Modeling of Diseases

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15. December 2019

Abstract

We solve the SIRS model with a Runge Kutta 4 and Monte Carlo approach. We add vitality, seasons and vaccines to the model and plott the results. Then we find that there are steps one can take to reduce and even remove illnesses from our population.

1 Introduction

Winter is coming, and as we all know it, so is the flue season. Many people are affected by this time, and it would be practical to know just how it might effect us. In this report we will look at a model for diseases called the SIRS model, solve it with two different approches add some additional cases to make it a bit more realistic.

2 Theory

2.1 SIRS Model

The SIRS model considers an isolated population of N people, which is then divided into three separate groups:

- S: susceptible, those without immunity to the disease.
- I: infected, those currently infected with the disease.
- R: recovered, those who have been infected and are now immune.

This model is circular, a person can only move from one group to another in the order $S \to I \to R \to S$. For a simple case where we look at a small time scale, we ignore the effect of birth and death. We then have a set of coupled differential equations, which forms the classic SIRS model:

$$\begin{aligned} S' &= cR - \frac{aSI}{N} \\ I' &= \frac{aSI}{N} - bI \\ R' &= bI - cR \end{aligned} \tag{1}$$

Here we have implemented the rate of transmission (a), the rate of recovery (b), and the rate of immunity loss (c). The population mixes homogeneously and we start by assuming total population remains constant, so we have

$$N = S(t) + I(t) + R(t) \tag{2}$$

This set does not have any analytic solutions, but the equilibrium solutions are given by rewriting the differential equations with 2, and setting them equal to zero. That is;

$$\begin{aligned} S' &= c(N - S - I) - \frac{aSI}{N} = 0 \\ I' &= \frac{aSI}{N} - bI = 0 \end{aligned} \tag{3}$$

Then we get the fractions of people in S, I, and R in equilibrium:

$$\begin{aligned} s^* &= \frac{b}{a} \\ i^* &= \frac{1 - \frac{b}{a}}{1 + \frac{b}{c}} \\ r^* &= \frac{b}{c}\frac{1 - \frac{b}{a}}{1 + \frac{b}{c}} \end{aligned} \tag{4}$$

Since this is fractions between 0 and 1, and must add up to 1, we see that we must have $b < a$ for the disease to establish itself.

2.2 Runge-Kutta 4

The Runge-Kutta methods are iterative methods used to approximate solutions to ordinary differential equations. The "classic" method is the Runge-Kutta 4 method, RK4. For the initial value problem;

$$y' = f(t, y), \quad y(t_0) = y_0 \tag{5}$$

we can find the approximation of y.

With a step-size $h > 0$ you can define

$$\begin{aligned} y_{n+1} &= y_n + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4 \\ t_{n+1} &= t_n h \end{aligned} \tag{6}$$

Using

$$\begin{aligned} k_1 &= hf(t_n, y_n) \\ k_2 &= hf(t_n + \frac{h}{2}, y_n + \frac{k_1}{2}) \\ k_3 &= hf(t_n + \frac{h}{2}, y_n + \frac{k_2}{2}) \\ k_4 &= hf(t_n + h, y_n + k_3) \end{aligned} \tag{7}$$

From this we get the approximation of y, y_{n+1}.

2.3 Monte Carlo

The variables S, I, and R are in reality discrete, and if you want to implement this you can use a Monte Carlo method. This uses randomness and probabilities for each transition between S, I and R. Using our differential equations 1 we can find the approximate amount of people moving from one state to another; $S \to I : \frac{aSI}{N}\Delta t$, $I \to R : bI\Delta t$, and $R \to S : cR\Delta t$. We want a Δt so small that at most one person can move from one state to another. Since

$$\begin{aligned} max\left\{\frac{aSI}{N}\Delta t\right\} &= \frac{aN}{4}\Delta t \\ max\left\{bN\Delta t\right\} &= bN\Delta t \\ max\left\{cN\Delta t\right\} &= cN\Delta t \end{aligned} \tag{8}$$

the time-step is given by

$$\Delta t = min\left\{\frac{4}{aN}, \frac{1}{bN}, \frac{1}{cN}\right\} \tag{9}$$

With this definition the transition probabilities are:

$$\begin{aligned} P(S \to I) &= \frac{aSI}{N}\Delta t \\ P(I \to R) &= bI\Delta t \\ P(R \to S) &= cR\Delta t \end{aligned} \tag{10}$$

For each possible transition you must draw a random number i between 0 and 1, and if $i < P$ it transitions.

2.4 Special cases

To look at different situations one can change or add parameters.

2.4.1 Vital dynamics

A more realistic model than the one we have above would take into account the birth and death cycle of the population. A simple way to do this is to add the birth rate (e), death rate (d) and the death as a result of illness (d_I) Here we would of cource also step away from the assumption in 2. New people who are born, must be added to the susceptible and is dependant on the birth rate and the total population N. People die from all three groups, so all three groups should subtract people, dependant on the population in each group and the death rate. Last of all, only the infected could die from the infection, so we need to subtract an element from this population, dependant on the death by illness rate and the infected population. Then the new model has the diffenential equations

$$\begin{aligned} S'_{new} &= S' - dS + eN \\ I'_{new} &= I' - dI - d_I I \\ R'_{new} &= R' - dR \end{aligned} \tag{11}$$

where we use the $S', I' and R'$ from 1.

