24) * 721 * 1 * 0.01155 = 0.34$. About one-third of a human in the first hour seems as a slow and not very aggressive disease. However

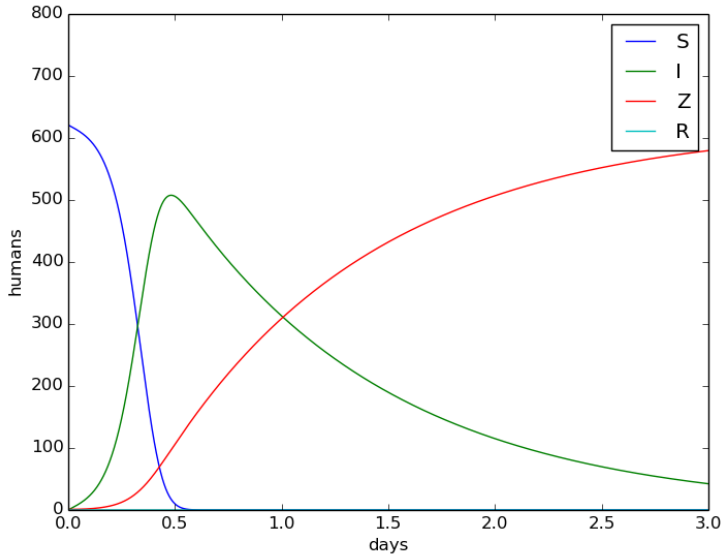

Figure 2.4: *Initial phase* for *Walking Dead*. $\beta = 0.3$, $\varrho = 1$ and $\alpha = 0$ leads to eradication.

when the number of *Zombies* slowly increases, the number of infected will be affected. By looking at the hour when the values are equal between humans and zombies, about 200 in each group, the number of infected will be 19.25 per hour. This result in about 10 percent of the humans. By changing β to the value from Fig.(2.4), the number of infected will be 500 per hour and it is quite easy to see that this will lead to eradication in a short amount of time. The last parameter α controls the number of zombies that dies in collisions between zombies and humans. While humans still think that the infected can be saved, it is still a chance that the result from a collision can end with a zombie kill. These results can therefore be seen as realistic values.

2.4.3 The Hysterical phase

Now the humans start to avoid the infected and some try to fight them. The humans often gather in groups and try to find safe spots away from the zombies. Important supplies as weapons and food are their main priorities. Barricades are built and the guarding is strict. When Rick Grimes wakes up, the hospital is abandoned and the halls are filled up with dead people. Quite fast he understand that he needs to reach safety. After a couple of days he ends up in a camp outside Atlanta city. A couple of elementary changes has happened with the interaction between humans and infected/zombies. In the *Initial phase*, the humans tried to help the infected humans. This resulted in a high percent of infected. Now they

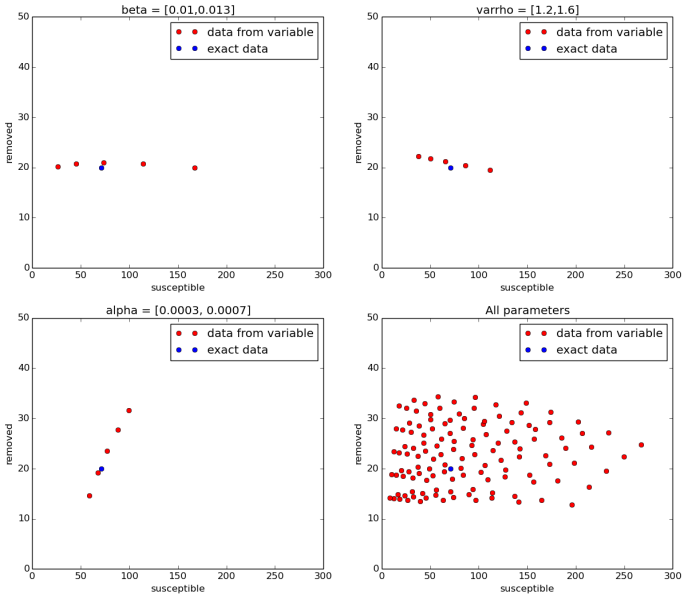

Figure 2.5: The final result for susceptible and removed group. These plots give a knowledge in the effect of varying the parameters. β and ϱ mainly affects the number of susceptible humans at final time, while α affects them both.

understand this risk and keep distance to those who are infected. This will give β a lower value. The morality for a zombie kill has dramatically changed. While this was seen as no option in the *Initial phase*, this is now okay. The humans have started to treat zombies and infected as enemies instead of sick allies. This results in a higher death rate among the zombies, which is described by α.

The hysterical model can be constructed based on the data found in the *Initial phase*.

Hysterical phase	initial values	final values
S	71.3	62
I	230.8	-
Z	298.9	360
R	21	200

Here, the infected and zombies are counted as one group for the final values, since it is difficult to separate these groups in the series. The time aspect will be modeled for 30 days, which results in a ten times longer simulation. Since the final results are known here, a similar adjustment of the parameters can be done.

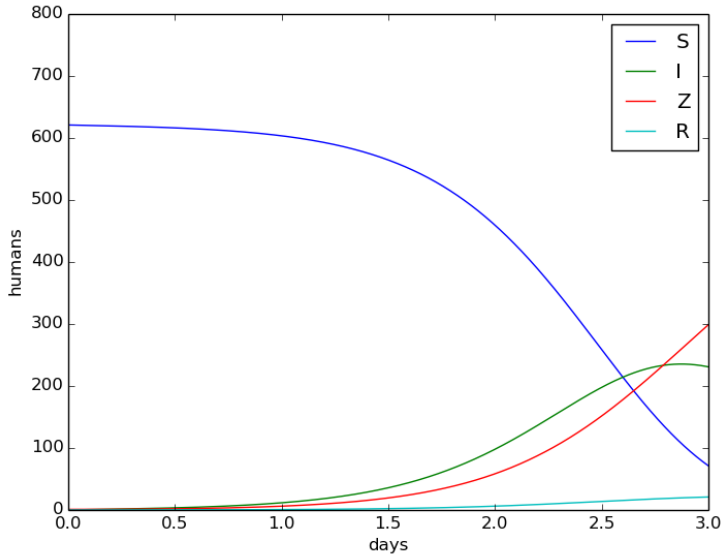

Figure 2.6: *Initial phase* for *Walking Dead*. The parameter values are set to $\beta = 0.01155$, $\varrho = 1.37$ and $\alpha = 0.00044$. The final values are $S_n = 71.3, I_n = 230.8, Z_n = 298.9$ and $R_n = 21$, which is quite close to the result from the movie.

The range of the parameter values have been found by some test simulations similar as shown in Fig.(2.5). The following parameter values can be used to simulate the *Hysterical phase*: $\beta = 0.000011$, $\varrho = 1.4$ and $\alpha = 0.000208$. The simulation is shown in Fig.(2.7).

Fig.(2.7) fulfills the result that was predicted based on the series. These final numbers correspond with the number in each group when Rick woke up at the hospital. The plot shows that the number of zombies increases quickly and reaches its maximum value after a couple of days in this phase, similar to the number of infected that dramatically decreased. Here the humans have been able to stabilize. Since the clashes between humans and zombies are dramatically decreased, nearly no humans get infected. And in the cases where humans have to face zombies, the killing rate has increased. The increase of the removed group is close to proportional to the decrease of the zombie group, which means that it is mostly zombies that die.

2.4.4 The Counter attack phase

This *Counter attack phase* is more complicated to model, since this phase appears simultaneously as the *Hysterical phase* in *Walking Dead*. The group of humans

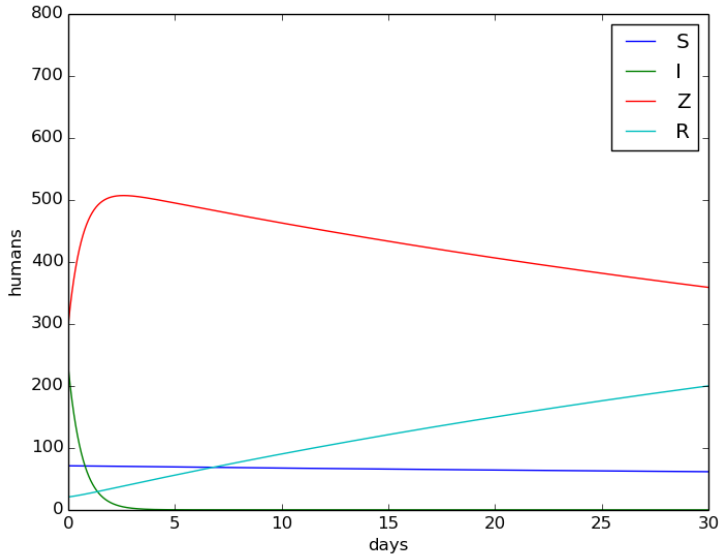

Figure 2.7: *Hysterical phase* with parameter values $\beta = 0.000011$, $\varrho = 1.5$ and $\alpha = 0.000208$.

are trying to avoid the zombies, but when the zombies get too close, the humans need to fight back. These situations are caused by a high density of zombies in some areas, which force the zombies to spread. In *Walking dead* the *Counter attack phase* appears when a group of 30 zombies reaches the camp. This triggers a fight where all the zombies are killed and 4 of the humans get bitten. This shows that a *Counter attack phase* from the humans causes a lot of damage. The time aspect is set to 6 hours. Now the function $\omega(t)$ will be used. This can be seen in Fig.(2.8):

To get some start values, $SZ\omega(t) = 30$ can be used. Where $\omega(t)$ is the area under the function. By inserting the final values from *Hysterical phase* for S and Z, the area shall be $\omega(t) = 1.34 \cdot 10^{-3}$. This result can be reproduced by using $a = 0.00103$ and $\sigma = 0.005$ in $\omega(t)$. The *Counter attack phase* is set to appear during the last part of the day [0.75,1]. The value of T is then set to T=[0.875].

This simulation in Fig.(2.9) results in some deaths. However, the total number should be higher. Another problem is that no humans died during this battle. The ODE model (2.12) is based on *The Night of the Living Dead*, where the amount of humans who are killed is close to zero. This is not the case in *Walking dead*. Therefore the risk of dying is higher for human during a *Counter attack phase*. This is solved by adding $\mu\omega(t)SZ$, where μ is the risk for a human

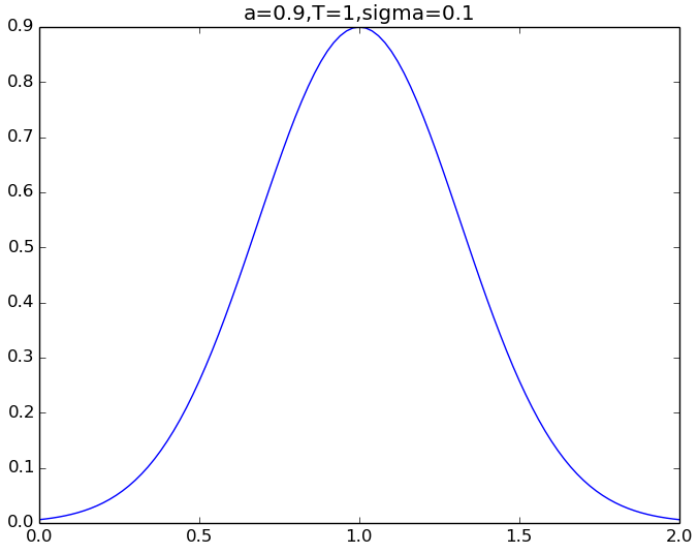

Figure 2.8: $\omega(t)$ is a Gaussian function where a controls the maximum value, T controls the time for maximum value and σ controls the length of the attack.

getting infected compared to a zombie kill during this attack. The model (2.12) can then be expanded to system(2.15),

$$\begin{aligned}
\frac{dS}{dt} &= \Sigma - (\beta + \mu\omega(t))SZ - \delta_S S \\
\frac{dI}{dt} &= (\beta + \mu\omega(t))SZ - \varrho I - \delta_I I \\
\frac{dZ}{dt} &= \varrho I - (\alpha + \omega(t))SZ + \zeta R \\
\frac{dR}{dt} &= \delta_S S + \delta_I I - \zeta R + (\alpha + \omega(t))SZ
\end{aligned} \tag{2.15}$$

Fig.(2.10) is modeled with the initial values given when Rich woke up, explained in the *Initial phase*. The result after this day is that the humans are reduced to 58 humans. The number in the infected group is increased to 2.47, which can be explained with the two characters in the series, Amy and Jim. The number of removed humans is increased to 231, and is a combination of killed zombies and humans who are attacked. By modelling this for another day, the removed group will increase with a couple of new deaths.

It would be interesting to check what would happen if this *Counter attack phase* was repeated over time. Who would survive? An attack every other day

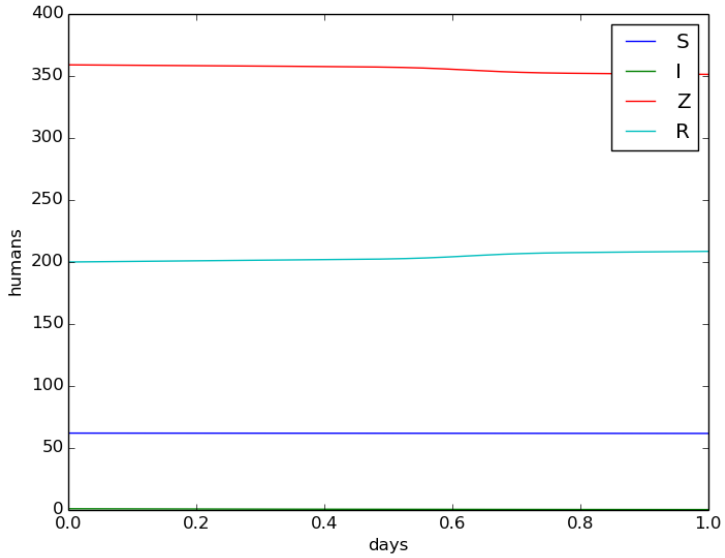

Figure 2.9: The *Counter attack phase* with parameter values $a = 0.00103$, $\sigma = 0.005$ and $T = 0.875$. 8-9 zombies are killed and all humans survive

will give the following result shown in Fig.(2.11). After 200 days there would be about 15 humans and 12 zombies left. Then the humans would be able to survive since they are more efficient in battles.

2.4.5 The three phases in Walking Dead

By adding these three phases together, the final result after the attack should be possible to match. The simulation here will be done with the parameters used in the earlier sections. This can lead to a small error since the result of the final number in each phase is given with decimals and the initial values are based on assumptions and round off numbers. The different parameter values are listed in Tab.(3.3).

parameter	Initial phase	Hysterical phase	Counter attack phase
β	0.01155	0.000011	0.000011
ϱ	1.37	1.5	1.5
α	0.00044	0.000208	0.000208
a	0	0	0.0073
σ	0	0	0.005
μ	0	0	0.14

The simulation is run for 34 days. The three first days are in the *Initial phase*, the resisting days are in the *Hysterical phase*. The *Counter attack phase* is released

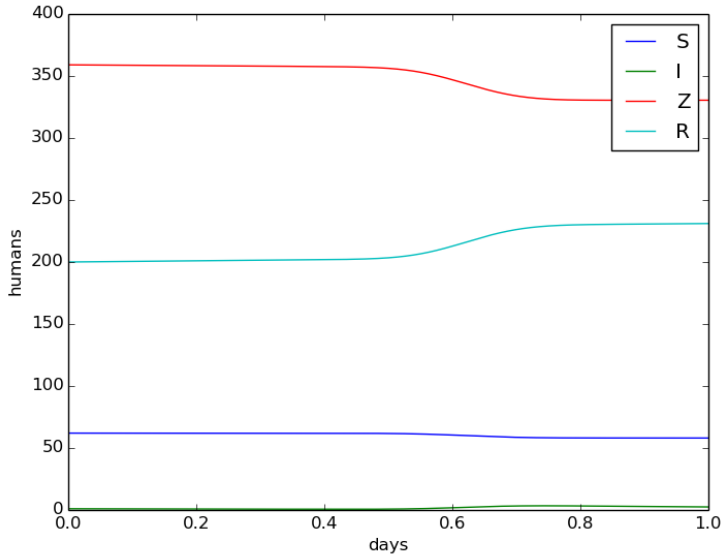

Figure 2.10: *Counter attack phase* with parameter values $a = 0.0073$ and $\mu = 0.14$.

on day 33 and lasts for about 6 hours. The plot is shown in Fig.(2.12). This clearly shows that the change in parameter values affects the different phases. The different values are shown in the Tab.(2.4.5), where the values are given at the initial time. The last column consist of the final values after 34 days.

values	Initial phase	Hysterical phase	Counter attack phase	final values
S_0	621	71	62	58
I_0	0	231	0	1
Z_0	1	299	359	332
R_0	0	21	202	231

Considering the uncertainty of the parameters, this simulation gives a result close to the expected result.

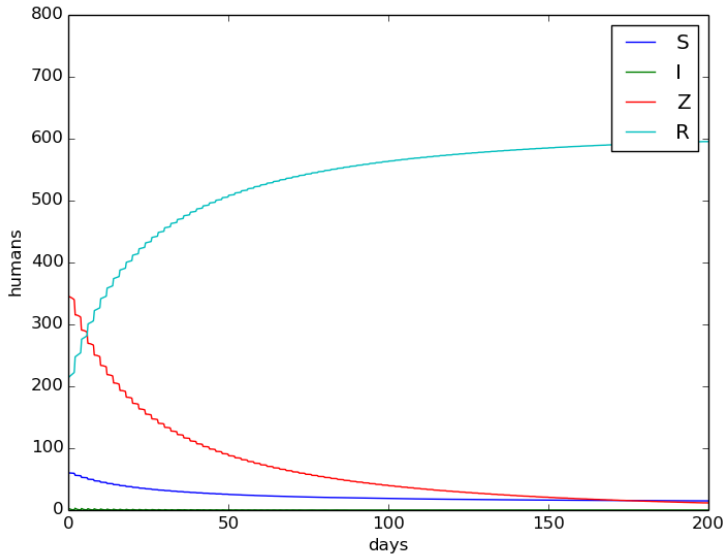

Figure 2.11: 100 counter attacks during 200 days will result in a higher population of humans.