2.4.2 Season Variations

One can also look at how the seasons affect the disease by changing the parameter a (rate of transmission), and making it dependent on time:

$$a(t) = A\cos(\omega t) + a_0 \tag{12}$$

Here we have average transmission rate (a_0), maximum deviation (A), and frequency of oscillation (ω). We have made the parameter cyclic, as one would expect the a to vary withe the seasons, but to end up as the same after a whole year has passed. As this model is using a cosin function, we could think of the year as pasing from $t = 0$ as the season with higest transmission rate, to $t = \frac{\pi}{2\omega}$ where the rate would be at is lowest, and back to $t = \frac{\pi}{\omega}$ where the rate would be at it's lowest again.

2.4.3 Vaccination

The effect of vaccination can also be included, by allowing people to move directly from S to R. This effect can depend on time and we choose it to be linearly dependant on time.

$$f(t) = f_0 \cdot t \tag{13}$$

This parameter can therefore be changed for each case. All you have to do is subtract the rate of vaccination (f) from S and add it to R, thus obtaining the equations

$$\begin{aligned} S'_{new} &= S' - f \\ I'_{new} &= I' \\ R'_{new} &= R' + f \end{aligned} \tag{14}$$

where we use the $S', I'\text{and}R'$ from 1 or if you want to combine models, it is the new ones in 11.

3 Method

First we wrote a program to solve the set of differential equations for the SIRS model with a Runge Kutta 4 solver. We used the parameters

$$\begin{aligned} N &= 400 \\ S_0 &= 300 \\ I_0 &= 100 \\ R_0 &= 0 \\ a &= 4 \\ c &= 0.5 \end{aligned}$$

for four different models, A, B, C and D with

$$\begin{aligned} b &= 1 \\ b &= 2 \\ b &= 3 \\ b &= 4 \end{aligned}$$

respectivly.

Then we wrote a new solver for the model with a Monte Carlo solution. With the same parameters as earlier, but solving the equations 10 times and averaging over them.

Afterwards, we added the vital dynamics model, using

$$\begin{aligned} d &= 0.006 \\ d_I &= 0.002 \\ e &= 0.012 \end{aligned}$$

d and e are taken from the the Norwegian values for these parameters, as the CIA give them [1], [2]. And we have used the d_I value for cancer in Norway, given by kreftforeningen [3]. We deducted the d_I value from the normal d value since the CIA just gives the total death rate and dont specify from what people die.

Then we implemented season dynamics, by making the a parameter time dependant. Here we used the same parameters as earlier, but with

$$\begin{aligned} A &= 1 \\ a_0 &= 4 \\ \omega &= \frac{2\pi}{365.25} \end{aligned}$$

to make the rate cyclic over half a year.

Lastly, we implemented vaccines, and used a base value of $f_0 = 0.1$ for the rate.

4 Results

First of all, we see that the Runge Kutta 4 method, and the Monte Carlo Solver practically agree on all the results except a few special ones.

4.1 Runge Kutta and Monte Carlo solutions for SIRS

We can clearly see in Figure one, two, three, four, five, six, seven and eight that the base mode, with $b = 1, 2, 3, 4$ all give models that stabilises after a short time. $b = 1$ give a model with values ending at $S = 200, I = 100, R = 100$. For $b = 2$ we can se that the values are higher for the S and R end values, as one would expect since the recovery rate is higher. With $b = 3$ the illness is almost extinguished, and with $b = 4$ the illness dies out affer a very short time.

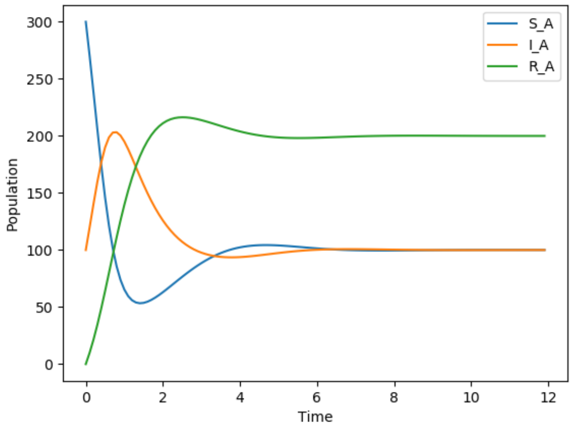

Figure 1 RK4 solution of SIRS, population distribution for population A with $a = 4$, $b = 1$ and $c = 0.5$

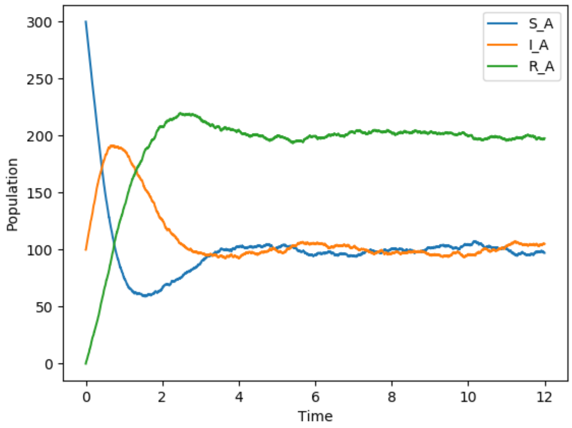

Figure 2 Monte Carlo solution of SIRS, population distribution for population A with $a = 4$, $b = 1$ and $c = 0.5$