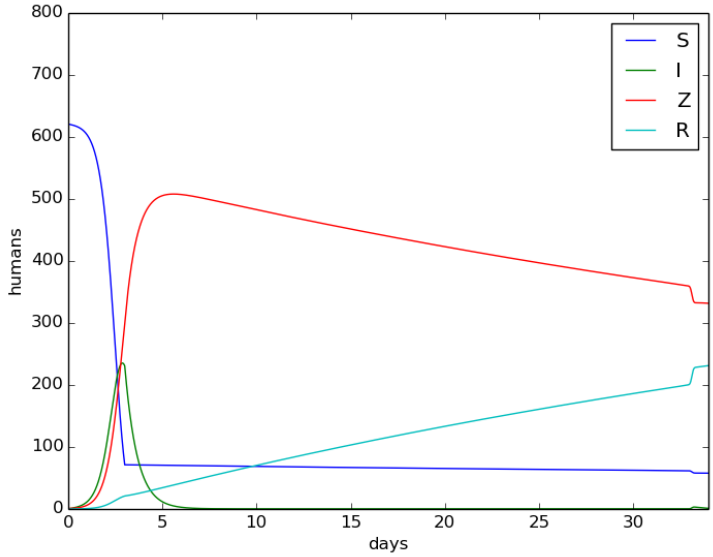

Figure 2.12: Walking Dead simulated after 5 episodes. Based on the three different phases.

2.5 Discussion

The simulations of the example English boarding school were based on a basic SIR model, shown in Eq.(2.1), and expected results were achieved. The maximum concentration of the infected group could be found by using Eq.(2.10). The value of $I_{\max}$ was first calculated for the example from section 2.3 with the given parameter values, and this resulted in $I_{\max} = 292$. The numerical solution shown in Fig.(2.2) gave the same result for $I_{\max}$.

With variations in the parameter value ρ, different epidemic results were achieved. In section 2.3, the value of ρ was set to 202. By decreasing this value to 50, all students would be infected during the 10 first days. Increasing the value of ρ up to 400 on the other hand, would result in 170 remaining students in the susceptible group after 30 days.

The *Zombiefication* part was based on the model and phases from Langtangen, Mardal and Røtnes Ref.[3]. The parameters and the length of the phases were adjusted to simulate *Walking Dead*. Since the simulations were based on observations from the TV series *Walking Dead*, the parameter values in the model were adjusted to fulfill the result.

The parameter values β, ϱ and α from the model in Eq.(2.12) were adjusted for the different phases in section 2.4. The effect of varying these parameters could be seen for the two groups *Susceptible* and *Removed* in Fig.(2.5). Varying β, which describes the number of susceptible humans that become infected, had a major effect on the result for the susceptible group. The changes in α, which describes the number of zombies killed by susceptible humans, affects the result in the removed group. The changes in ϱ, which describes the probability for an infected human to wake up as a zombie, affects the susceptible group in the *Initial phase*. By varying the different parameters in Eq.(2.12), the expected result from *Walking Dead* was achieved.

The parameters found in this model will be used for all three chapters. This model is easy to use. The parameter values can easily be adjusted to fit a known solution, shown for the example from *Walking Dead*. However,it gives no information about the spatial spread of the disease. It will therefore be useless in describing how a disease can spread abroad countries and borderlines. The next two chapters will introduce more complicated models which will take the spatial position into account.

Chapter 3

PDE models

This chapter will introduce a spatial model for epidemic diseases. The ODE system from the previous chapter 2 can be expanded with a term for geographic spread of the disease. The first section 3.1 will be based on the simple SIR model presented in previous chapter, and the chapter *Geographic spread and Control of epidemics* by Murray [6]. The parameter values from the section 2.3 will be used for the model and the results will be compared. The position of the different groups will be studied to see if it affects the numbers in the groups. The last section 3.3, will study and expand the system from Langtangen, Mardal and Røtnes [3]. The results and parameter values used to calculate *Walking Dead* will be compared with the previous ODE system and variations of this PDE model.

3.1 Simple system for spatial spread

A spatial variable, $\mathbf{x}$, will be introduced to the model. This results in both temporal and spatial variations. The difference from a standard ODE system will be the diffusion part added to each equation. The system can be seen in Eq.(3.1).

$$\begin{aligned} \frac{\partial S}{\partial t} &= -rIS + D\nabla^2 S \\ \frac{\partial I}{\partial t} &= rIS - aI + D\nabla^2 I \\ \frac{\partial R}{\partial t} &= aI + D\nabla^2 R \end{aligned} \tag{3.1}$$

Here S describes the susceptible group, I describes the infected group and R describes the removed group. The following conditions are set for the boundary and initial values:

$$\begin{aligned} u_x(0,t) = u_x(X,t) = 0, \quad u = S, I, R \\ u(x,0) = f_u(x), \quad u = S, I, R \end{aligned} \tag{3.2}$$

This results in Neumann conditions at the boundary. The following implementation can be used at the boundary

$$\begin{aligned} \frac{u_{-1}^n - u_1^n}{2\Delta x} &= 0 \\ u_{-1}^n &= u_1^n \end{aligned} \tag{3.3}$$

This is solved by adding an extra point on each side, called ghost points. The values in these ghost points are updated every time step with values from u_1^n and u_{X-1}^n. All three groups, S, I, R in Eq.(3.1) have the same diffusion coefficient, D. This gives the three groups the same diffusion speed. This can vary between systems. Later in the chapter, in section *Zombiefication*, different diffusion terms are given to the groups. The two probabilities rIS and aI will work in the same way as in the ODE system. Since this model takes the position into account, a group of infected that move into a uniform population with susceptible humans can be model. The group of susceptible has the density S_0. A simulation can show the geotemporal spread of the disease. The problem can first be considered as one-dimensional. The system can be nondimensionalised by writing

$$\begin{aligned} I^* = \frac{I}{S_0}, \quad I^* = \frac{I}{S_0}, \qquad R^* = \frac{R}{S_0}, \\ x^* = \left(\frac{rS_0}{D}\right)^{1/2} x, \quad t^* = rS_0 t, \qquad \lambda = \frac{a}{rS_0}, \end{aligned} \tag{3.4}$$

S_0 is used as a representative population. Now Eq.(3.1) can be expressed as in Eq.(3.5). The asterisks have been dropped to make it easier to read.

$$\begin{aligned} \frac{\partial S}{\partial t} &= -IS + \frac{\partial^2 S}{\partial x^2}, \\ \frac{\partial I}{\partial t} &= IS - \lambda I + \frac{\partial^2 I}{\partial x^2}, \\ \frac{\partial R}{\partial t} &= \lambda I + \frac{\partial^2 R}{\partial x^2}, \end{aligned} \tag{3.5}$$

The three parameters r, a and D have been replaced by λ. The *reproduction rate* that was presented for the ODE model can be seen as $1/\lambda$.

$$R_0 = \frac{1}{\lambda} = \frac{rS_0}{a} \tag{3.6}$$

The number of secondary infections produced by one primary infected can be seen as $1/\lambda$. It can also be used to measure two different time scales. The first one, $1/(rS_0)$, measures the contagious time of the disease. The second one looks at the life expectancy for an infected. This can be described as $1/a$ [6].

3.1.1 Travelling wave 1D

In this case the travelling wave describes how a group of infected travels through a geographic area of susceptible humans. This will be shown by sending a pulse

from the infected group into a group of susceptible. A travelling wave solution can be described as follows,

$$I(x,t) = I(z), \quad S(x,t) = S(z), \quad R(x,t) = R(z), \quad z = x - ct, \tag{3.7}$$

The value c describes the wave speed. This represents a wave of constant shape that travels in the positive x-direction. Eq.(3.7) can be inserted into Eq.(3.5). This result in the ordinary system Eq.(3.8)

$$\begin{aligned} S'' + cS' - IS &= 0, \\ I'' + cI' + I(S-\lambda) &= 0 \\ R'' + cR + I\lambda &= 0 \end{aligned} \tag{3.8}$$

This makes an eigenvalue problem. The value of λ needs to stay in a range where $c > 0$ is fulfilled. The values S, I and R have to stay nonnegative. This leads to

$$\begin{aligned} 0 \leq S(-\infty) < S(\infty) &= 1 \\ I(-\infty) = I(\infty) &= 0, \\ 1 \geq R(-\infty) \geq R(\infty) &= 0 \end{aligned} \tag{3.9}$$

An epidemic wave can be seen in Fig.(3.1). The value of λ is set to 0.5. The initial value of the susceptible group is 1 for the area and the removed group is set to 0. The infected group has a Gauss curve around 0 at initial time. In the four subplots in Fig.(3.1), the epidemic wave travels towards the other side. The value z, which is defined in Eq.(3.7), is used to plot the travelling wave measured at a specific point, in this case $x = 15$. This travelling wave is shown in figure(3.2). The infected group in Eq.(3.8) can be linearised when $z \to \infty$. This leads to $S \to 1$ and $I \to 0$. The result can be seen in Eq.(3.10).

$$I'' + cI' + I(S-\lambda) \approx 0 \tag{3.10}$$

This can be found by

$$I(z) \propto \exp\left[(-c \pm c^2 - 4(1-\lambda)^{1/2})z/2\right] \tag{3.11}$$

Since it is required that $I(z) \to 0$ and $I(z) > 0$, oscillations around 0 must be prevented. If a travelling wave exist, it has to satisfy

$$c \geq 2(1-\lambda)^{1/2}, \lambda < 1 \tag{3.12}$$

If $\lambda > 1$, no travelling wave will exist. Then the disease will die out. The terms defined in Eq.(3.4) will give the threshold conditions,

$$\lambda = \frac{a}{rS_0} < 1 \tag{3.13}$$

This is the same value that was given for the ODE model in the previous chapter.

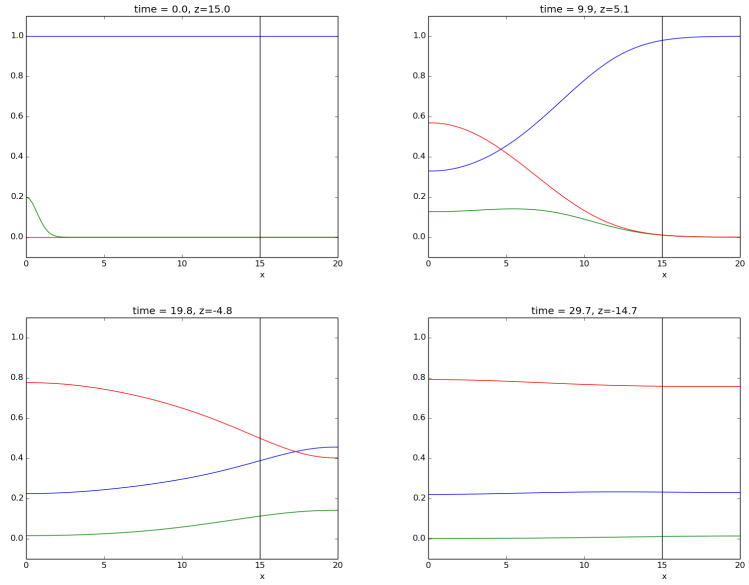

Figure 3.1: A Gaussian function of infected with height 0.2 is placed on the left side. This causes an epidemic wave controlled by the parameter $\lambda = 0.5$. The size of the epidemic wave is measured at point $x = 15$ and can be seen in Fig.(3.2) Movie.

3.1.2 Verifying the solution

To verify the implementation of the model, two manufactured solutions are used. A solution that fulfills the boundary conditions is selected for the manufactured solution. The solver is then tested to see if is reproduces the known solution. The solver will be tested against a constant solution and a cosinus solution.

3.1.3 Constant solution

A constant solution uses preproduced constant values for the concentrations S, I and R. These can be replaced by $S = C_s, I = C_i, R = C_r$. The value of C_i can only be 0 in Eq.(3.5). This results in a poor test where several bugs can escape. The system can be expanded by adding a term βR to the susceptible group and subtracting the same term from the removed group. Then all three values can be tested. The system will then look like this:

$$\begin{aligned} \frac{\partial S}{\partial t} &= -IS + \beta R + \frac{\partial^2 S}{\partial x^2}, \\ \frac{\partial I}{\partial t} &= IS - \lambda I + \frac{\partial^2 I}{\partial x^2}, \\ \frac{\partial R}{\partial t} &= \lambda I - \beta R + \frac{\partial^2 R}{\partial x^2}, \end{aligned} \tag{3.14}$$

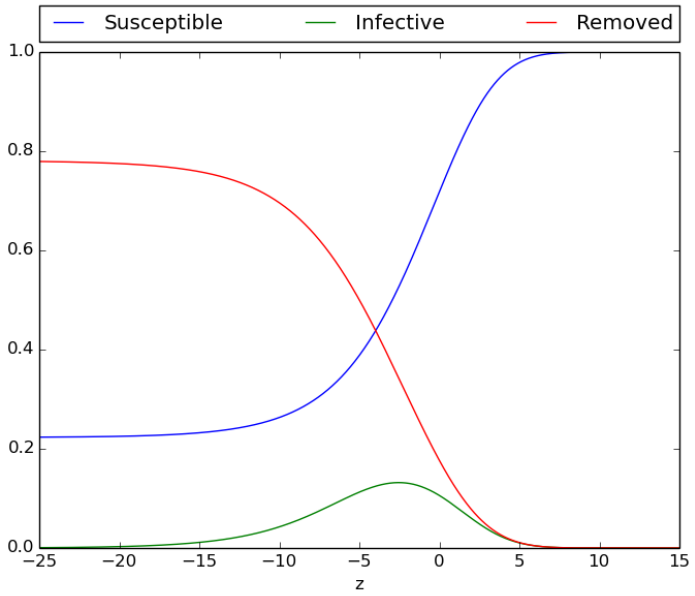

Figure 3.2: The travelling wave measured at $x = 15$ in figure(3.1). The value of z is defined as $x - ct$. The initial value the travelling wave can be seen when $z = 15$.

By deriving Eq.(3.14), the following system Eq.(3.15) has to be solved

$$\begin{aligned} C_i C_s &= \beta C_r \\ C_i C_s &= \lambda C_i \\ \lambda C_i &= -\beta C_r \end{aligned} \tag{3.15}$$

The values β and λ are based on the constants C_s, C_i, C_r, which can be chosen freely. Here they are set to $C_s = 1.2, C_i = 0.8, C_r = 0.6$. This results in $\lambda = C_s = 1.2$ and $\beta = \frac{C_s C_i}{C_r} = 1.6$. A test is made in python and can be seen below.

```
def _test_constant_solution():
    """
    Test problem where u=u_const is the exact solution, to be
    reproduced (to machine precision) by any relevant method.
    """
    def exact_solution(t):
        return C_s,C_i,C_r

    def lam(t,x):
        return C_s

    def beta(t,x):
        return (C_s*C_i)/float(C_r)
```

```
#Constant values
C_s = 1.2
C_i = 0.8
C_r = 0.6

#lam = C_s
#beta = (lam*C_i)/float(C_r)

T = 2; Nt = 200
X = 20; Nx = 40
S_1 = np.ones(Nx+3)*C_s
I_1 = np.ones(Nx+3)*C_i
R_1 = np.ones(Nx+3)*C_r

t,x,S,I,R = simple_PDE(T,Nx,Nt,X,lam,beta,S_1,I_1,R_1)

S_e,I_e,R_e = exact_solution(t)
difference = abs(S_e - S).max()  # max deviation
tol = 1E-14
assert difference < tol

difference = abs(I_e - I).max()  # max deviation
tol = 1E-14
assert difference < tol

difference = abs(R_e - R).max()  # max deviation
tol = 1E-14
assert difference < tol
```

The test was run with no error, and the three constant values were produced correctly. This test is not good enough to qualify the program alone, however an error here would result in a large error in the program.

3.1.4 Manufactured solution

By constructing a function to each equation in the Eq.(3.5), a manufactured solution can be created. Here S,I and R are pre produced. The system will be

$$\begin{aligned} \frac{\partial S}{\partial t} &= -IS + \frac{\partial^2 S}{\partial x^2} + f(x,t), \\ \frac{\partial I}{\partial t} &= IS - \lambda I + \frac{\partial^2 I}{\partial x^2} + g(x,t), \\ \frac{\partial R}{\partial t} &= \lambda I + \frac{\partial^2 R}{\partial x^2} + h(x,t), \end{aligned} \tag{3.16}$$

where f, g and h are source terms used to achieve the expected results for S, I and R. In this case the functions will be:

$$\begin{aligned} f(x,t) &= \frac{\partial S}{\partial t} + IS - \frac{\partial^2 S}{\partial x^2} \\ g(x,t) &= \frac{\partial I}{\partial t} - IS + \lambda I - \frac{\partial^2 I}{\partial x^2} \\ h(x,t) &= \frac{\partial R}{\partial t} - \lambda I - \frac{\partial^2 R}{\partial x^2}, \end{aligned} \tag{3.17}$$

When choosing the expected function for the groups, it is important that the boundary conditions from Eq.(3.2) is fulfilled.

$$u_x(0,t) = u_x(X,t) = 0 \tag{3.18}$$

The quantities have been set to:

$$\begin{aligned} S(x,t) &= \cos(\frac{\pi}{X}x)t \\ I(x,t) &= \cos(\frac{\pi}{X}x)t \\ R(x,t) &= \cos(\frac{\pi}{X}x)t \end{aligned} \tag{3.19}$$

`sympy` is used to find the corresponding source terms f, g and h. This results in the following equations seen in Eq.(3.20)

$$\begin{aligned} f(x,t) &= (t^2\cos(\frac{\pi}{X}x) + (\frac{\pi}{X})^2 t + 1)\cos(\frac{\pi}{X}x) \\ g(x,t) &= (\lambda t - t^2\cos(\frac{\pi}{X}x) + (\frac{\pi}{X})^2 t + 1)\cos(\frac{\pi}{X}x) \\ h(x,t) &= (-\lambda t + (\frac{\pi}{X})^2 t + 1)\cos(\frac{\pi}{X}x) \end{aligned} \tag{3.20}$$

A similar test made for the constant solution can be used here. While the constant test expected a difference on machine precision, this is not the case here. In this test, an expected convergence rate can be measured. The implementation of the manufactured test can be seen below.

```
def _test_manufactured_solution(T,Nt,X,Nx):

    def exact_solution_S(t,x):
        return np.cos(np.pi*x)*t

    def exact_solution_I(t,x):
        return np.cos(np.pi*x)*t

    def exact_solution_R(t,x):
        return np.cos(np.pi*x)*t


    def beta(t,x):
        return exact_solution_S(t,x)*exact_solution_I(t,x)/exact_solution_R(t,x)

    def f(t,x):
        return (t**2*np.cos(np.pi*x) + (np.pi/float(X))**2*t + 1)*np.cos(np.pi*x)

    def g(t,x):
        return (lam*t - t**2*np.cos(np.pi*x) + (np.pi/float(X))**2*t + 1)*np.cos(np.pi*x)

    def h(t,x):
        return (-lam*t + (np.pi/float(X))**2*t + 1)*np.cos(np.pi*x)


    dx = X/float(Nx)
    dt = T/float(Nt)
    S_1 = exact_solution_S(0,np.linspace(0-dx,X+dx,Nx+3))
```

```
I_1 = exact_solution_I(0,np.linspace(0-dx,X+dx,Nx+3))
R_1 = exact_solution_R(0,np.linspace(0-dx,X+dx,Nx+3))

t,x,S,I,R = simple_PDE(T,Nx,Nt,X,lam,beta,S_1,I_1,R_1,f,g,h)
S_e = exact_solution_S(t[-1],x)
I_e = exact_solution_I(t[-1],x)
R_e = exact_solution_R(t[-1],x)

difference_S = abs(S_e - S).max()  # max deviation
difference_I = abs(I_e - I).max()  # max deviation
difference_R = abs(R_e - R).max()  # max deviation

return difference_S,difference_I,difference_R
```

3.1.5 Convergence rate

The solver can be verified by checking the convergence rate. Here, a common discretization parameter h can been used. Since the *stability criteria* demands that the following term in Eq.(3.21) is fulfilled:

$$\Delta t <= \frac{\Delta x^2}{2} \tag{3.21}$$

The common discretization parameter has be set to $h = \Delta t = \frac{\Delta x^2}{2}$ and can be used in Eq.(3.22) to study the convergence rate.

$$\epsilon = C_x h + C_t h = Ch \tag{3.22}$$

The value of h has been set to 0.005, which result in $\Delta t = 0.005$ and $\Delta x = 0.1$. By reducing the value of h, the convergence rate is expected to be 1. The error, ϵ has been produced for four different values of h. The result can be seen in Tab.(3.1.5).

	h	$\frac{h}{4}$	$\frac{h}{16}$	$\frac{h}{64}$
ϵ	9.9E-3	2.5E-3	6.1E-4	1.5E-4

The convergence rate can now be found by using

$$\epsilon \propto h^r \tag{3.23}$$

The error values from Tab.(3.1.5) can be inserted with the different values of the discretization parameter in Eq.(3.24).

$$r_{12} \simeq \frac{\log(\epsilon_1/\epsilon_2)}{\log(h_1/h_2)} \tag{3.24}$$

Where $h_1 = h, h_2 = \frac{h}{4}, ...$, This gives the following result

	ϵ_1/ϵ_2	ϵ_2/ϵ_3	ϵ_3/ϵ_4
r	1.00178	1.00044	1.00011

The expected convergence rate for this model is fulfilled.

3.1.6 Travelling wave in 2D

The Eq.(3.5) can be discretized for a 2D area. This is more realistic when simulating a geographic spread of an epidemic disease. The nondimensional system can be discretized with Forward Euler in time and centered difference in space.

$$\begin{aligned}
\frac{S_{i,j}^{n+1}-S_{i,j}^{n}}{\Delta t} &= -I_{i,j}^{n}S_{i,j}^{n}+\left(\frac{S_{i-1,j}^{n}-2S_{i,j}^{n}+S_{i+1,j}^{n}}{\Delta x^2}+\frac{S_{i,j-1}^{n}-2S_{i,j}^{n}+S_{i,j+1}^{n}}{\Delta y^2}\right)\\
\frac{I_{i,j}^{n+1}-I_{i,j}^{n}}{\Delta t} &= I_{i,j}^{n}S_{i,j}^{n}-\lambda I_{i,j}^{n}+\left(\frac{I_{i-1,j}^{n}-2I_{i,j}^{n}+I_{i+1,j}^{n}}{\Delta x^2}+\frac{I_{i,j-1}^{n}-2I_{i,j}^{n}+I_{i,j+1}^{n}}{\Delta y^2}\right)\\
\frac{R_{i,j}^{n+1}-R_{i,j}^{n}}{\Delta t} &= \lambda I_{i,j}^{n}+\left(\frac{R_{i-1,j}^{n}-2R_{i,j}^{n}+R_{i+1,j}^{n}}{\Delta x^2}+\frac{R_{i,j-1}^{n}-2R_{i,j}^{n}+R_{i,j+1}^{n}}{\Delta y^2}\right)
\end{aligned} \tag{3.25}$$

The known values can be placed on the right side. The system will then be

$$\begin{aligned}
S_{i,j}^{n+1} &= S_{i,j}^{n}+\Delta t\left(-I_{i,j}^{n}S_{i,j}^{n}+\left(\frac{S_{i-1,j}^{n}-2S_{i,j}^{n}+S_{i+1,j}^{n}}{\Delta x^2}+\frac{S_{i,j-1}^{n}-2S_{i,j}^{n}+S_{i,j+1}^{n}}{\Delta y^2}\right)\right)\\
I_{i,j}^{n+1} &= I_{i,j}^{n}+\Delta t\left(I_{i,j}^{n}S_{i,j}^{n}-\lambda I_{i,j}^{n}+\left(\frac{I_{i-1,j}^{n}-2I_{i,j}^{n}+I_{i+1,j}^{n}}{\Delta x^2}+\frac{I_{i,j-1}^{n}-2I_{i,j}^{n}+I_{i,j+1}^{n}}{\Delta y^2}\right)\right)\\
R_{i,j}^{n+1} &= R_{i,j}^{n}+\Delta t\left(\lambda I_{i,j}^{n}+\left(\frac{R_{i-1,j}^{n}-2R_{i,j}^{n}+R_{i+1,j}^{n}}{\Delta x^2}+\frac{R_{i,j-1}^{n}-2R_{i,j}^{n}+R_{i,j+1}^{n}}{\Delta y^2}\right)\right)
\end{aligned} \tag{3.26}$$

This results in an explicit system, which is easy to code. It consists of known values on the right side and only one unknown value on the left side.

3.1.7 A Gaussian wave

In the PDE system for the 1D equation, a Gaussian quantity of infected humans was placed on the left side in the initial value. This resulted in a wave of infected spreading along the x-axis. A similar procedure can be done for the 2D simulation. A couple of simulations have been produced for the 2D system. The first simulation is calculated with a Gaussian function along the points(0,y) for the infected group at initial time. The second simulation has placed the Gaussian function at point(0,0) for the infected group at initial value.

The size of the epidemic wave can be measured and compared by studying the travelling wave at a certain point. In these two 2D simulations in Fig.(3.3), the wave are measured in the point (15,15), while the travelling wave in the 1D simulation was measured at point(15).

The shapes of the two travelling waves in Fig.(3.3) are similar. The only difference is the time when the wave occurs. The plot for 1D wave in Fig.(3.2) has the same shape. With a closer study, the area under the function can be measured in all three cases. The result can be seen in Tab.(3.1.7)

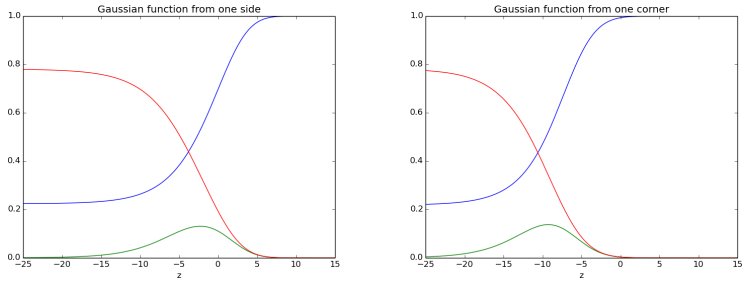

Figure 3.3: Travelling wave measured at point (15,15) with two different initial values for the infected group. I: The initial value is set as a Gaussian line along (0,y). II: The initial value is set as a Gaussian function at point (0,0).

1D wave	2D wave line	2D wave point
1.43	1.43	1.43

The area in all three simulations approach the same area when Δt and Δx are reduced. The size and shape will not change by expanding the system from 1D to 2D. However, by studying Fig.(3.3), one can see that the wave occurs at different times. This is caused by the distance from the start position for the Gaussian wave. The first subplot that starts with a Gaussian function along the $x = 0$ axis gets a wave from the infected group that flows along the x axis. This can be seen as a wave on the beach. Everyone that have the same distance from the ocean will be hit simultaneously. The travelling wave for the 1D simulation and the first subplot occurs at the same time, because they are measured at the same distance from the starting point. The last plot is also measured at (15,15), but occurs later. Since the wave starts at point (0,0), the distance to (15,15) is 21.21. This means that the wave will reach the point 6.21 time steps later. This is a reasonable conclusion based on the plot.

3.1.8 Changes in the initial flow

By increasing the initial wave of the infected group, the initial value of infected can be studied. The simulation is run with the same parameters as for the three simulations above and the only difference is the initial value for the infected group. The Gaussian wave of the infected group is placed at point(0,0) as for subplot II in Fig.(3.3). The simulation can be seen in Fig.(3.4).

The size and shape can be compared by measuring the travelling wave at point(15,15). The travelling wave for this simulation can be seen in Fig.(3.5) and the area for the travelling wave is measured to 1.43, which is similar to the three other simulations.

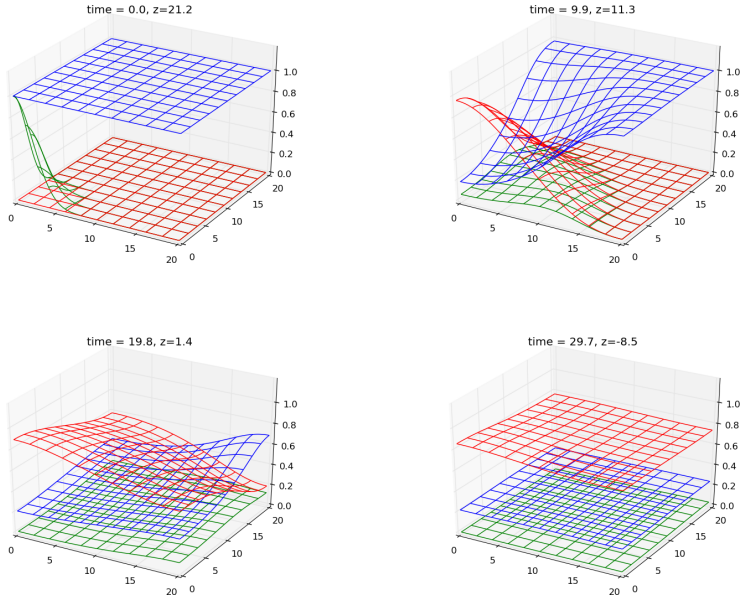

Figure 3.4: A major flow of infected spread outwards in the field. After a certain time, the wave has passed the area and the number in each group stabilized.Movie

The size of the travelling wave will not be affected by changing the value of the infected group. However there is a difference in the time when the wave occurs. In the simulation where the initial value is higher, the travelling wave reaches the measuring point (15,15) earlier. This can be explained by the idea of a ball dropped from a large height. If the ball is released or thrown to the ground, it will only affect the acceleration of the ball, not the terminal velocity. After a certain time the released ball and the thrown ball will reach the same maximum speed. This is the case for the speed of the travelling wave.

3.1.9 Changes in lambda

The one thing that affects the speed and size, is the λ variable in the PDE system(3.5). This λ is a combination of a, which controls deaths among the infected group, r, which controls the number from the susceptible group that gets infected in meetings between the infected and susceptible groups. The last parameter in λ is the concentration of Susceptible, S_0. By changing this parameter, the travelling wave will change in both size and shape. In Fig.(3.6), the simulation is run with four different values of λ. To understand the results in Fig.(3.6), the λ function can be studied,

$$\lambda = \frac{a}{rS_0}, \tag{3.27}$$

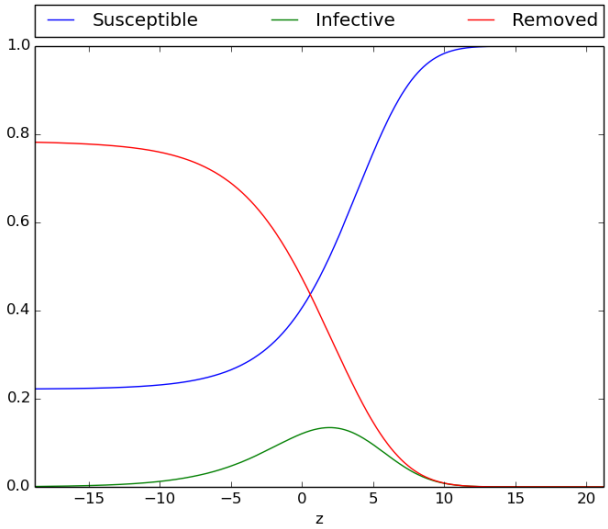

Figure 3.5: The travelling wave with a major increase of infected at the initial time.

A major and aggressive travelling wave is caused when $\lambda \to 0$. In Fig.(3.6), λ is run with value 0.01 in the first subplot. This results in a travelling wave of infected that eradicates the susceptible group in a short time. The wave starts decreasing when all susceptible humans are infected. By looking at Eq.(3.27),one can see that a small value is caused by a small a compared to r and S_0. If a is low, this results in few deaths/immune in the infected group. This means that the infected group will grow and be able to infect even more humans from the susceptible group. The same thing will happen if r is large. A result of a large r will be an aggressive disease that infects a major part of the population. The same result will happen if S_0 is large. Then there are several possible humans to infect. Therefore an outburst of a disease is more critical in a crowded city than in the wilderness, far from other humans.

If λ increases above 1, the disease will not be able to spread. The number of infected will decrease, since the number in the removed group caused by the infected group is higher than the amount of infected humans from the susceptible group. After a certain time, the number of infected will die out. If λ stays at 1, the number of infected will be equal the whole time.

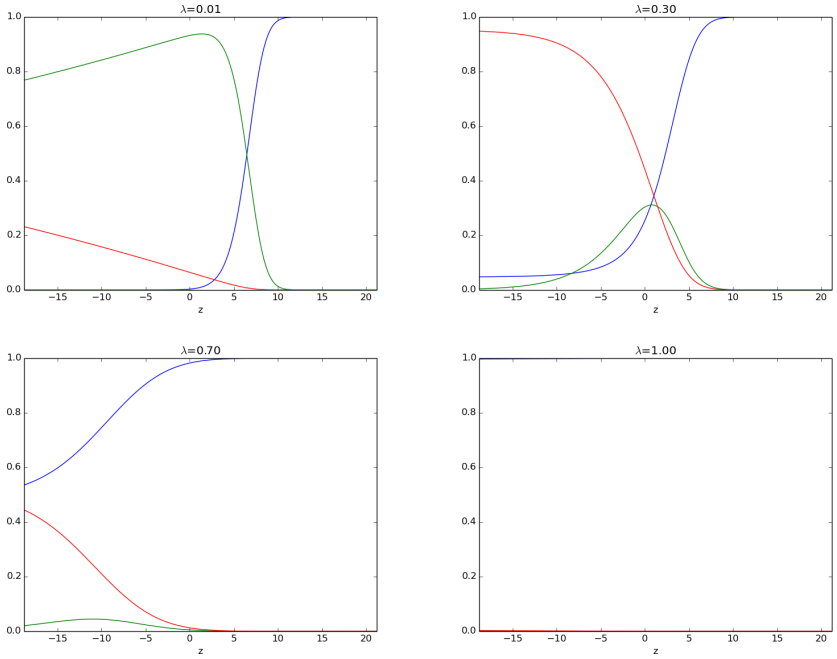

Figure 3.6: The travelling wave simulated with different λ values. The values that are used: $\lambda = 0.01$ for subplot I, $\lambda = 0.3$ for subplot II, $\lambda = 0.7$ for subplot III and $\lambda = 1$ for subplot IV.

3.2 English boarding school

An example from an English boarding school was presented in the previous chapter 2. This example was based on the book from J.D Murray [5], and was modeled for an ODE system. A similar result should appear for the PDE system with the same parameter values and a uniform distribution of the groups. The school had 763 students, and one of the students brought a disease back to the school. The following numbers were used for the ODE system in chapter one. $N = 763, S_0 = 762, I_0 = 1, R_0 = 0, \rho = 202$ and $r = 2.18 \cdot 10^{-3}$.

The first simulation is produced with uniform distributed concentration, This is done to verify the implementation. A person is defined as one cubic. The total volume of the whole group is spread over the area. The area is set to be 100 m x 100 m, which results in an average height of 1/10000 m per person. This is done to get a uniformed distribution. This would of course be more difficult in real life, particularly if the person would be alive. Since the infected group only consists of one person, the total height will be 0.0001 for the whole area. The susceptible group consists of 762 students and the total height at each point will be 0.0762.