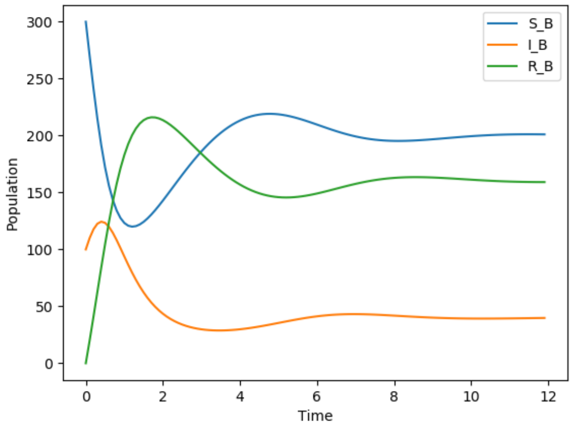

Figure 3 RK4 solution of SIRS, population distribution for population B with $a = 4$, $b = 2$ and $c = 0.5$

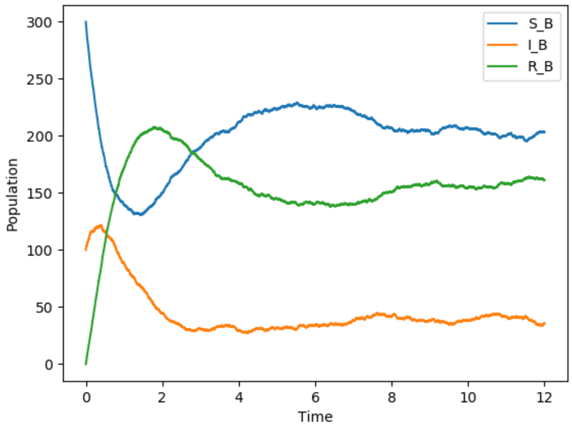

Figure 4 Monte Carlo solution of SIRS, population distribution for population B with $a = 4$, $b = 2$ and $c = 0.5$

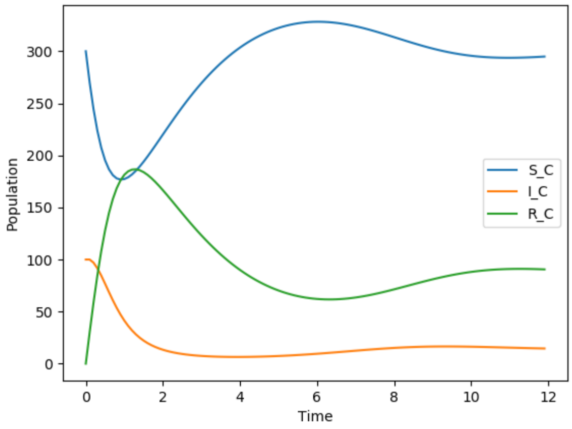

Figure 5 RK4 solution of SIRS, population distribution for population C with $a = 4$, $b = 3$ and $c = 0.5$

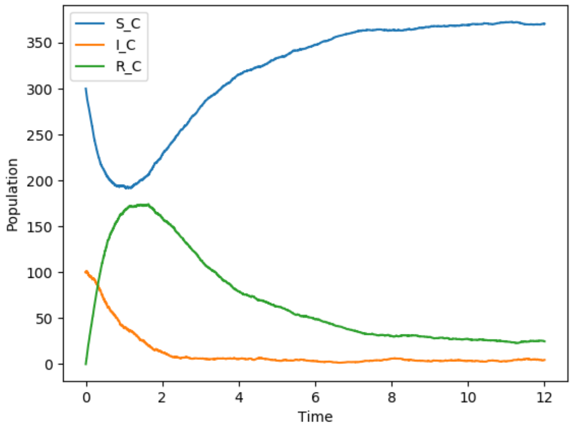

Figure 6 Monte Carlo solution of SIRS, population distribution for population C with $a = 4$, $b = 3$ and $c = 0.5$

Table 1. Approximate equilibrium values for Monte Carlo, read from plotted results

Equlibrium	A	B	C	D
s*	0.25	0.5	0.875	1.0
i*	0.25	0.125	0.0	0.0
r*	0.5	0.375	0.125	0.0

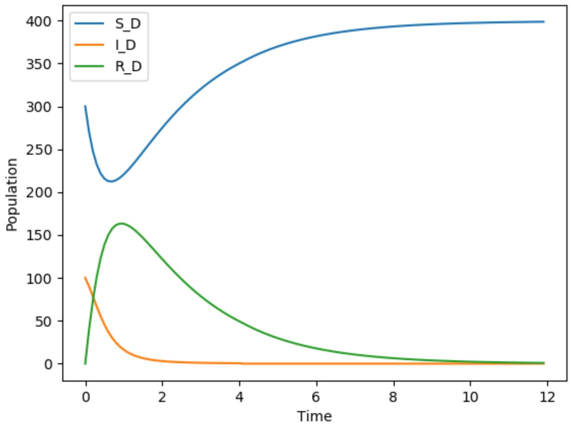

Figure 7 RK4 solution of SIRS, population distribution for population D with $a = 4$, $b = 4$ and $c = 0.5$

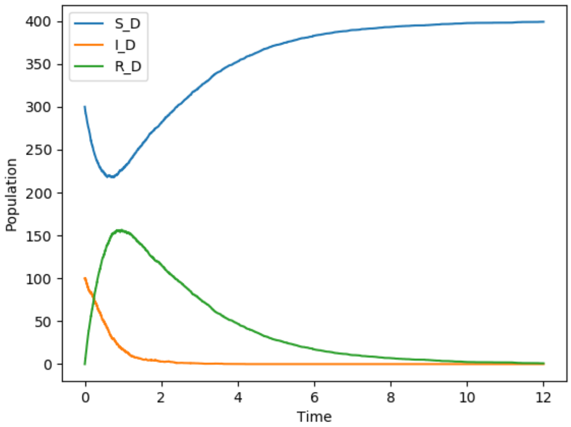

Figure 8 Monte Carlo solution of SIRS, population distribution for population D with $a = 4$, $b = 4$ and $c = 0.5$

[H]

4.2 Implemented vitals for SIRS with Runge Kutta and Monte Carlo

With vitality we can see from figure nine and ten that the population in our model now rises, but other then that it is about the same as earlier. As for figure eleven and twelve the look practicaly equal to the model before the implementation.