The results from subplot I in Fig.(3.7) are equal to the results from the ODE system modeled in the previous chapter.This can be seen in Tab.(3.2.2). This is as expected, since the diffusion term is negligible in this system. The simulation results in a group of separate ODE systems modeled over an area.

3.2.1 Maximum concentration of infected

The maximum concentration of the infected group was found for the ODE system in the previous chapter. The expected value of $I_{\max}$ was first calculated, and later verified with the numerical solution of the ODE system. The reproduction rate found for the PDE system in Eq.(3.6) was given by the same parameters as for the ODE system. A similar maximum value is expected from the PDE solution. The maximum value of the infected group from the numerical PDE solution is $I_{\max} = 292$ and is equal to the $I_{\max}$ for the ODE solution.

3.2.2 Introducing a Gaussian distribution of infected

An assumption one can make is that a person is not able to be evenly distributed over an area. In this example, with only one infected student at initial time, the chance of being infected increases the closer the susceptible group gets the infected student. The student is represented by a Gaussian function in the middle of the school yard, to see if the position affects the result. The height is set to 1 and the volume of the Gauss function is set to 1 cubic. The simulation can be seen in Fig.(3.8) and the total amount of students in each group can be be seen in Fig.(3.7).

The results from the uniform distributed and Gaussian distributed simulations show various results. The initial position of the infected group is the difference between the simulations. This has a major impact. Since the only ones that can be infected by the Gaussian distribution are the students close to the infected student, this restricts the spread of the epidemic. The chance of getting infected in this area is higher. The Fig.(3.8) shows that the infected group quickly grows in the center, where the infected was placed. Subplot IV in Fig.(3.8) shows that the amount from the removed group in the center is close to the maximum of the initial value of the susceptible group, while the students along the boundary of the schoolyard seem to be unaffected after 15 days. This simulation shows that the position of the infected group has a major role in the simulation.

The position of the infected group, here as a Gaussian function, also affects the outcome. Subplot III in Fig.(3.7) describes a simulation where the Gaussian function is placed in the corner with position(0,0). The total volume of the function is increased to 4 since only a quarter of the function is placed in the area. Tab.(3.2.2) shows that the total number of infected is lower than for the centered placed Gaussian function. The infected student is only able to spread

the disease to a quarter of the population compared to the infected student in the center.

If the simulations are run for a long time, the difference between each group will decrease. After 100 days there will be about 18 students in the susceptible group in the uniform distributed simulation, compared to 25 students in both of the Gaussian simulations. A table with the values from the three simulations performed for this English boarding school are compared to ODE system from chapter 2.

	ODE system	PDE uniform dist	PDE center	PDE corner
5 Days				
Susceptible	444.62	444.62	748.03	757.33
Infected	209.56	209.56	7.36	2.35
Removed	108.82	108.82	7.60	3.32
10 Days				
Susceptible	37.59	37.59	697.71	743.58
Infected	117.59	117.59	24.43	6.66
Removed	607.82	607.82	40.86	12.76
15 Days				
Susceptible	21.09	21.09	597.01	717.02
Infected	17.30	17.30	46.96	12.37
Removed	724.62	724.62	119.03	33.61

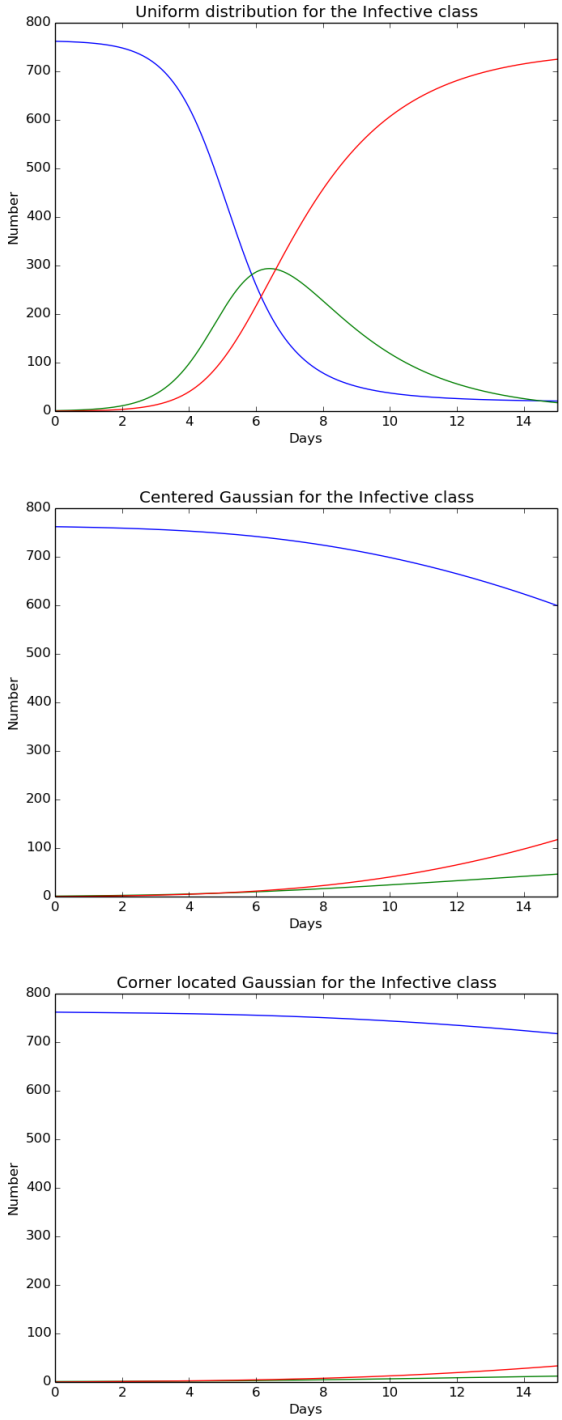

Figure 3.7: English Boarding School modeled with three different initial values for the infected student. The amount of students in each group modeled over 15 days. Subplot I: uniform distribution. Subplot II: The student is placed as a Gaussian function in center. Subplot III: The student is placed as a Gaussian function in the corner (0,0).

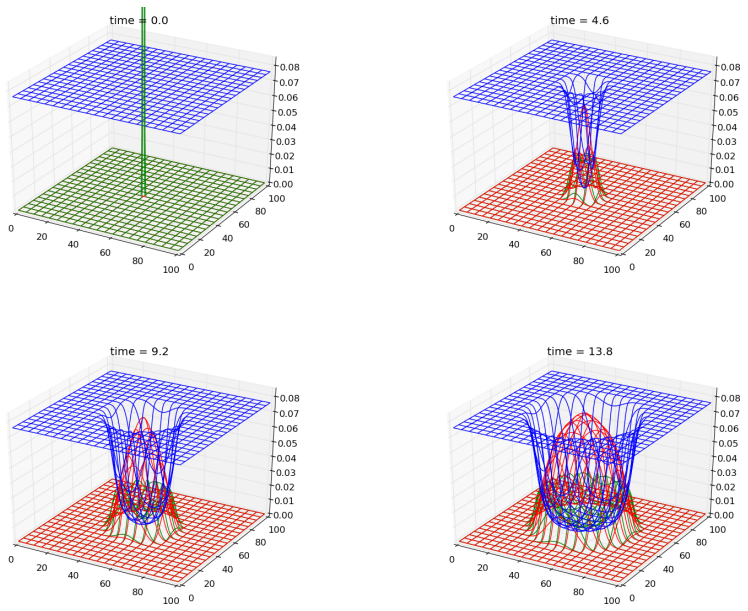

Figure 3.8: The infected student is placed in the center as a Gaussian function at initial time. The height of the Gaussian function is set to 1 m and volume is set to 1 cubic.Movie

3.3 Zombiefication

The previous chapter studied an ODE system designed to calculate the number in the four groups: *Susceptible*, *Infected*, *Zombie* and *Removed* during the five first episodes in the TV series *Walking Dead* Ref.[1]. The model was based on the model from Langtangen, Mardal and Røtnes Ref.[3], with an extra term in the *counter attack* phase. The ODE system from the chapter 2 can be expanded with a diffusion term in each group to make a PDE system. This can be seen in Eq.(3.28)

$$\begin{aligned}
\frac{\partial S}{\partial t} &= \Sigma - (\beta + \mu\omega(t))SZ - \delta_S S + D_s\nabla^2 S \\
\frac{\partial I}{\partial t} &= (\beta + \mu\omega(t))SZ - \varrho I - \delta_I I + D_i\nabla^2 I \\
\frac{\partial Z}{\partial t} &= \varrho I - (\alpha + \omega(t))SZ + \zeta R + D_z\nabla^2 Z \\
\frac{\partial R}{\partial t} &= \delta_S S + \delta_I I - \zeta R + (\alpha + \omega(t))SZ + D_r\nabla^2 R
\end{aligned} \tag{3.28}$$

The Eq.(3.28) can be solved numerically by finite difference. Forward Euler is used for the temporal discretization and centered difference for the spatial discretization. This is solved with the same technique as for the SIR model(3.25). The system can be seen in Eq.(3.29)

$$\begin{aligned}
\frac{S_{i,j}^{n+1} - S_{i,j}^n}{\Delta t} &= \Sigma - (\beta + \mu\omega(t))S_{i,j}^n Z_{i,j}^n - \delta_S S_{i,j}^n \\
&\quad + D_s\left(\frac{S_{i-1,j}^n - 2S_{i,j}^n + S_{i+1,j}^n}{\Delta x^2} + \frac{S_{i,j-1}^n - 2S_{i,j}^n + S_{i,j+1}^n}{\Delta y^2}\right) \\
\frac{I_{i,j}^{n+1} - I_{i,j}^n}{\Delta t} &= (\beta + \mu\omega(t))S_{i,j}^n Z_{i,j}^n - \varrho I_{i,j}^n - \delta_I I_{i,j}^n \\
&\quad + D_i\left(\frac{I_{i-1,j}^n - 2I_{i,j}^n + I_{i+1,j}^n}{\Delta x^2} + \frac{I_{i,j-1}^n - 2I_{i,j}^n + I_{i,j+1}^n}{\Delta y^2}\right) \\
\frac{Z_{i,j}^{n+1} - Z_{i,j}^n}{\Delta t} &= \varrho I_{i,j}^n - (\alpha + \omega(t))S_{i,j}^n Z_{i,j}^n + \zeta R_{i,j}^n \\
&\quad + D_z\left(\frac{Z_{i-1,j}^n - 2Z_{i,j}^n + Z_{i+1,j}^n}{\Delta x^2} + \frac{Z_{i,j-1}^n - 2Z_{i,j}^n + Z_{i,j+1}^n}{\Delta y^2}\right) \\
\frac{R_{i,j}^{n+1} - R_{i,j}^n}{\Delta t} &= \delta_S S_{i,j}^n + \delta_I I_{i,j}^n - \zeta R_{i,j}^n + (\alpha + \omega(t))S_{i,j}^n Z_{i,j}^n \\
&\quad + D_r\left(\frac{R_{i-1,j}^n - 2R_{i,j}^n + R_{i+1,j}^n}{\Delta x^2} + \frac{R_{i,j-1}^n - 2R_{i,j}^n + R_{i,j+1}^n}{\Delta y^2}\right)
\end{aligned} \tag{3.29}$$

By setting the unknown to the left, the following system in Eq.(3.30) can be solved:

$$\begin{aligned}
S_{i,j}^{n+1} &= S_{i,j}^n + \Delta t\Big(\Sigma - (\beta + \mu\omega(t))S_{i,j}^n Z_{i,j}^n - \delta_S S_{i,j}^n \\
&\quad + D_s\left(\frac{S_{i-1,j}^n - 2S_{i,j}^n + S_{i+1,j}^n}{\Delta x^2} + \frac{S_{i,j-1}^n - 2S_{i,j}^n + S_{i,j+1}^n}{\Delta y^2}\right)\Big) \\
I_{i,j}^{n+1} &= I_{i,j}^n + \Delta t\Big((\beta + \mu\omega(t))S_{i,j}^n Z_{i,j}^n - \varrho I_{i,j}^n - \delta_I I_{i,j}^n \\
&\quad + D_i\left(\frac{I_{i-1,j}^n - 2I_{i,j}^n + I_{i+1,j}^n}{\Delta x^2} + \frac{I_{i,j-1}^n - 2I_{i,j}^n + I_{i,j+1}^n}{\Delta y^2}\right)\Big) \\
Z_{i,j}^{n+1} &= Z_{i,j}^n + \Delta t\Big(\varrho I_{i,j}^n - (\alpha + \omega(t))S_{i,j}^n Z_{i,j}^n + \zeta R_{i,j}^n \\
&\quad + D_z\left(\frac{Z_{i-1,j}^n - 2Z_{i,j}^n + Z_{i+1,j}^n}{\Delta x^2} + \frac{Z_{i,j-1}^n - 2Z_{i,j}^n + Z_{i,j+1}^n}{\Delta y^2}\right)\Big) \\
R_{i,j}^{n+1} &= R_{i,j}^n + \Delta t\Big(\delta_S S_{i,j}^n + \delta_I I_{i,j}^n - \zeta R_{i,j}^n + (\alpha + \omega(t))S_{i,j}^n Z_{i,j}^n \\
&\quad + D_r\left(\frac{R_{i-1,j}^n - 2R_{i,j}^n + R_{i+1,j}^n}{\Delta x^2} + \frac{R_{i,j-1}^n - 2R_{i,j}^n + R_{i,j+1}^n}{\Delta y^2}\right)\Big)
\end{aligned} \tag{3.30}$$

A simulation with uniform distributed groups can be done to verify the implementation of the system. The result is expected to be similar to the ODE system in the previous chapter. A zombie attack can be separated into three different phases, based on the paper from Langtangen, Mardal and Røtnes [3]. The first phase is short, and it is called the *Initial phase*. The humans are unfamiliar with the disease in this phase and are as a consequence quite naive to the disease. This result in a high chance of getting infected. The next phase is called the *Hysterical phase*. The humans are now more familiar with the situation and try to avoid the infected group. This result in a lower chance of getting infected. The last phase, which happens at the same time as the *Hysterical phase*, is the *Counter attack*. This phase is often initiated when humans are attacked by zombies. The following parameters that were used for simulating the first episodes of *Walking Dead* will be used here. These can be seen in Tab.(3.3). By computing the system for all three phases, the value in each phase can be compared to the ones from the ODE system. This will give an indication of whether the discretization is done correct.

parameter	Initial phase	hysterical phase	counter attack
β	0.01155	0.000011	0.00011
ϱ	1.37	1.5	1.5
α	0.00044	0.000208	0.000208
a	0	0	0.0073
σ	0	0	0.005
μ	0	0	0.14

The simulation in Fig.(3.9) seems to match the results from the ODE system. For further verification, comparison of the groups in each phase is done. This result can be seen in Tab.(3.3)

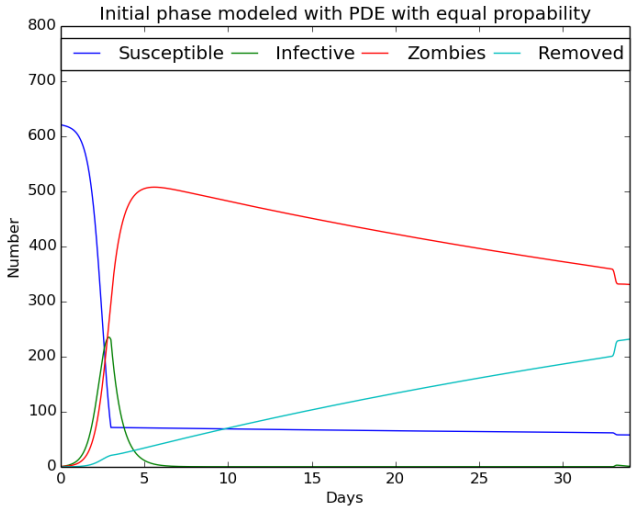

Figure 3.9: The Eq.(3.30) modeled with uniformed distributed groups. Initial values $S_0 = 621$, $I_0 = 0$, $Z_0 = 0$ and $R_0 = 0$ with parameters from (3.3).

The initial values for the four groups are set to $S_0 = 621$, $I_0 = 0$, $Z_0 = 1$ and $R_0 = 0$ in all simulations. The values in Tab.(3.3) are measured at the final time for each phase. The *Initial phase* lasts for three days and the values are measured at $time = 3$. The *Hysterical phase* is a continuous phase, and will not stop until an eventual eradication. The values are therefore given before the *Counter attack* at $time = 33$. The *Counter attack* lasts for some hours, and is measured at $time = 34$, which is a day after the attack. The value of Δt is set to 1E-3.

	ODE system	PDE uniform dist	PDE gauss center
Initial phase	———	———	———
Susceptible	71.3	71.3	81.12
Infected	230.8	230.8	210.94
Zombie	298.9	298.9	310.11
Removed	21.0	21.0	20.60
Hysterical phase	———	———	———
Susceptible	61.6	61.6	70.55
Infected	0.3	0.3	0.34
Zombie	358.6	355.6	334.33
Removed	201.5	201.5	217.56
Counter attack	———	———	———
Susceptible	57.8	57.8	66.50
Infected	1.2	1.2	1.23
Zombie	331.8	331.8	305.86
Removed	231.3	231.3	249.19

These results shows that the PDE system gives the same results as the ODE system.

3.3.1 Spatial spread of the susceptible group

In the previous section, 3.2, the location of the infected group was proven to have a major influence on the result. However here the susceptible group was uniformly distributed over the schoolyard. The number in each group, based on the study of *Walking Dead*, was seen in three different locations in the TV series. By only studying the TV series, it is hard to decide the geographical distance between these three locations. Since this paper focus on a small group of people, the following simulations are done on a grid with size 40m x 40m and for a group of 622 persons. Three susceptible groups will be divided out at initial time. The three susceptible groups will now be called constellations, to avoid any confusion with the groups *Susceptible*, *Infected*, *Zombie* and *Removed. The three constellations are represented as Gaussian functions. A person is defined as one cubic. The following initial positions for the constellations :

- Small constellation with center in position(6,6) with the volume of 21 cubic, correspond to the population of 21 humans
- Middle constellation with the center in position(12,25) with voulme of 200 cubic, correspond to the population of 200 humans
- Large constellation with the center in position(25,12) with volume of 400 cubic, correspond to the population of 400 humans

The diffusion term describes the diffusion for each group. This can be seen as the speed towards equilibrium for each group. If the diffusion constant is large, the flow towards equilibrium will go faster. In these simulations, the diffusion

constant for the groups *Susceptible*, *Infected* and *Zombie* is set to 1, while the diffusion constant for the group *Removed* is set to 0.

The parameters from Tab.(3.3) will be used here, and the three phases will be modeled as shown for the uniformed distributed PDE system. The values will be used for three different simulations with the similar initial value for the different groups. The position of initial values can be seen in Fig.(3.10) and are based on the data given for each constellation above. The difference in the three simulations will be the position of the zombie at initial time. The zombie will be placed in center of the small, middle and large constellation.

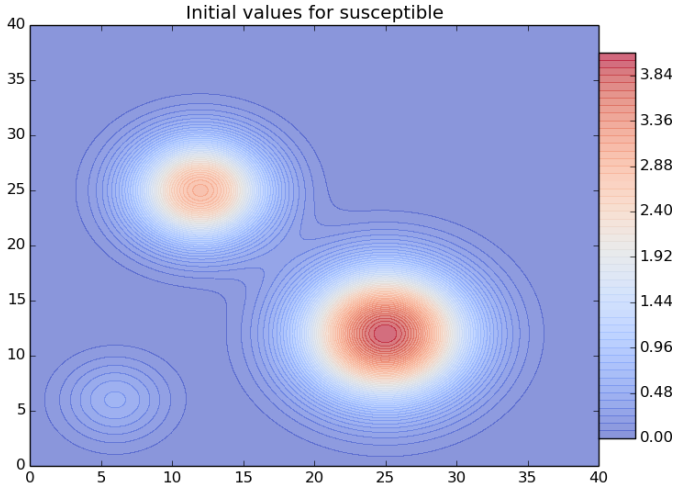

Figure 3.10: The initial value for the susceptible group for three simulations. Small constellation at position(6,6) with volume of 21 cubic, middle constellation at position(12,25) with volume of 200 cubic and large constellation(25,12) with volume of 400 cubic. All three groups are build up with a Gaussian function.

Fig.(3.11) shows the simulation where the zombie is placed in the large constellation. The four subplots are from the different phases that arise during a zombie attack. The different groups have the same color as introduced in Fig.(3.9). It is difficult to separate the three groups *Infected*, *Zombie* and *Removed*, since they all have a low value at initial time. The development of the amount can easier be seen in the Tab.(3.3.1). Since the amount of the susceptible group is quite low in the small constellation where the zombie arises, the disease is not able to infect too many before the society has moved to the next phase, assuming that the broadcasting about the disease works okay for the first days.

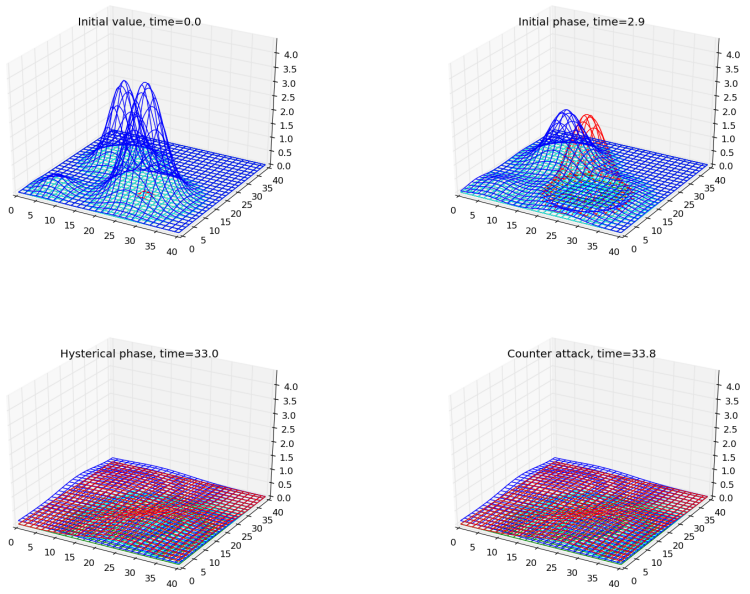

Figure 3.11: *Walking Dead* simulated with the zombie at initial time in the large constellation. Subplots shown at each phase. Movie

By placing the zombie in the middle constellation, the amount in the zombie group increases to a higher level. The damages are higher, and after a month the total population of the susceptible group is reduced to 427. The last calculation done for the large constellation in Fig.(3.11) shows major damages. Here the amount in the zombie group increases above the number of susceptible humans. The infected group also increases to above 100 after a couple of days in the initial phase. This can be explained by the high number of meetings between susceptible and zombies. By studying the subplot II in Fig.(3.11), the zombies are grouped in the large constellation, while the middle and small constellation mostly consist of susceptible humans. By counting the loss of susceptible humans during the first phase, the Tab.(3.3.1) shows that this amount corresponds with the size of the constellations where the zombie was placed, given by the number 17, 188 and 362 in the small,middle and large constellation.

The results from the uniformed distributed simulation is still much higher for the zombie group the in these three simulations. This shows that using the parameters from the ODE system in a geographical area makes little sense. A realistic assumption is that a zombie is restricted to a given area, and therefore the parameters will not be equal for all. The chance of getting infected is much higher if a person from the susceptible group is close to an infected. There is also a greater chance of getting infected if the susceptible group has a high density.

	Small constellation	Middle constellation	Large constellation
Initial phase	———	———	———
Susceptible	602.93	425.31	246.18
Infected	3.09	25.96	49.29
Zombie	14.30	162.28	311.26
Removed	0.65	7.42	14.25
Hysterical phase	———	———	———
Susceptible	602.31	420.11	237.41
Infected	0.03	0.20	0.36
Zombie	6.40	96.21	205.37
Removed	12.23	104.45	177.83
Counter attack	———	———	———
Susceptible	602.05	418.17	233.65
Infected	0.08	0.59	1.14
Zombie	4.60	82.64	179.09
Removed	14.24	119.57	207.09

3.3.2 Free areas for the susceptible group

To model a realistic zombie attack, humans ability to think logically is crucial in the fight. The mobility was presented as a factor in the previous section. Another important skill that the susceptible group holds, is the ability to decide the safety of an area. In the TV series *Walking Dead*, the humans build barricades to keep the zombies outside. This gives the susceptible group free areas where they can stay. This idea can be transferred to the PDE system by rewriting the Eq.(3.28) with spatial dependent diffusion terms. The diffusion constant D_u is now replaced with a diffusion function $\gamma_u(x)$ for $u = S, I, Z, R$, which is spatial discretized. Since a diffusion equation always goes towards equilibrium, this rewriting will only slow down/stop the selected group to diffuse into an area. In this case it will stop the zombie group from diffusing into the buildings.

$$\begin{aligned}
\frac{\partial S}{\partial t} &= \Sigma - (\beta + \mu\omega(t))SZ - \delta_S S + \nabla(\gamma_S(x)\nabla S) \\
\frac{\partial I}{\partial t} &= (\beta + \mu\omega(t))SZ - \varrho I - D_i\delta_I I + \nabla(\gamma_I(x)\nabla I) \\
\frac{\partial Z}{\partial t} &= \varrho I - (\alpha + \omega(t))SZ + \zeta R + \nabla(\gamma_Z(x)\nabla Z) \\
\frac{\partial R}{\partial t} &= \delta_S S + \delta_I I - \zeta R + (\alpha + \omega(t))SZ + \nabla(\gamma_R(x)\nabla R)
\end{aligned} \tag{3.31}$$

The diffusion term is the difference between this system and Eq.(3.28). The discretization can be shown for for a general γ. This will be similar for all groups.

A centered difference is used for the spatial discretization.

$$\begin{aligned}
&= \nabla(\gamma(x)\nabla S) \\
&= (\gamma(x)S_x)_x + (\gamma(x)S_y)_y \\
&= \left(\gamma(x)\frac{S^n_{i+1/2,j} - S^n_{i-1/2,j}}{\Delta x}\right)_x + \left(\gamma(x)\frac{S^n_{i,j+1/2} - S^n_{i,j-1/2}}{\Delta y}\right)_y \\
&= \left(\frac{\gamma(x_{i+1/2,j})(S^n_{i+1,j} - S^n_{i,j}) - \gamma(x_{i-1/2,j})(S^n_{i,j} - S^n_{i-1,j})}{\Delta x^2}\right) \\
&+ \left(\frac{\gamma(x_{i,j+1/2})(S^n_{i,j+1} - S^n_{i,j}) - \gamma(x_{i,j-1/2})(S^n_{i,j} - S^n_{i,j-})}{\Delta y^2}\right)
\end{aligned} \tag{3.32}$$

Since the calculations are based on spatial points, the values inside the function of γ need to be adjusted. This can be done by the use of an arithmetic mean, which can be seen in Eq.(3.33). The notation $q_{i+1/2}$ is a simplification of the function $q(x_{i+1/2})$ with $x_{i+1/2} = x_i + 1/2\Delta x$

$$q_{i+1/2} \approx \frac{1}{2}(q_i + q_{i+1}) \tag{3.33}$$

This arithmetic mean can be inserted for all γ's in the system. The system can be expressed:

$$\begin{aligned}
S^{n+1}_{i,j} &= S^n_{i,j} + \Delta t\Big(\Sigma - (\beta + \mu\omega(t))S^n_{i,j}Z^n_{i,j} - \delta_S S^n_{i,j} \\
&+ \frac{1}{2\Delta x^2}\left(\gamma_S(x_{i-1,j})(S^n_{i-1,j} - S^n_{i,j}) + \gamma_S(x_{i,j})(S^n_{i-1,j} - 2S^n_{i,j} + S^n_{i+1,j}) + \gamma_S(x_{i+1,j})(-S^n_{i,j} + S^n_{i+1,j})\right) \\
&+ \frac{1}{2\Delta y^2}\left(\gamma_S(x_{i,j-1})(S^n_{i,j-1} - S^n_{i,j}) + \gamma_S(x_{i,j})(S^n_{i,j-1} - 2S^n_{i,j} + S^n_{i,j+1}) + \gamma_S(x_{i,j+1})(-S^n_{i,j} + S^n_{i,j+1})\right)\Big) \\
I^{n+1}_{i,j} &= I^n_{i,j} + \Delta t\Big((\beta + \mu\omega(t))S^n_{i,j}Z^n_{i,j} - \varrho I^n_{i,j} - \delta_I I^n_{i,j} \\
&+ \frac{1}{2\Delta x^2}\left(\gamma_I(x_{i-1,j})(I^n_{i-1,j} - I^n_{i,j}) + \gamma_I(x_{i,j})(I^n_{i-1,j} - 2I^n_{i,j} + I^n_{i+1,j}) + \gamma_I(x_{i+1,j})(-I^n_{i,j} + I^n_{i+1,j})\right) \\
&+ \frac{1}{2\Delta y^2}\left(\gamma_I(x_{i,j-1})(I^n_{i,j-1} - I^n_{i,j}) + \gamma_I(x_{i,j})(I^n_{i,j-1} - 2I^n_{i,j} + I^n_{i,j+1}) + \gamma_I(x_{i,j+1})(-I^n_{i,j} + I^n_{i,j+1})\right)\Big) \\
Z^{n+1}_{i,j} &= Z^n_{i,j} + \Delta t\Big(\varrho I^n_{i,j} - (\alpha + \omega(t))S^n_{i,j}Z^n_{i,j} + \zeta R^n_{i,j} \\
&+ \frac{1}{2\Delta x^2}\left(\gamma_Z(x_{i-1,j})(Z^n_{i-1,j} - Z^n_{i,j}) + \gamma_Z(x_{i,j})(Z^n_{i-1,j} - 2Z^n_{i,j} + Z^n_{i+1,j}) + \gamma_Z(x_{i+1,j})(-Z^n_{i,j} + Z^n_{i+1,j})\right) \\
&+ \frac{1}{2\Delta y^2}\left(\gamma_Z(x_{i,j-1})(Z^n_{i,j-1} - Z^n_{i,j}) + \gamma_Z(x_{i,j})(Z^n_{i,j-1} - 2Z^n_{i,j} + Z^n_{i,j+1}) + \gamma_Z(x_{i,j+1})(-Z^n_{i,j} + Z^n_{i,j+1})\right)\Big) \\
R^{n+1}_{i,j} &= R^n_{i,j} + \Delta t\left(\delta_S S^n_{i,j} + \delta_I I^n_{i,j} - \zeta R^n_{i,j} + (\alpha + \omega(t))S^n_{i,j}Z^n_{i,j}\right)
\end{aligned} \tag{3.34}$$

The diffusion term for the removed group is taken away, since dead people are not able to move. This system looks quite messy, but it is straight forward to calculate. All values on the right side are known values and the system is easy to solve. Now every point will be controlled by the diffusion constants given

in $\gamma(x)$. This makes it easier to control the flow in each group. With a high diffusion constant, the diffusion will spread fast. When the diffusion constant goes towards zero, the flow will decrease towards zero flow. This will result in a set of ODE systems modeled for each point.

3.3.3 Ten minutes at Frederikkeplassen

Frederikkeplassen at the University of Oslo is a possible area for an upcoming zombie attack. This simulation will try to model a ten minute sequence with the diffusion parameter added in this section. Since students often learn and interact fast, they will only use three minutes before they realize the danger and transitions into the *Hysterical phase*. A map of Frederikkeplassen is used to define the safe and critical areas. The buildings are set as areas where only the susceptible humans are allowed to move. This is done by setting the diffusion constant to zero for the zombie and infected groups. Since the buildings are safe spots for the susceptible humans, an idea would be to express this in the diffusion term by forcing the susceptible humans for other areas into the buildings. This is more difficult, since the concentrations in each group wants to diffuse towards equilibrium. A way to delay this process is by setting the diffusion constant to be low in the buildings and high outside. This will result in a fast diffusion in the open areas and a slow diffusion inside the buildings.

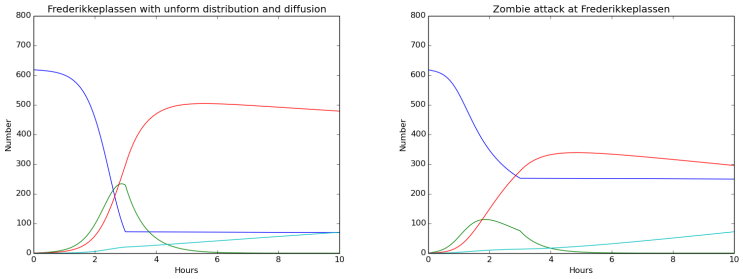

Figure 3.12: The amount in each group for two simulations of Frederikkeplassen modeled same parameters for 10 minutes. Subplot I with uniformed distributed groups and same diffusion constants for all groups. Subplot II is based on Fig.(3.13) with different initial values for each group.

Two simulations have been done at Frederikkeplassen. The amount in each group can be seen in Fig.(3.12). The first simulation has a solution based on the ODE system, with uniformed distributed groups, equal diffusion constants and no free areas for the susceptible humans. The second simulation is modeled with three groups of susceptible humans, as in the previous section. The small group with 21 students is placed at point(4,4), the middle group with 200 students is placed at point(15,8) and the large group with 400 students is placed at point(8,13). The zombie is placed at point(8,10). The $\gamma(x)$ is set to zero in the

buildings for the zombie and infected group, and one in the rest of the area. For the susceptible group, $\gamma(x)$ is set to 0.1 in the buildings, which causes slow diffusion. In the outside areas, $\gamma(x)$ is set to 5 for the susceptible group. The desired result is to push them into the buildings, but this will only happen if there is a lower concentration inside the buildings. Therefore this will not reflect a realistic flow of a susceptible population. This simulation can be seen in Fig.(3.13)

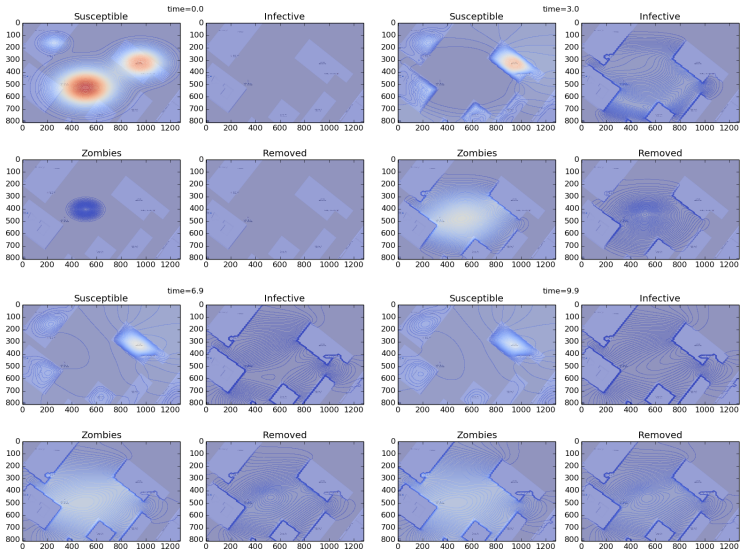

Figure 3.13: Frederikkeplassen modeled with free areas for the susceptible groups. The diffusion function $\gamma(x)$ is set to zero for the zombie and infected groups in the buildings. The zombie at initial time is placed in the center of Frederikkeplassen. Movie

The results in Tab.(3.3.3) shows that the three first minutes are crucial. The number after three minutes shows that only 72 humans survived the attack in the uniformed solution, compared to 252 in the free areas. The number in the zombie group is quite similar for the simulations with uniformed distribution and free areas measured at $t = 3$. However at $t = 7$ the difference is major. This can be explained by looking at Fig.(3.13) and the building with the middle group placed inside. When the zombie starts attacking at $t = 0$, the large group is exposed. This group is placed close to the zombie and the position is in an open area. The zombie can attack right away and the number in the infected and zombie groups increases fast. In the two first minutes, a major part of the large group is infected and the zombie group starts to spread. After 2-3 minutes, the group has reached the building with the middle group. Here the diffusion is set to 0, and the spread of zombies stop. Since the diffusion variable for the

susceptible group is quite low inside the buildings, it takes time before the group diffuses. Maybe the right diffusion value along the buildings would be 0, to avoid any leakage. This would again cause problem for the diffusion of the susceptible group into the buildings. It is also reasonable to think that the susceptible group needs to diffuse after a certain time. The lack of supplies would force them out.