With the lower, and higher values for the different parameters used in Figure 113, 14, 15 and 16, we see that almost all the infected die. We can also see that the S value grows in the monte carlo solution, but not in the RK4.

And with the starting values, but over a longer time, we can see from figure 17, 18, 19 and 20 that the illness growes, but settles after some time and we gain a stable model in the end, but with much higher amount of infected.

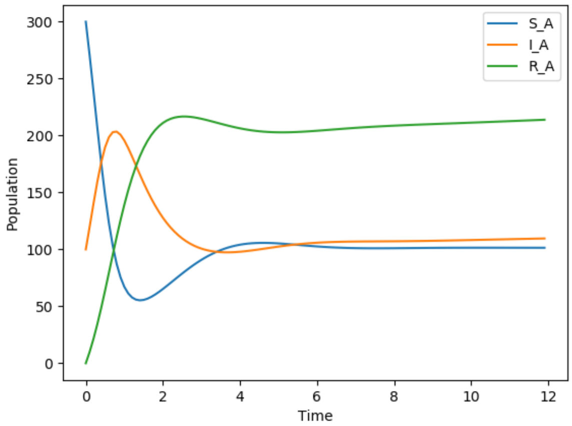

Figure 9 RK4 solution of SIRS, population distribution for population A with $d = 0.006$, $d_I = 0.002$, $e = 0.012$, $a = 4$, $b = 1$ and $c = 0.5$

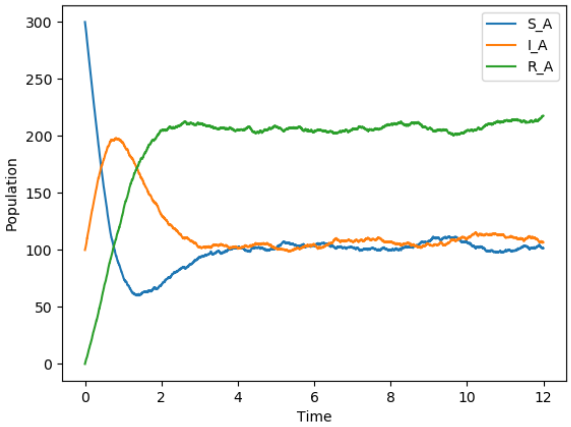

Figure 10 Monte Carlo solution of SIRS, population distribution for population A with $d = 0.006$, $d_I = 0.002$, $e = 0.012$, $a = 4$, $b = 1$ and $c = 0.5$

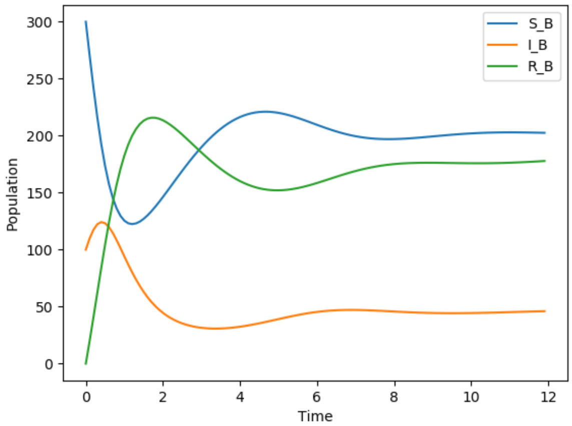

Figure 11 RK4 solution of SIRS, population distribution for population B with $d = 0.006$, $d_I = 0.002$, $e = 0.012$, $a = 4$, $b = 2$ and $c = 0.5$

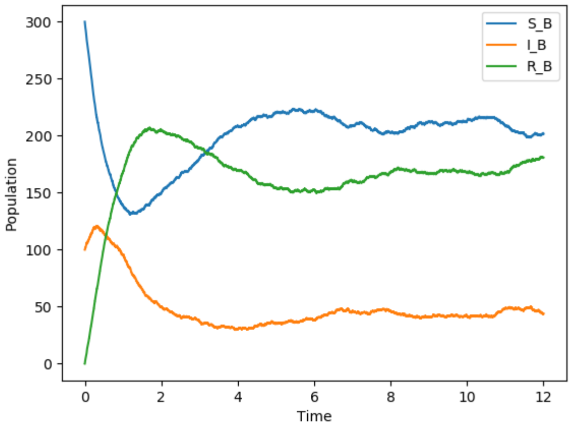

Figure 12 Monte Carlo solution of SIRS, population distribution for population B with $d = 0.006$, $d_I = 0.002$, $e = 0.012$, $a = 4$, $b = 2$ and $c = 0.5$