	Uniform distribution	Free areas
3 Minutes		
Susceptible	72.23	252.72
Infected	229.65	75.69
Zombie	296.67	276.55
Removed	20.84	13.94
7 Minutes		
Susceptible	70.78	251.35
Infected	0.83	0.51
Zombie	498.72	325.54
Removed	49.12	41.26
10 Minutes		
Susceptible	69.69	249.84
Infected	0.25	0.38
Zombie	479.00	295.71
Removed	70.55	72.36

3.4 Discussion

This PDE model made it possible to analyze epidemic diseases for a spatial area. The travelling wave is essential for a disease to spread within one area. If the reproduction rate seen in Eq.(3.6) was below 1, the travelling wave would decrease towards zero and the disease would disappear. By varying λ, one could see that a low value would cause a total eradication of the susceptible group. By setting $\lambda >= 1$, the damage from the epidemic wave would be close to zero and the disease would die out.

The results from the English boarding school shows that the position of the infected student has a major impact on the result. A uniform distribution was first calculated and compared with the ODE simulation in the previous chapter. This gave the same result. However, placing the infected student in the center of the schoolyard, resulted in 68 percent more susceptible after in days than with an uniform distribution. The amount of susceptible is even higher if the student is placed in the corner. Then the amount is 70 percent higher than in the uniform group. The results can be seen in Tab.(3.2.2). The uniform distribution shows that there are 21 students left in the susceptible group and 724 in the removed group in 15 days. The opposite result can be seen for the simulation where the infected is placed in the corner. Here, there are 717 susceptible and 33 removed left.

Section 3.3 verified the uniformly distributed PDF solution with the ODE solution from the previous chapter. These were expected to be similar. The English boarding school studied the variations in the position of the infected with a uniformly distributed group of susceptible. This section tried to expand this idea by splitting the group of susceptible into three constellations. One zombie was placed in all three constellations, and the simulations showed that the loss of susceptible was proportional to the size of the constellation. For the small, middle and large constellation the loss of susceptible were 18,196 and 375 based on the Tab.(3.3.1). The middle group lost 97 percent susceptible based on the size of the constellation, which was the highest percentage in all three constellations. This can be explained by the overlapping between the middle and the large constellations, seen in Fig.(3.10). This overlapping resulted in a minor spread of the disease to the constellation next to it. As seen in the section 3.2, the position of the infected student has an impact on the spread of the disease. This section shows that the susceptible group also affects the result. It is therefore better to use a PDE model than an ODE model. It is realistic to assume that different groups will never be uniformly distributed, and that the positions have a major effect.

The last section 3.3.3 tried to implement human behavior by giving the susceptible group the ability to keep zombies outside the buildings. This was done by giving the groups: *Zombie* and *Infected* restricted areas. This was crucial factor for the humans in *Walking Dead* to prevent meetings between them and the zombies. Houses and buildings were used as shields. The three constellations from the previous section was used. However, the position was changed. The middle constellation was placed in one of the buildings. By studying Fig.(3.13), one can see that the zombie group was not able to diffuse into the buildings. As a result, the middle constellation avoided attacks. However, since the concentrations for each group will go towards equilibrium, the movement pattern for each group will differ from human behavior. The next chapter will use a Random walk model to simulate this zombie outburst. This will be based on the section 3.3.3, and introduce different conditions depending on the phase the zombies and humans are in.

Chapter 4

Random walk

The last chapter will study a third way to model epidemic diseases. This will be done by using a Random walk model. This technique is quite different from the two models presented earlier. Here, Monte Carlo simulations and probabilities are used instead of differential equations, which have been in focus earlier. The first section will be an introduction to general principles for Monte Carlo methods and Random walk based on the paper from M.H. Jensen Ref.[2]. The next sections will use the parameters from the English boarding school and *Walking Dead* to see if a Random walk model can expand the knowledge about epidemics by adding human behavior.

4.1 Monte Carlo methods

Techniques from Monte Carlo are widely used in several fields as chemistry, physics, medicine, biology and in finance Ref. [2]. These numerical methods can be seen in general terms as statistical simulation methods, which use random numbers to perform the simulations. Four terms are required to understand the Monte Carlo strategy:

- Random variable
- Probability distribution functions (PDF)
- Moments of a PDE
- The pertinent variance σ^2

The two first terms are important when modelling a Random walk simulation, while the two last terms are important when studying the result. The four terms are explained below.

4.1.1 Random variable

Random variable can be seen as a stochastic variable, where the outcome cannot be presumed. Examples as tossing dice, flipping coins or gambling are based on this principle. Although the outcome is unknown, knowledge about the probability and the range can be studied. The numbers in the *domain* for two dice are

$$\{2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12\}$$

with the corresponding *probabilities* are

$$\{1, 2, 3, 4, 5, 6, 5, 4, 3, 2, 1\}\frac{1}{36}$$

By throwing two dice once, there is no guarantee that the result will be 7, though this has the highest probability. However, by repeating this operation, the distribution would reflect the *probabilities* above. A stochastic variable can either be discrete or continuous, but will in both cases be denoted as capital letters, X, Y. A discrete example is the example above, where the domain is given with exact values, $x_1, x_2, x_3, ..., x_n$. The continuous case can be seen as the probability in a given area. An example can be the distance from a dart to the center, after trowing a dart randomly.

This chapter will use random variable for several decisions. The path of the walker will be controlled by two random variables. The first will control the direction of the walker, by drawing a random number between 0 and 2π. The second random variable will control the number of time steps walked in the chosen direction. Here a number between 1 and 20 is drawn. This is done to create a more realistic movement pattern. Random variables will be drawn for each parameter value given in the previous ODE and PDE systems. Here the outcome will be based on the random variable and the probability given by the parameter value.

4.1.2 Probability distribution functions (PDF)

The PDF is a function $p(x)$ on the domain that gives the probability or relative frequency for a outcome. In the discrete case, the function can be seen as

$$p(x) = Prob(X = x) \tag{4.1}$$

The PDF in the continuous case is not able to directly depict the actual probability. The probability is instead defined as the density around x with an infinitesimal interval. This can therefore be seen as an integral, since it is the density of the probability rather than the probability Ref.[2]. This can be defined.

$$Prob(a \leq X \leq b) = \int_a^b p(x)dx \tag{4.2}$$

To quote M.H. Jensen "Qualitatively speaking, a stochastic variable represents the values of numbers chosen as if by chance from some specified PDF so that the selection of a large set of these numbers reproduces this PDF." Ref.[2]. This sums up the relation between random variables and the PDF. If this is not fulfilled, the group of stochastic variables does not fulfill the criteria for random numbers.

The size of $p(x)$ has to be in the interval $0 \leq p(x) \leq 1$, since the probability cannot be negative or larger than 1 for an event to happen. The sum of all events has to be 1, both for discrete and continuous PDFs, and can be seen as follows

$$\begin{aligned} \sum_{x_i \in \mathbb{D}} p(x_i) &= 1 \\ \int_{x \in \mathbb{D}} p(x)dx &= 1 \end{aligned} \tag{4.3}$$

There are several distributions that are essential when looking at continuous PDFs. The main PDF in this chapter will be uniform distribution and can be seen in Eq.(4.4).

$$p(x) = \frac{1}{b-a}\theta(x-a)\theta(b-x) \tag{4.4}$$

with:

$$\begin{aligned} \theta(x) &= 0, \quad x < 0 \\ \theta(x) &= 1, \quad x \geq 0 \end{aligned} \tag{4.5}$$

This is used to disperse the group of walkers at initial time over the area. The chance will be equal for all positions. This PDF is also used in the movement pattern and for the spread of the disease. To get a correct estimate, it is important that the set of random numbers is large enough. Gaussian distribution is the second PDF used in this chapter. This is often called normal distribution and can be seen in Eq.(4.6)

$$p(x) = \frac{1}{\sigma\sqrt{2\pi}} \exp(-\frac{(x-\mu)^2}{2\sigma^2}) \tag{4.6}$$

This will give the same distribution as the Gaussian function used in the previous chapter. Here it will be used for the simulations of all three phases, to describe the initial positions of the walkers.

4.1.3 Moments of a PDF

By defining $h(x)$ as an arbitrary function, the *expectation value* can be written

$$\langle h \rangle_X \equiv \int h(x)p(x)dx \tag{4.7}$$

Here, defined on the domain of the stochastic variable X, with PDE $p(x)$. A more general way to write the expectation is by adding a power of, n, to the

equation. This can now be seen as the *moments*. The n-th moment is defined

$$\langle x^n \rangle \equiv \int x^n p(x) dx \tag{4.8}$$

The value of n can be set to zero. This results in $\langle 1 \rangle$ and creates a normalized condition for p. The first order is called *mean* and is often defined with a μ.

$$\langle x \rangle = \mu \equiv \int x p(x) dx \tag{4.9}$$

This represents the average value of PDF and is often called the expectation value of p Ref.[2]. Since this system consists of small group of walkers, which is modeled over a short period, the results from the simulations will vary. Therefore a set of simulations will be performed and the average values will be used.

4.1.4 The pertinent variance σ^2

Central moments is a special case of moments defined as

$$\langle (x - \langle x \rangle)^n \rangle \equiv \int (x - \langle x \rangle)^n p(x) dx \tag{4.10}$$

The first two central-moments are trivial and only result in 1 and 0, respectively for $n = 0$ and $n = 1$. However, the second central-moment is more interesting to study. This is denoted as σ_X^2 or Var(X), called the variance. This can be shown.

$$\sigma_X^2 = \langle x^2 \rangle - \langle x \rangle^2 \tag{4.11}$$

The square root of the variance, $\sigma = \sqrt{\langle (x - \langle x \rangle)^2 \rangle}$ is called *standard deviation*. This can be seen as the spread around the mean of the PDF. Since the result is based on the average value of a set of simulations, the *standard deviation* also gives essential information. If the *standard deviation* is major, one can expect large variations when modelling a system. This will make it more difficult to predict the result of an outcome. Since these systems are quite small, one can expect major variations and a large *standard deviation*.

4.2 English boarding school

The parameters in this example has been equal for all three systems. The chance of getting infected by influenza requires a meeting between an infected person and a susceptible person. A random walker will after a sufficient number of steps cover the whole area. A simulation is done for a student with a random position at initial time. 1000 random steps are taken every day, which results in a step every 90 seconds. The step length is set to 5.7024 m, and is based on the average distance a person walks every day. The simulation is performed for 15 days, which results in 15000 random steps. The size of the schoolyard is set to 100 m x 100 m, and the disease can spread within a distance of 5 meters.

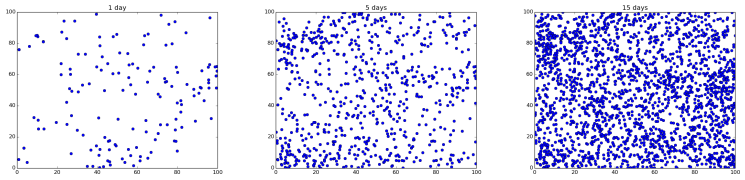

Figure 4.1: The positions a random walker has covered in 1, 5 and 15 days. A random step with length 5.7024 m is performed every minute. The positions are plotted for every ten minutes.

Fig.(4.1) shows that a random walker will be distributed over the area after enough steps. The students in the school are divided into three groups.

- The *Susceptible* group: This consists of susceptible students, who are at risk of getting infected. This group is described by S.
- The *Infected* group: This consists of infected students. The group is described by I.
- The *Removed* group: This consists of students who are immune to the disease. This group is described by R.

The total number of students is $N = 763$. The initial values are: $S_0 = 762$, $I_0 = 1$ and $R_0 = 0$. There are two parameters that are used in the simulation. The first parameter r, describes the gain of infected students from the susceptible group. This rate is proportional to the number of susceptible and infected students and is given by rSI. The second parameter a describes the rate of removal from the infected group to the removed group. These two parameters are set to $r = 2.18 \cdot 10^{-3}$ and $a = 0.44036$ for the ODE system simulated in chapter 2. The ODE system can be seen in Eq.(4.12)

$$\begin{aligned} \frac{dS}{dt} &= -rSI \\ \frac{dI}{dt} &= rSI - aI \\ \frac{dR}{dt} &= aI \end{aligned} \tag{4.12}$$

The parameters r and a must be adapted to the Random walk simulation. The parameter r is used in

$$rSI \tag{4.13}$$

and is based on the fact that all possible combinations of S and I are executed during one time unit. This is not necessarily the case in a random simulation. The meetings in a random simulation depends on the number of random walkers, the possibility of a meeting and the number of time steps during one time unit. If the possibility of a meeting is small, the students have to be close to transmit

the disease. If the number of time steps is high, the chance of one meeting another is higher. The following term has to be fulfilled:

$$r_r m_0 = r S_0 I_0 \tag{4.14}$$

Here m_0 is a constant value and represents number of meetings between the susceptible group and the infected group at initial time. This can be found by a numerical simulation of the random walkers. The number of meetings for the infected student during one day is simulated for 1000 days, and the average result per day is used. The average number of meetings during one time unit is $m_0 = 1905.223$. Now Eq.(4.14) can be rewritten and r_r can be expressed by known values:

$$r_r = \frac{r S_0 I_0}{m_0} \tag{4.15}$$

The parameter r_r is now used to calculate the risk of getting infected in a meeting between a susceptible student and an infected student.

The value of a has to be adjusted as well. This parameter is only affected by the time. If 1000 random steps a day are simulated, the parameter value for a_r can be found by studying the average period of illness. This can be found by $\frac{1}{a}$. The average period is 2.27 days. The value of a_r can be set to 0.00044036. With a numerical simulation of 100 000 random walkers and the parameter value $a_r = 0.00044036$ for becoming immune, one can see that the average number will be 2.27 days. The simulation of the English boarding school can be seen in Fig.(4.2).

4.2.1 Lower maximum concentration for the infected group

In the previous chapters, the threshold value was found for the epidemic systems. The reproduction rate could be used to check if the disease would develop into an epidemic disease. The reproduction rate can be seen in Eq.(4.16)

$$R_0 = \frac{r S_0}{a} \tag{4.16}$$

If $R_0 > 1$ was fulfilled, an epidemic situation would occur. With the parameters from the ODE simulation, he result would be $R_0 = 3.77$. This information could be used to find the maximum concentration of the infected group. This was shown in Section 2.2. In the two previous chapters, the maximum value of infected, given by I_{max} has been set to 292. By studying the Fig.(4.2), one can see that the maximum value of the Random walk simulation is lower, and occur later. The maximum value of the infected group is here measured to be 263.

Since the transformation of a student from the susceptible group to the infected group only requires one successful meeting, where successful is seen as the transmission of the disease. There will be no difference in the result if

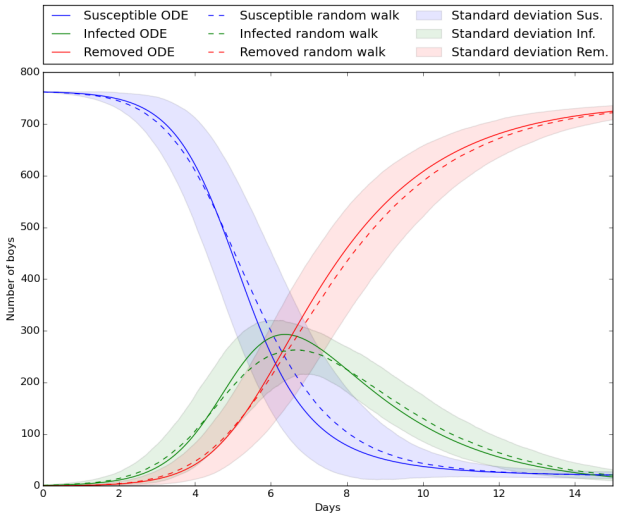

Figure 4.2: Random walk compared to an ODE simulation of Eq.(4.12). The random function is shown with a dashed line, with the standard deviation shown as the colored area around the dashed line. The random function is based on the average of a set of simulations.

the transmission of the disease happens once or several times during one time step. However, if the number of infected increases, the risk of one person getting infected several times increases as well. By studying Fig.(4.2), one can see that the differs between the simulations occur when the concentration of infected is high.

4.2.2 The chance for a disease to spread

When calculating the group of simulations, only 75 percent of the simulations resulted in an epidemic disease. 25 percent resulted in a transmission of the infected student to the removed group, before the student was able to infect other students. These simulations were performed on a small group, and the results may differ in larger groups. A removal rate above one will not necessarily lead to an epidemic disease, if the group is small enough.

4.3 Zombiefication

The ODE system given in the chapter 2 will be used for this simulation. This can be seen in Eq.(4.17). The parameters have to be adjusted for this simulation, similarly to the parameters for English boarding school. Frederikkeplassen at Blindern will be used as the area where the simulations will be done. The area

is estimated to be 100m x 100m and the disease will be able to spread if the distance is closer than 4 meters. There will be done four different simulations in this section, where the influence from human behavior to the model will be studied. The time unit will be set to minutes, and the simulations will be done for 10 minutes for the two first simulations. The last simulations will be performed for 34 minutes. 100 random steps will be performed every minute.

$$\begin{aligned}\frac{dS}{dt} =&\Sigma - (\beta + \mu\omega(t))SZ - \delta_S S \\ \frac{dI}{dt} =&(\beta + \mu\omega(t))SZ - \varrho I - \delta_I I \\ \frac{dZ}{dt} =&\varrho I - (\alpha + \omega(t))SZ + \zeta R \\ \frac{dR}{dt} =&\delta_S S + \delta_I I - \zeta R + (\alpha + \omega(t))SZ\end{aligned} \tag{4.17}$$

Similarly to the English boarding school, the parameters in Eq.(4.17) have to be adjusted. The parameters from the two first phases in *Walking Dead* will be used. These can be seen in the table below. The number of meetings per minute is set to $m_0 = 98.64$, based on the average from 300 time steps. This is used to find the value of β_r and α_r, similar to the method shown in the previous section. The value for ϱ has been adjusted by first finding the average incubation time for the infected group. This has been done by setting $1/\varrho$. The average incubation time is 0.72 minutes. This is really fast, and not a realistic number, based on the TV Series *Walking Dead*. By numerical simulations, the value of ϱ_r can be set to 0.0137 for each simulation. This will result in an average incubation time of 0.72 minutes. The same can be done for the value in the hysterical phase.

parameter	Initial phase	hysterical phase
β	0.01155	0.000011
β_r	0.07271	0.000693
ϱ	1.37	1.5
ϱ_r	0.0137	0.015
α	0.00044	0.000208
α_r	0.00277	0.001309

These parameter values are used for all simulations. The previous chapter 3 introduced the spatial effect and the ability for humans to seek safe areas. This chapter will introduce different conditions for the walkers. These conditions will affect the interaction between the groups. In chapter 2, the simulated period was estimated to 34 days. This will be different in this chapter. The section 3.3.3 in the previous chapter will be used as preference for the results.

4.3.1 Random walk

Random walk will be the first condition for each walker. This results in a smooth distribution of the whole group. The simulation will be done for ten minutes at

Frederikkeplassen. The simulations are shown with the python package `Pygame`, where the random walkers are represented with different images. These can be seen in Fig.(4.3).

Figure 4.3: Figures used in the simulation. I: The walkers in the susceptible group can be seen as humans with green sweater. II: The walkers in the infected group can be seen with a red and green sweater, with one arm in front. III: The walkers in the zombie group can be seen with a white sweater and both arms in front. IV: the walkers in the removed group can be seen as a tombstone.

The initial values for the four groups are equal as for the previous chapter. $S_0 = 621$, $I_0 = 0$, $Z_0 = 1$ and $R_0 = 0$. The walkers are randomly distributed over Frederikkeplassen at initial time. The initial positions in one simulation can be seen in subplot I in Fig.(4.4).The probability distribution function for the walkers are here set to be uniform. The walkers will therefore have the same probability for walking in all directions. The step length is based on an average pace of 5 kilometers per hour. This result in a step length of 0.83 m for each random walk. The first simulation is run for 10 minutes. The parameters from the *Initial phase* are used from 0 to 3 minutes. From 3 to 10 minutes, the parameters from the *Hysterical phase* are used. The result after 10 minutes can be seen in subplot II in Fig.(4.4).

100 simulations with these parameter values are performed, and the average and standard deviation of the simulations are plotted in Fig(4.5). 95 percent of the simulations led to an epidemic disease. However, the standard deviation is large. By studying the second phase from 3 minutes to 10 minutes, one can see that the amount in each group varies. In the *Hysterical phase*, the standard deviation is high for the susceptible and zombie groups. Therefore the outcome from a random chosen simulation is hard to predict.

By comparing the average result with the PDE simulation from section 3.3.3 in the previous chapter, one can see that the average results differ from the PDE results. The average number of the susceptible group is higher than the result from the PDE simulation.

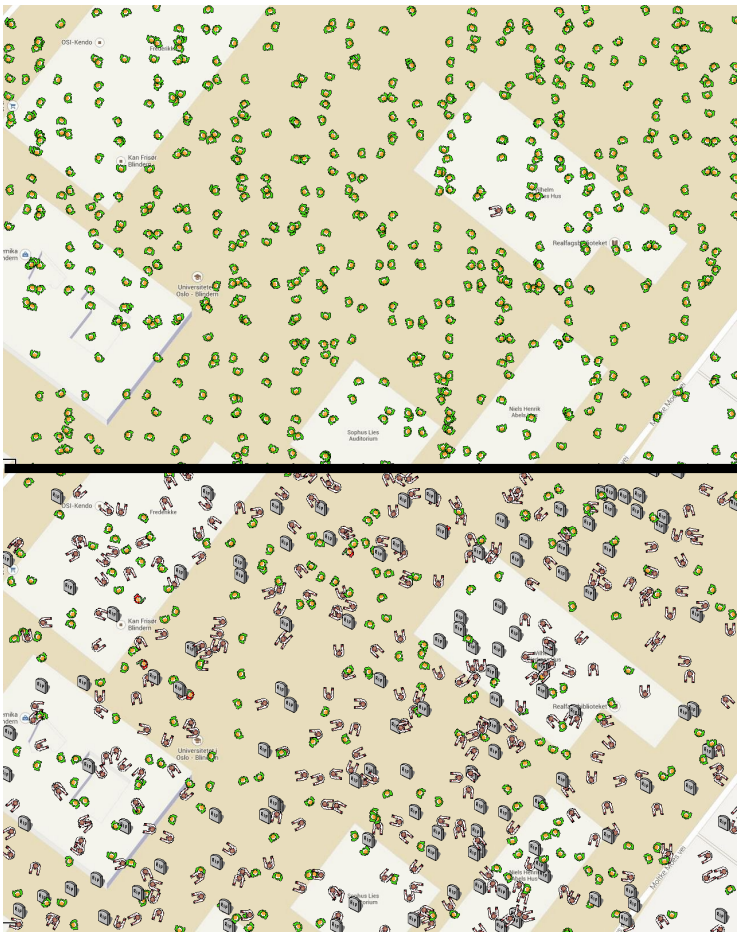

Figure 4.4: Positions from the simulations of Frederikkeplassen. I: Initial position for 621 susceptible humans and 1 zombie. II: Final position of a simulation of Frederikkeplassen. Movie

	PDE	Random walk	Moving smart
3 Minutes			
Susceptible	72.23	279.2	87.51
Infected	229.65	162.05	229.02
Zombie	296.67	167.57	284.88
Removed	20.84	13.168	20.59
7 Minutes			
Susceptible	70.78	276.36	82.79
Infected	0.83	0.6421	35.35
Zombie	498.72	278.87	397.46
Removed	49.12	66.115	106.4
10 Minutes			
Susceptible	69.69	274.34	79.96
Infected	0.25	0.4736	34.87
Zombie	479.00	243.48	350.15
Removed	70.55	103.69	157.02

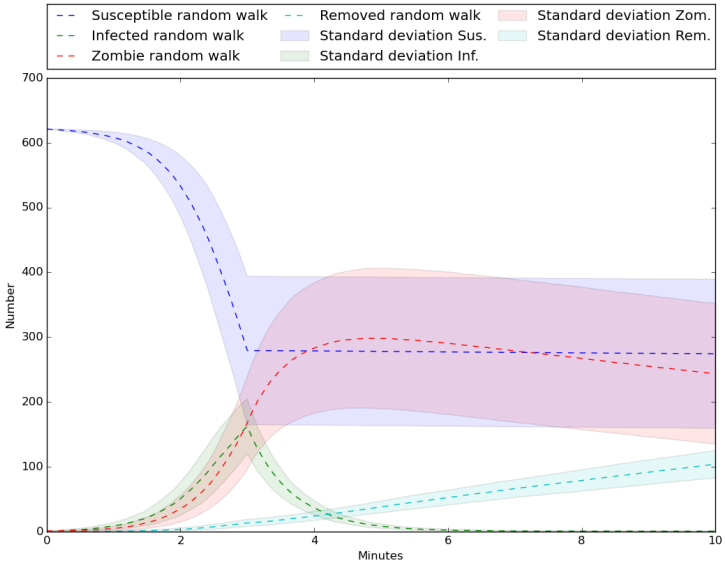

Figure 4.5: The average and standard deviation of a set of simulations on Frederikkeplassen. The *Initial phase* lasts from 0 to 3 minutes.The *Hysterical phase* lasts from 3 to 10 minutes. The parameter values can be seen in Tab.(4.3).

4.3.2 Moving smart

Next phase is based on the movement pattern that would be more realistic based on the TV series *Walking Dead*. Here the zombie group searches after humans from the susceptible group in the area around them. If there are humans that are close enough, the zombies will start moving towards the humans. The same is done for the humans in the susceptible group. The humans search after possible attacks from the zombies. When the zombies get to close, the humans try to escape by moving away. If the distance between the zombie and human is to high, they will randomly walk around.

Similar to the Random walk condition above, the Moving smart condition is calculated based on 100 simulations. The step length is equal for the susceptible group and the zombie group. Therefore the number of zombies are set to 10, to avoid a chasing game, where one zombie runs after the group of susceptible with the equal distance the whole time. A screenshot of one simulation can be seen in Fig.(4.6). One can see that the zombies chase the humans around. The zombies have to cooperate to be able to get close enough to attack the humans.

Some simulations were first tried where only one zombie was initialized at the start. This resulted in zero infected humans and a chasing zombie as explained

above. However, when the amount of zombies was increased to 10, the difference in the result was major. One can see in Tab.(4.3.1) that after the *Initial phase*, there are only 100 susceptible humans left in the average Moving smart. The cooperating force from the zombie group gets stronger as the group increases. Then they are able to chase the susceptible group from several fronts, and it is difficult for the susceptible group to avoid fights. Similar situations are seen in *Walking Dead*. In the city Atlanta, where the amount of zombies is high, the ability to escape is difficult. However, when the main character Rick Grimes meets individual zombies, he can easily escape the danger. A plot of the average result with the standard deviation can be seen in Fig.(4.7).

A result of this cooperating force from the zombie group is that the group is able to eradicate the susceptible group in several simulations. After the *Initial phase*, 15 of the 100 simulations results in total eradication for the susceptible group. At final time the number of simulations that causes eradication have increased to 29 simulations. This Moving smart condition seems to give the zombie group the greatest advantage, when the density of zombies gets high.

4.3.3 Three phases in Walking Dead

A natural idea is to use different conditions for different phases. The first phase, *Initial phase*, will include a Random walk condition for all groups. While the *Hysterical phase* will include a smart moving condition for the susceptible and zombie group. The infected group will move randomly around as in the *Initial phase*. The third phase will be the *Counter attack*, where the susceptible group will stop running and then counter attack the zombies. The strength of the attack depends on the density of humans around. If the density of humans is high in an area, the strength of the susceptible group will increase. This is not the case for the zombie group. The simulation will be performed for 34 minutes, where the three phases have been scaled down from days to minutes. This simulation will not be able to say anything about the result for 34 days. This will demand other values. This result will give an insight into how human behavior will affect the result.

The susceptible group will at initial time be split into three groups. The distribution in the groups will be based on a Gaussian distribution explained section 4.1. The susceptible groups are placed at the following positions: 21 humans at position(6,6), 200 humans at position(12,25) and 400 humans at (25,12). The initial position for the zombie is randomly placed around for all simulations. 100 simulations are performed. Screenshots from a simulation can be seen in Fig.(4.8).

By studying the Tab.(4.3.3), the three phases gives the susceptible group a greater chance of staying alive. One can see that there is only 1 person from

the susceptible group that dies in the Hysterical phase compared to 4 in the ODE simulation. The similar result can be seen for the zombie group. There are several that dies in the ODE simulation that in the Random walk simulation. This can be explained by the fact that the susceptible group tries to avoid fights by running away.

	ODE	Random walk	Free areas
Initial phase			
Susceptible	71	274	331
Infected	231	157	130
Zombie	299	178	149
Removed	21	14	12
Hysterical phase			
Susceptible	62	256	330
Infected	0	0	0
Zombie	359	31	256
Removed	202	335	37
Counter attack			
Susceptible	58	256	330
Infected	1	0	0
Zombie	332	28	255
Removed	231	338	37

4.3.4 Free areas for the susceptible group

The last advantage the susceptible group will get, is to be able to move into buildings to escape the zombies. A similar thing was done for in the previous chapter, 3. However, the effect is better here. The free areas are found by using the pixel values for the backgroud picture. The value of the buildings is similar for all buildings, and is used to control the direction of the zombie group. Nothing is done for the susceptible group. The movement pattern for the susceptible students will only be affected by the positions of the zombies. A screenshot after 10 minutes can be seen in Fig.(4.10)

One can see from Fig.(4.10) that the humans moves into the buildings. These are not defined as any free areas. However, the zombies are not able to go in here, and the result is that this becomes the desired area for the humans. By studying Fig.(4.11), one can see that the change in amount of zombies and humans flattens out over time, this can be explained by the fact that the humans are now able to avoid battles. The *Counter attack* phase in negligible in the simulation with free areas. Since the humans are able to avoid connections with the zombies, the counter attack disappears.

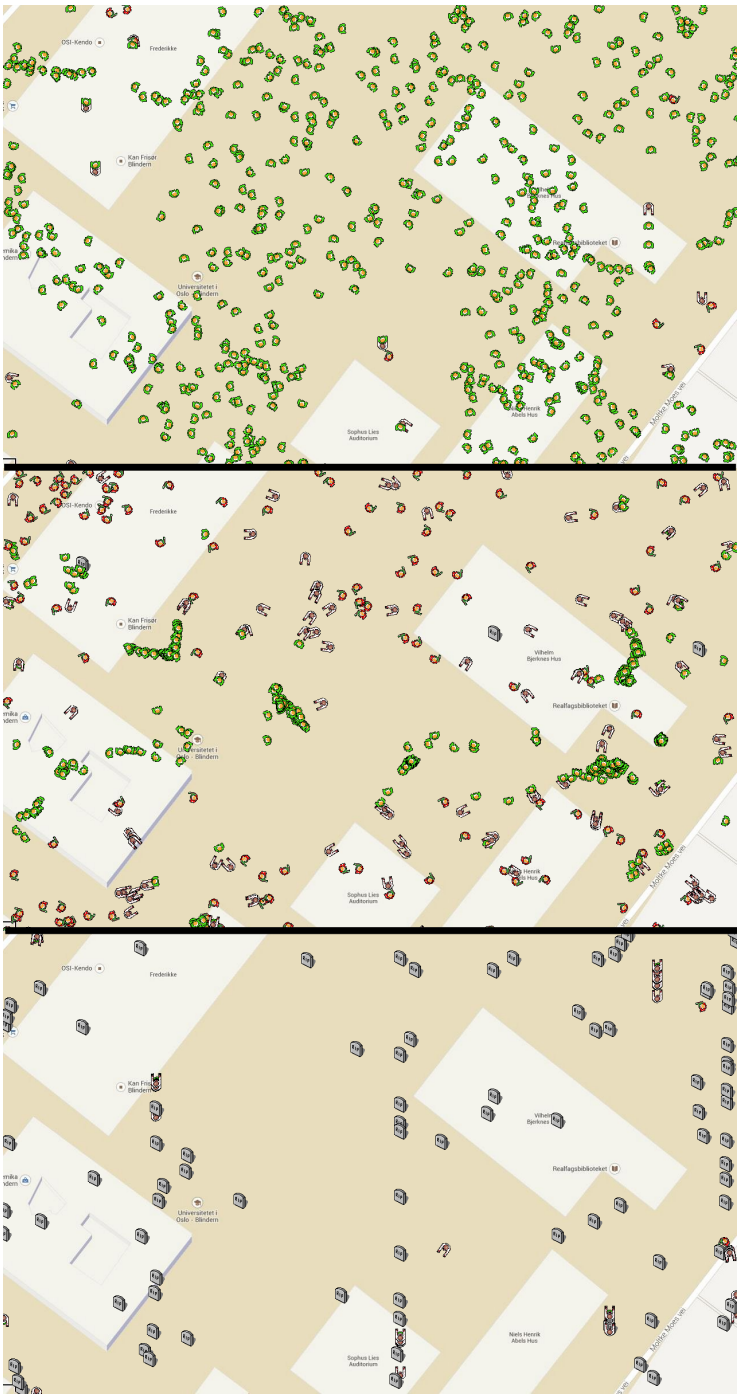

Figure 4.6: Three Screenshots of the moving pattern for the zombie and susceptible groups with the Moving smart condition.I:Close after initial time. The zombies are chasing the humans.II: A large group of humans have recently been infected in the upper left corner. III: Close to total eradication for the human group. Only a small group left in the center of Frederikke. Movie

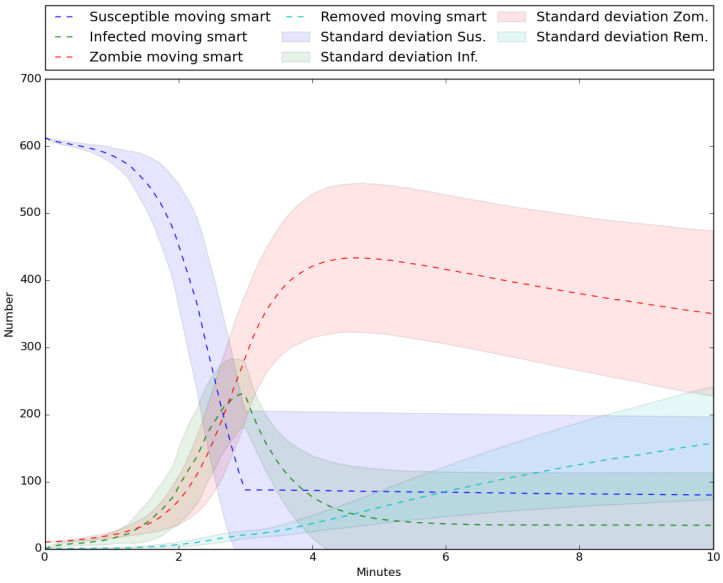

Figure 4.7: The average and standard deviation of for the Moving smart conditionon Frederikkeplassen. The *Initial phase* lasts from 0 to 3 minutes.The *Hysterical phase* lasts from 3 to 10 minutes. The parameter values can be seen in Tab.(4.3).