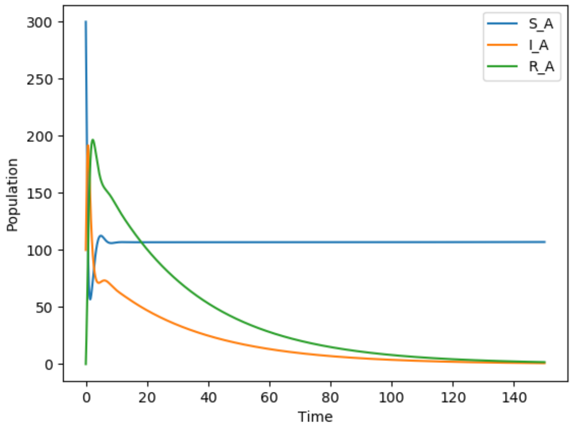

Figure 13 RK4 solution of SIRS, population distribution for population A with $d = 0.00002242299$, $d_I = 0.1$, $e = 0.00002948891$, $a = 4$, $b = 1$ and $c = 0.5$

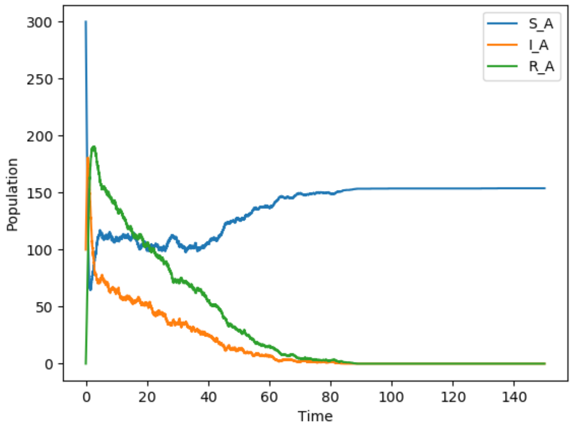

Figure 14 Monte Carlo solution of SIRS, population distribution for population A with $d = 0.00002242299$, $d_I = 0.1$, $e = 0.00002948891$, $a = 4$, $b = 1$ and $c = 0.5$

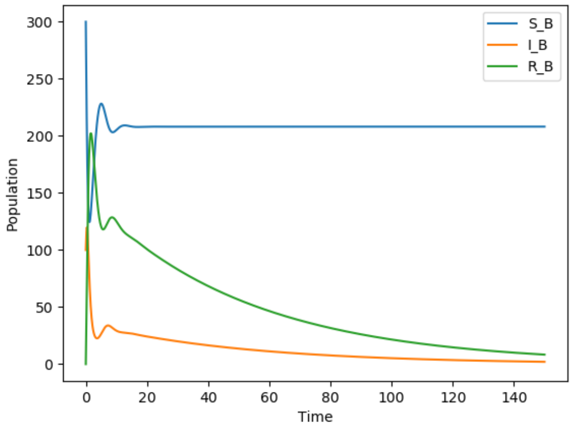

Figure 15 RK4 solution of SIRS, population distribution for population B with $d = 0.00002242299$, $d_I = 0.1$, $e = 0.00002948891$, $a = 4$, $b = 2$ and $c = 0.5$

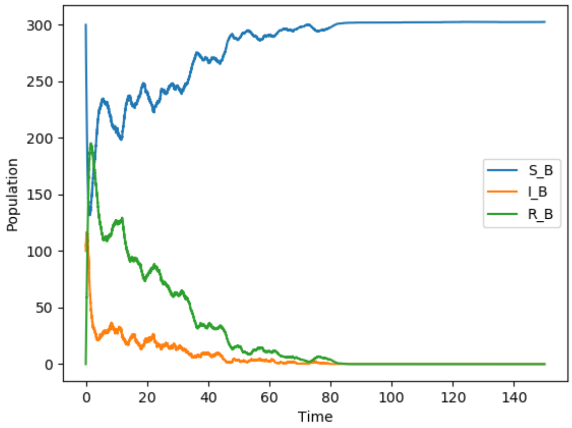

Figure 16 Monte Carlo solution of SIRS, population distribution for population B with $d = 0.00002242299$, $d_I = 0.1$, $e = 0.00002948891$, $a = 4$, $b = 2$ and $c = 0.5$

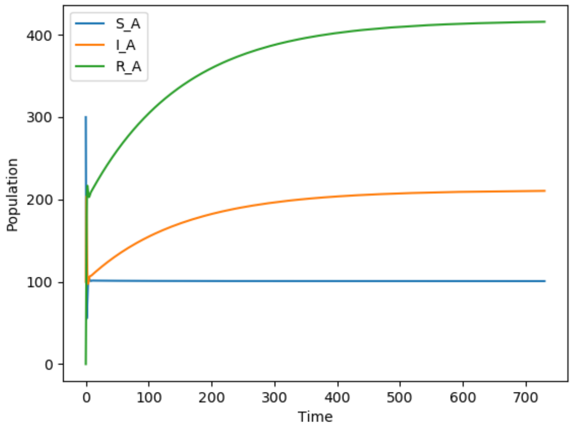

Figure 17 RK4 solution of SIRS, population distribution for population A for two years with $d = 0.006$, $d_I = 0.002$, $e = 0.012$, $a = 4$, $b = 1$ and $c = 0.5$

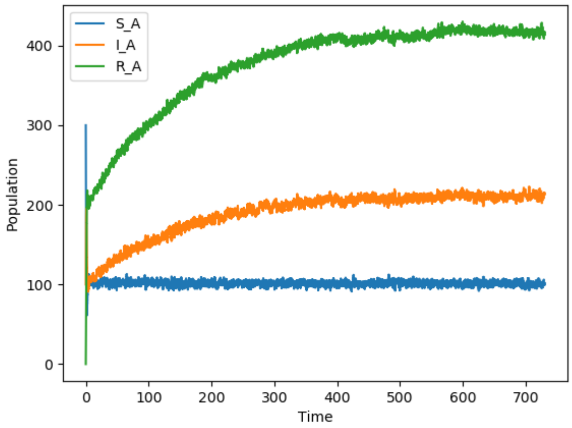

Figure 18 Monte Carlo solution of SIRS, population distribution for population A for two years with $d = 0.006$, $d_I = 0.002$, $e = 0.012$, $a = 4$, $b = 1$ and $c = 0.5$

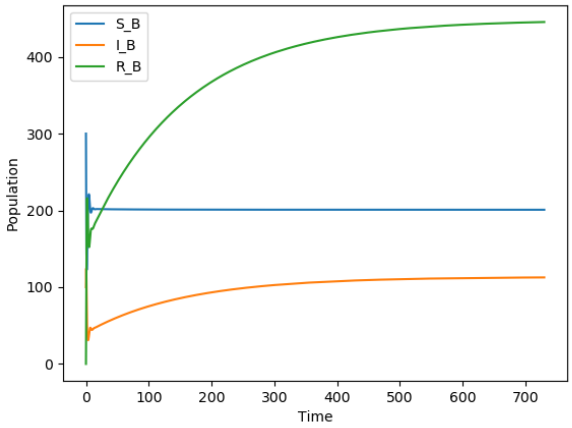

Figure 19 RK4 solution of SIRS, population distribution for population B for two years with $d = 0.006$, $d_I = 0.002$, $e = 0.012$, $a = 4$, $b = 2$ and $c = 0.5$

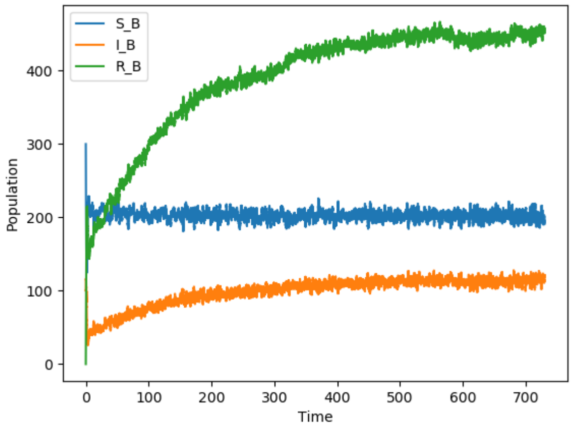

Figure 20 Monte Carlo solution of SIRS, population distribution for population B for two years with $d = 0.006$, $d_I = 0.002$, $e = 0.012$, $a = 4$, $b = 2$ and $c = 0.5$

4.3 Seasonal variation of SIRS with Runge Kutta and Monte Carlo

With season variations implemented, we can see in figure 21, 22, 23 that we get cyclic motions through the year. In figure 24 however, the Illness dies out and the cyclic motion starts anew from here.

With the shorter diviation of A, used in figures 25, 26, 27 and 28 we see the same result, but with less cyculation.

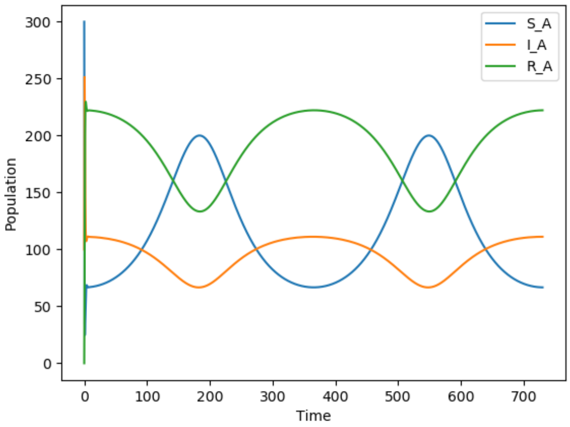

Figure 21 RK4 solution of SIRS, population distribution for population A with $\omega = 2\pi/365.25$, $A = 2$, $a_0 = 4$, $b = 1$ and $c = 0.5$

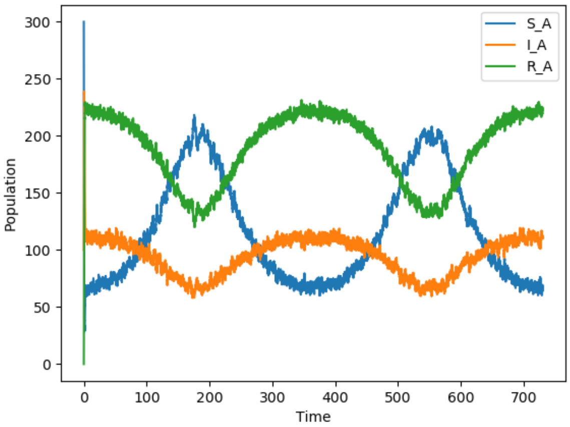

Figure 22 Monte Carlo solution of SIRS, population distribution for population A with $\omega = 2\pi/365.25$, $A = 2$, $a_0 = 4$, $b = 1$ and $c = 0.5$