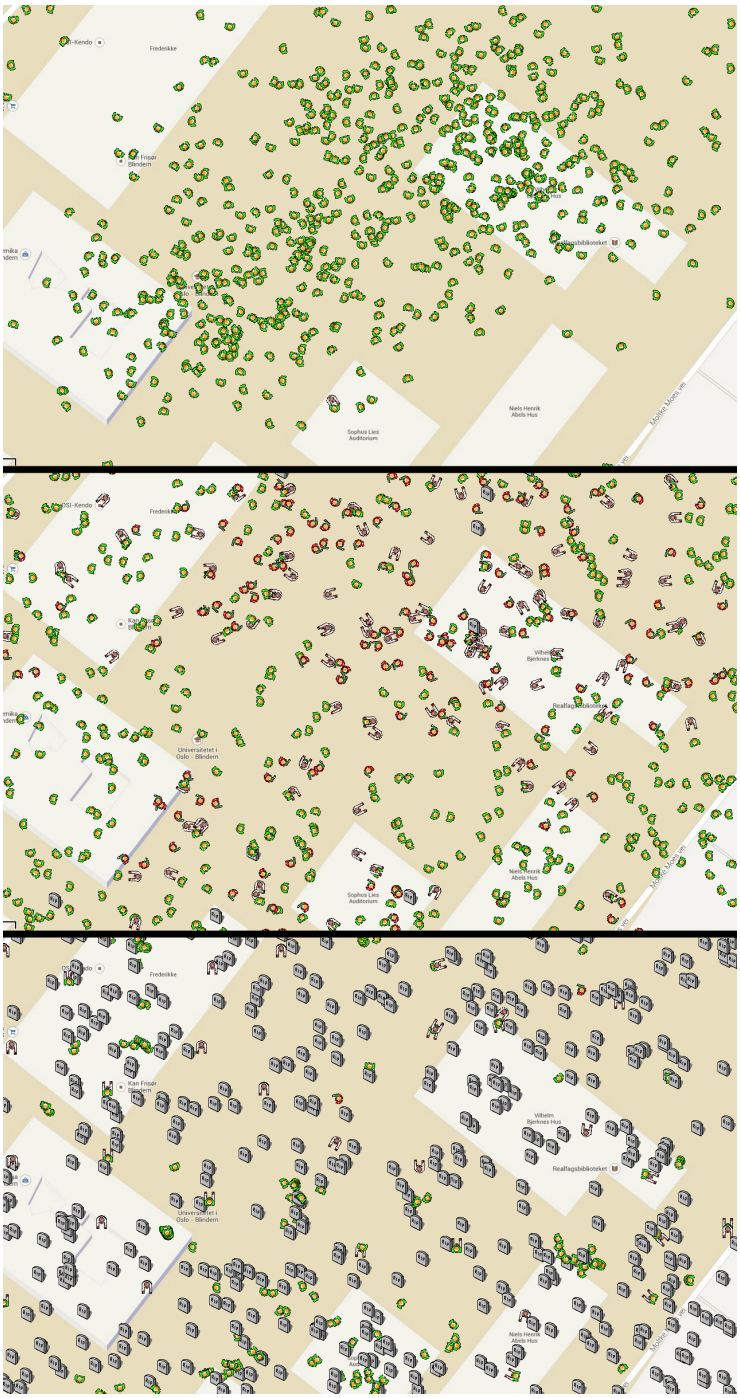

Figure 4.8: Three screenshots from a simulation of the three phases. I: Shows the initial position of the susceptible and zombie group. II: Shows the position and number before the *Hysterical phase*. III: shows the result after the *Hysterical phase*. Movie

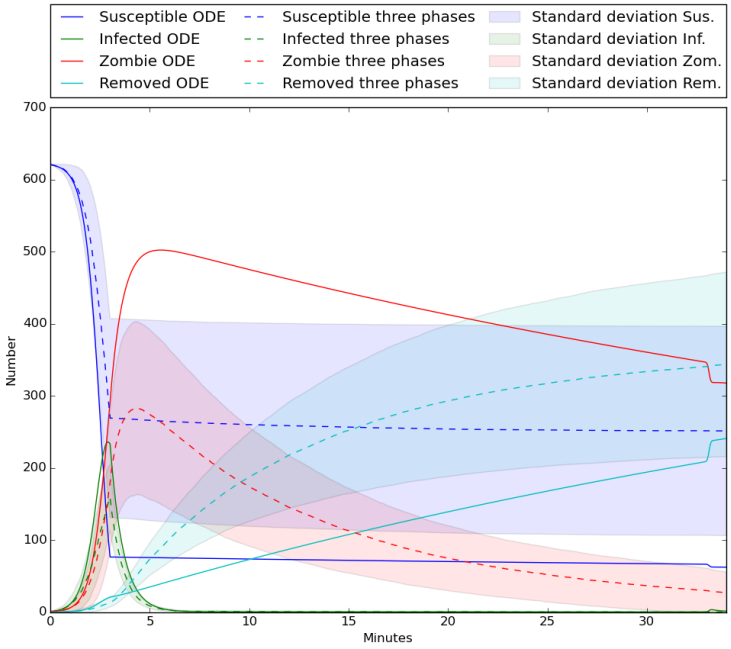

Figure 4.9: The average and standard deviation for a set of simulations over three phases. An ODE simulation withthe same parameters is added to the plot.

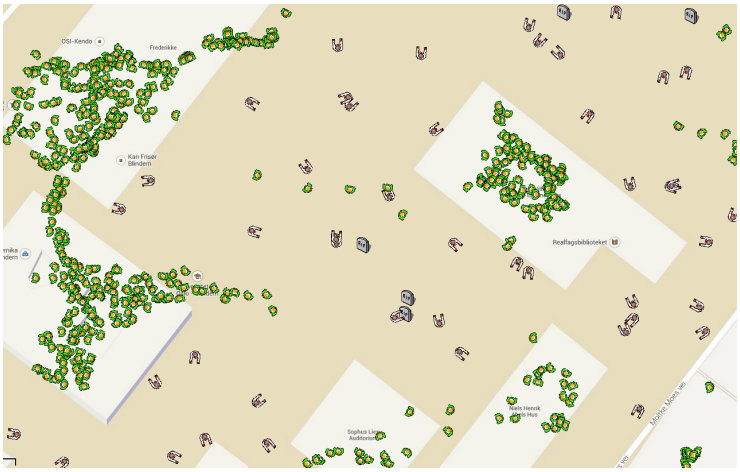

Figure 4.10: A screenshot of a simulation over three phases with free areas for the susceptible group inside the buildings. The screnshot is taken 10 minutes into the simulation. In the *Hysterical phase*. Movie

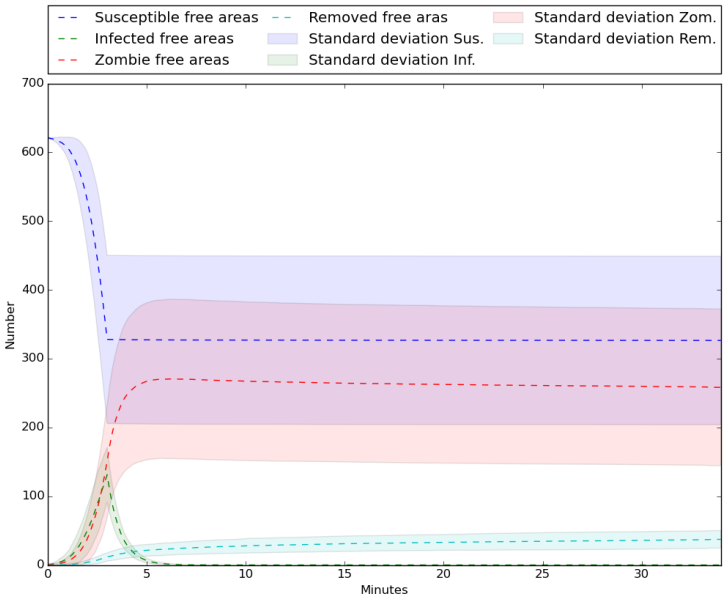

Figure 4.11: The average and standard deviation for a set of simulations over three phases, with free areas inside the buildings. Initial values $S_0 = 621$, $I_0 = 0$, $Z_0 = 1$ and $R_0 = 0$.

4.4 Discussion

The results from the English boarding school shows that the maximum concentration of the infected group, $I_{\max}$, is reduced when using Random walk to simulate the disease. From the ODE and PDE simulations in the previous chapters, the value was $I_{\max} = 292$. For the Random walk, the average $I_{\max}$ was 263. A susceptible person can only be infected in each time step, and it can only happen once. This may affect the value of $I_{\max}$. To study this further, a couple of variations could be made in the simulations. Here, the number of simulations for the group was set to 200. A larger set of simulations would perhaps have given a different result. The second is to study the Random walk model with shorter time steps, and see if this affected the result.

As shown in section 2.2, the reproduction rate, R_0, had to be above 1 for an epidemic situation to occur. The reproduction rate was calculated to $R_0 = 3.77$ for the English boarding school. However, 25 percent of the simulations resulted in no epidemic occurrence because the infected student was transposed to the removed group before he was able to infect other students. 200 simulations were performed for this example, and the percent may differ for an even larger set of simulations. However, this result shows that when modelling closed systems, especially with a small group, an epidemic situation may not occur, even with a reproduction rate, R_0, above one.

In section 4.3 the effect of human behavior in an epidemic model was studied. To achieve the most realistic situation, the simulations were performed in minutes, instead of days as in the previous models. The two conditions *Random walk* and *Moving smart* were simulated and compared with the uniform PDE solution from section 3.3.3. The Random walk was based on a random movement pattern for all groups. The Moving smart mode gave humans and zombies a more realistic behavior. Based on *Walking Dead*, the humans would avoid the zombies, while the zombies would strive to take the humans. When simulating the condition *Moving smart* with only one zombie at initial time, the zombie was never able to reach any of the susceptible humans. In other words, the result of this was that the zombie group did not increase. The simulations were therefore later done with 10 zombies at initial time. When studying Tab.(4.3.1), one can see this variation in the condition *Moving smart* gives the zombie group an advantage. There were 72 susceptible left after 3 minutes in the uniform PDE simulation, while the average simulation of Random walk resulted in 279 susceptible humans. A random walker can only be at one place at the time, compared to the PDE simulation, which covers the whole area. This supports the conclusion from section 3.4, which said that the position of the groups plays a key role in modelling the spread of a disease. The variations in Moving smart, makes the zombie attack more aggressive. The average result for the susceptible group after 3 minutes was 87 humans. The condition *Moving smart* resulted in eradication for the susceptible group in 15 of the 100 simulations after three

minutes. At final time, the number was increased to 29 cases of eradication for the susceptible group.

The two lasts sections consist of simulations of all three phases from *Walking Dead*, with a shorter time frame than in the series. These simulations gave some interesting results. The movement pattern for the *Initial phase* was random for both cases, while the *Hysterical phase* consisted of the condition *Moving smart*. The effect of restricted areas for the zombies gave a higher amount of susceptible humans shown in Tab.(4.3.3), than in the other simulations. While there were 274 humans left in the average Random walk simulation after the *Initial phase*, there were 331 susceptible humans left for the average simulations with restricted areas for the zombie group. By comparing this to the ODE simulation where there were 71 susceptible humans left, one can say that the susceptible group gets an advantage by adding human behavior. As follows, the conclusion is that Random walk models will be able to produce more realistic simulations, than the two previous models.

Chapter 5

Discussion and conclusion

In this thesis, two examples have been used to simulate the three different epidemic models. The results have been analyzed and compared throughout the paper. Here, the most important analyzes and comparisons will be discussed and summarized. Based on this some conclusions will be made, and ideas for further work will be presented in section 5.0.1

The first example was an English boarding school which was first simulated by the ODE model. This simulation was based on given parameter values from the British medical journal. One could see that the maximum concentration of the infected group could be found by Eq.(2.10), and the numerical simulation gave the same result. By adjusting the parameter ρ in Fig.(2.2), the result from the epidemic disease changed. When ρ was set to 50, it lead to total eradication of susceptible students during the first 10 days. However, by increasing ρ to 400, the amount of susceptible students was 170.

The introduction of the PDE model, made it possible to compare results of different simulations. The PDE model was first simulated for the English boarding school with uniform distribution. This gave the same result as in the ODE model, which was expected. However, when the infected student was placed in center, the amount of susceptible students increased with 68 percent in 5 days. The disease was now less effective and one can see from Fig.(3.8) that the disease only spread to the students in the center. Another variation was made. By placing the student in the corner, the number of susceptible students increased to 70 percent in 5 days. To summarize, the same parameter values and size was used for all three simulations mentioned above, but the results differed widely.

In both the ODE model and the PDE model, the maximum value of infected was $I_{\max} = 292$. This was not the result from the Random walk simulation. In

the Random walk simulation the average maximum value of the infected group was $I_{\max} = 263$, which is lower than for the other models. By studying Fig.(4.2), one can see that the infected ODE is always within the range of the standard deviation for the Random walk simulation. The average value for the Random walk is based on 200 simulations. It would be interesting in further work to increase this number even more, to see in what degree that would affect the average value. Another element that the Random walk model added, was the chance of an epidemic disease to die out. 25 percent of the simulations resulted in no epidemic occurrence. The infected student was transposed to the removed group before he was able to infect other students. This would not be the case for the ODE and PDE model, since the reproduction rate was above one, as explained in section 2.2.

The second example was based on the TV series *Walking Dead*. Here, the amount in each group was known, and the parameter values for the ODE model were adjusted to fit the expected result. The parameter values β, ϱ and α from the model in Eq.(2.12) were adjusted for the different phases in *Walking Dead*, and based on this, the evolution in *Walking Dead* can be seen as realistic. However, the ODE model does not take the spatial factor into account. The position of the infected student had an effect on the result for the English boarding school. In the simulation of the PDE model one of the goals were to see if the size of the group of susceptible also had an effect on the result. The susceptible group was therefore split into three constellations of different sizes, called the small-,middle and large constellation. One zombie was placed in all three constellations, and the simulations showed that the loss of susceptible was proportional to the size of the constellation. For the small, middle and large constellation the loss of susceptible were 18,196 and 375 based on the Tab.(3.3.1). The middle group lost 97 percent susceptible based on the size of the constellation, which was the highest percentage in all three constellations. To summarize, the PDE simulations showed that the size of the susceptible group also affects the result. The last simulations of the PDE model were made in an attempt to implement human behavior. This was done by giving the zombie and infected restricted areas, in other words keeping them outside the buildings. The simulation shown in Fig.(3.13) gave the susceptible group in the buildings a greater chance of surviving. However, since the concentrations for each group in an PDE model goes towards equilibrium, the movement pattern differs from human behavior. As a conclusion, the goal of implementing human behavior would be easier to attain using a Random walk model.

To study the effect of the human behavior, the simulations of the Random walk model were run for a short amount of time. The condition *Moving smart*, where the zombies chase the susceptible humans, was used. With only one zombie at initial time, the result was zero loss for the susceptible group. This result was also due to equal moving speed for humans and zombies, which made the humans able to avoid battles. As a variation the simulation was performed

with 10 zombies at initial time. This resulted in 87 humans after 3 minutes, compared to 297 humans in the Random walk simulation. These results are based on the average value of a set of simulations. However, if one look more closely at the different results of the simulations with the condition *Moving smart*, 15 of 100 simulations resulted in eradication of the susceptible group after 3 minutes. After 10 minutes the result was increased to 29 simulations. This was not the case for any of the simulations with the Random walk condition. However, the condition *Moving smart* would not be a realistic movement pattern in all situations.

The last simulations of the Random walk model, combined the conditions *Random walk* and *Moving smart*. In the *Initial phase*, the condition was set to Random walk, while it was changed to the Moving smart condition in the *Hysterical phase*. One set of simulations were run with the ability for all groups to move freely within one area, while another set of simulations were modeled with restricted areas for the zombie group. These were compared to the ODE simulation from the second chapter. The parameter values and the amount wass equal for all simulations. After the *Initial phase*, there were 71 susceptible left in the ODE simulation, 278 in the simulation where the groups could move freely and 331 in the simulation with restricted areas for the zombies. To summarize, adding human behavior to the model increases the chance for humans to survive.

As a final summary of the main results in this thesis, one can say that the ODE model can be adapted to problems, where the result is already known. The model can then be used to study the evolution of the epidemic disease. However, it does not take the spatial factor into account. This makes the model weak, predicting the spread of a disease. The PDE model is able to implement the spatial factor. The results from the English boarding school and the TV series *Walking Dead* showed the effect of the position. However, when wanting to add human behavior, this model becomes weak. It offers limited possibilities of applying movement pattern that can be seen as realistic, especially for small groups. The Random walk model was able to take the spatial effect into account and implement human behavior. These two factors gave the most realistic simulations. A drawback was the high calculating capacity. The longest Random walk simulation was 34 minutes long. Making longer simulations with a higher amount would demand more calculating capacity than in the other models.

5.0.1 Further work

As said in the introduction of the thesis, a couple of choices were made. The first one was that systems would be modeled for a short period of time. The second one was that all models would be simulated as closed systems, which meant using a certain number of people and a certain time frame. In further work it would be interesting to expand the Random walk model by using parallelization.This would make it possible to make longer simulations with a higher amount.

Another idea for further work is to add more skills to the different groups in Random walk model. The effect of these changes could be compared to the effect of varying the parameter values. The skills and strength of a human was similar for all in the susceptible group. This is not authentic. In the real world, all humans have different skills and would behave differently when meeting a zombie. Interesting skills to add could be:

- weapons for the susceptible group
- noise sensitivity for the zombie group
- the ability to cooperate within the groups.

This would make the Random walk model more authentic in simulation of a zombie outburst.

A final suggestion for further study is based on the movement speed of the three groups *Susceptible*, *Infected* and *Zombie*. In this thesis the movement speed of the three groups has been equal. However, in *Walking Dead*, the average speed was higher for the susceptible group, than for the two others. Further studies of how this would affect the results could be interesting.

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