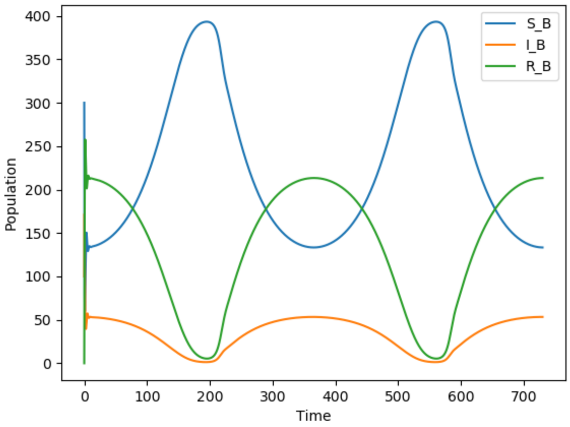

Figure 23 RK4 solution of SIRS, population distribution for population B with $\omega = 2\pi/365.25$, $A = 2$, $a_0 = 4$, $b = 2$ and $c = 0.5$

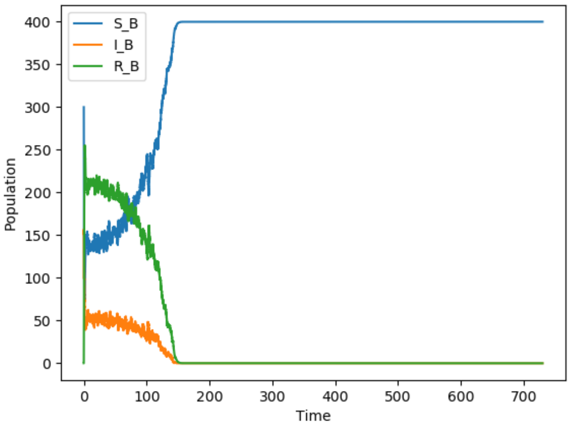

Figure 24 Monte Carlo solution of SIRS, population distribution for population B with $\omega = 2\pi/365.25$, $A = 2$, $a_0 = 4$, $b = 2$ and $c = 0.5$

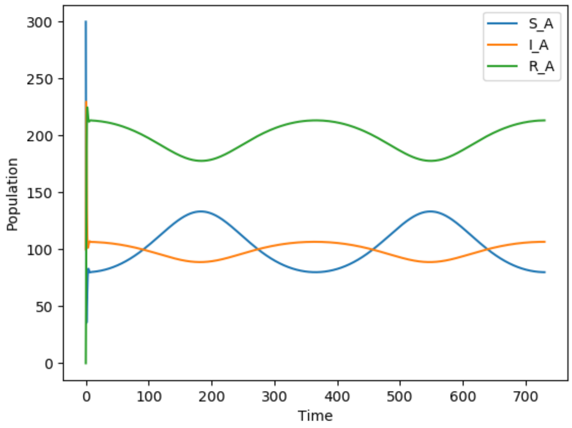

Figure 25 RK4 solution of SIRS, population distribution for population A with $\omega = 2\pi/365.25$, $A = 1$, $a_0 = 4$, $b = 1$ and $c = 0.5$

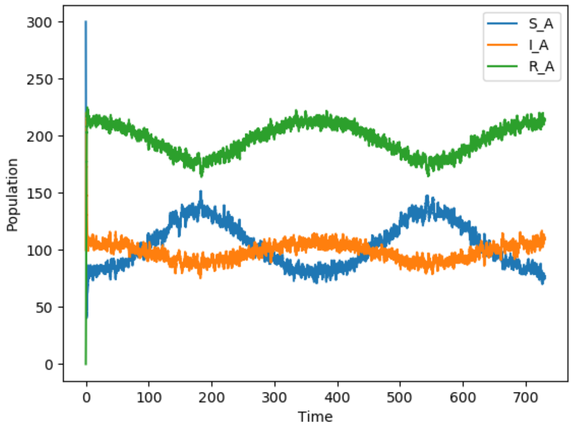

Figure 26 Monte Carlo solution of SIRS, population distribution for population A with $\omega = 2\pi/365.25$, $A = 1$, $a_0 = 4$, $b = 1$ and $c = 0.5$

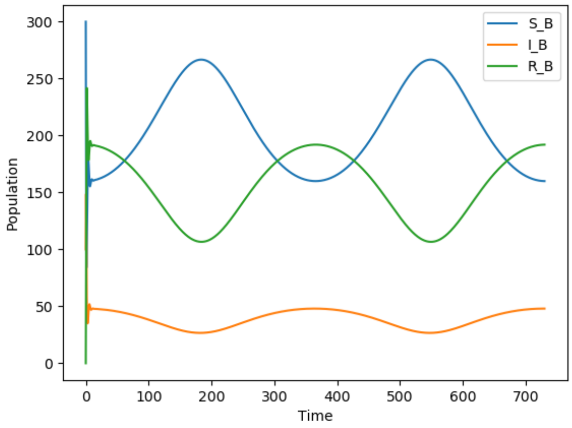

Figure 27 RK4 solution of SIRS, population distribution for population B with $\omega = 2\pi/365.25$, $A = 1$, $a_0 = 4$, $b = 2$ and $c = 0.5$

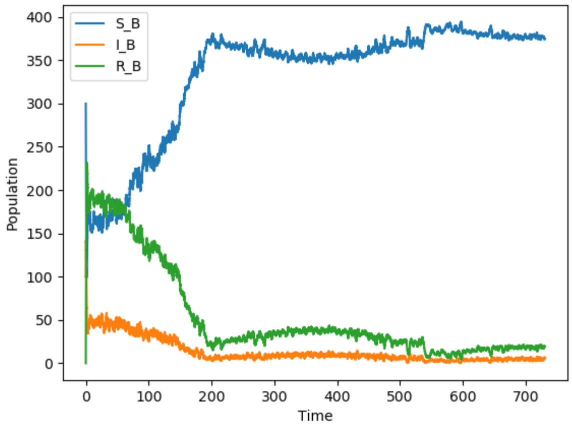

Figure 28 Monte Carlo solution of SIRS, population distribution for population B with $\omega = 2\pi/365.25$, $A = 1$, $a_0 = 4$, $b = 2$ and $c = 0.5$

4.4 Vaccines in SIRS model with Runge Kutta and Monte Carlo

We can see differnece from figure 29, 30, 31 and 32 and the first four figures, except for the longer time frame

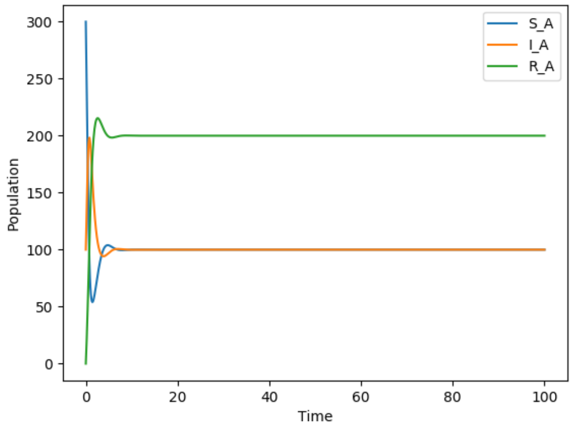

Figure 29 RK4 solution of SIRS, population distribution for population A with $f = 0.1$

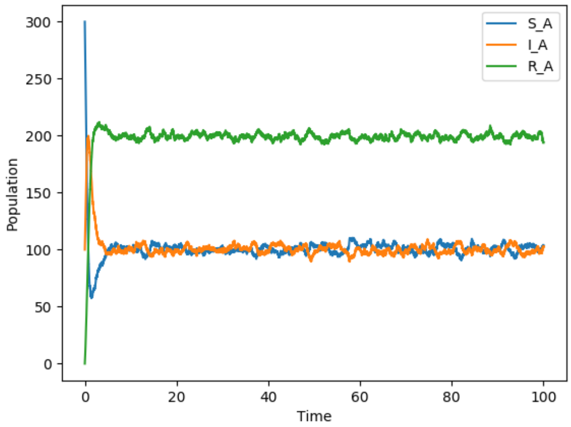

Figure 30 Monte Carlo solution of SIRS, population distribution for population A with $f = 0.1$

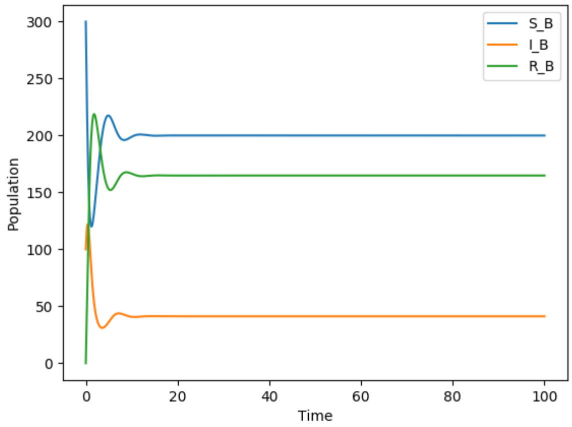

Figure 31 RK4 solution of SIRS, population distribution for population B with $f00.1$

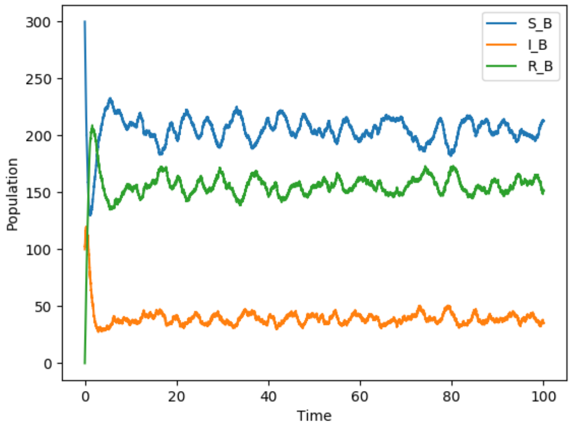

Figure 32 Monte Carlo solution of SIRS, population distribution for population B with 0.1

5 Discussion

Most of the results gave us a good idea of how illness will spread through different kinds of populations, how it can vary with seasons, and how we can limit the spread. However we got a few pequliar results.

Our implementation of vitals, which was supposed to give us a more realistic look at the illness over longer periods of time. But our results did not look exactly the way we expected, this could be that we have not found the correct parameters, or that we have implemented the code wrong.

The seasonal variation also had some strange results from the Monte Carlo method, since we expected the results from Runge Kutta to correspond, but both the results from population B flattens out in Monte Carlo and not in Runge Kutta. This might come from the different methods of calculation, where the Monte Carlo method can die out faster due to the discrete values. But we can not know if this comes from an error or not, so we should probably look at these particular with some scepticism.

The Implementation of the vaccination just showes us the base model again. There is obviously something with the implementation that makes it not effect the calculations, but we don't have time to investigate.

References

Lectures https://github.com/CompPhysics/ComputationalPhysics/blob/master/doc/Lectures/lectures2015.pdf

[0] [1] https://www.cia.gov/library/publications/the-world-factbook/fields/345.html

[2] https://www.cia.gov/library/publications/the-world-factbook/fields/346.html

[3] https://kreftforeningen.no/en/patients-and-next-of-kin/cancer-information/cancer-in-norway/

[4] https://github.com/AdaMathea/Fys3150_Project5