CX 4230 Mini Project 1 Report

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Introduction

This report is for CX 4230 Mini-project 1: Contagion. This report will briefly discuss our results for the given problems and our approach to the project. Initially, we were given a model with the following scenario: there is an epidemic going on, and we're able to separate people into three different groups. The first group is susceptible people who haven't had the disease, and the second group is infected people who already have the disease. Finally, the third group is recovered people who had the disease, but no longer have it. Here are some basic assumptions of this model - the disease can only spread from infected people to susceptible people. An infected person stays sick for some period, but then recovers; once they have recovered, they can never get sick again. Furthermore, the population stays the same as we're assuming no one will die or be born.

The mathematical model

$$\vec{x} = \vec{x}(t) = \begin{bmatrix} S(t) \\ I(t) \\ R(t) \end{bmatrix}$$

Above is the three-dimensional vector representing the state of the system, where t represents the continuous time variable. $S(t)$, $I(t)$, $R(t)$ denote the fractions of the population who are susceptible, infected, or recovered at time *t*. From our assumption the population remains the same, we can conclude $S(t) + I(t) + R(t) = 1$. *Suppose the state* $\vec{x}$ *evolves as an ordinary differential equation* $D\vec{x} = \vec{f}(\vec{x})$ *.*

$$\vec{f}(\vec{x}) = \begin{bmatrix} -\tau S(t)I(t) \\ \tau S(t)I(t) - \dfrac{I(t)}{\kappa} \\ \dfrac{I(t)}{\kappa} \end{bmatrix}$$

The parameter τ ≥ 0 measures how quickly the disease can spread, with higher values corresponding to faster rates of spread. The parameter κ > 0 measures how quickly an infected

person recovers, with higher values corresponding to longer recovery times.

#1.1 - finding fixed points

To find the fixed points of this system,

DS = 0 => S=0 or I=0

DI = 0 => S= 1/(τk) or I=0

DR= 0 => I=0

There is one fixed point (S,I,R) => (S, 0, 1-S*)*

(S is any value when the condition finished)*

There are two different cases when 1/τk >= 1 and 1/τk < 1.

1. *When 1/τk => 1, there is one stable fixed point at (S*, 0, 1-S*) for any S.*

   -Nullclines

   DS = 0: 1) S = 0 a) DI = -I/k => {<0 if I > 0

   b) DR = I/k {>0 if I <0

   2) I = 0 a) DI = 0 ~ (S, 0, 1-S) is <u>stable</u>

   DI = 0: 1) S = 1/(τk) a) DS = -I/k

   b) DR = I/k

   -Since 1/τk => 1, S can not equals to 1/(τk)

   2) I = 0 a) DS = 0

   b) DR = 0

   DR = 0: 1) I = 0 a) DS = 0

   b) DI = 0

2. *When 1/τk < 1, there is a fixed points (S*, 0, 1-S*) for any S.*

   -Nullclines

   DS = 0: 1) S = 0 a) DI = -I/k => {<0 if I > 0

   b) DR = I/k {>0 if I <0

   ~ (S, 0, 1-S) is <u>stable</u>

   2) I = 0 a) DI = 0

   b) DR = 0

When 1 > S(t) >= 1/τk

DI = 0: 1) S = 1/(τk) a) DS = -I/k => {<0 if I > x(is a I(t) value when S = 1/(τk)

b) DR = I/k {<0 if I < x

~ (S, 0, 1-S) is unstable

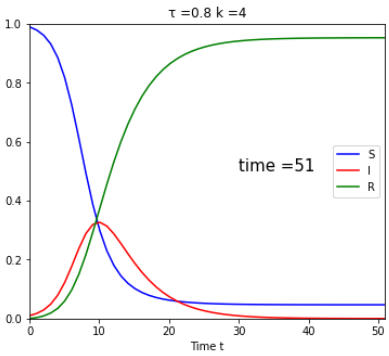
2) I = 0 a) DS = 0

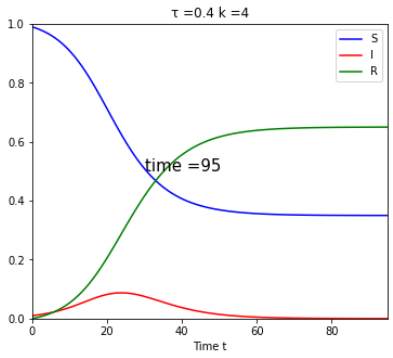
b) DR = 0

DR = 0: 1) I = 0 a) DS = 0

b) DI = 0

#1.2 - comparing three different scenarios





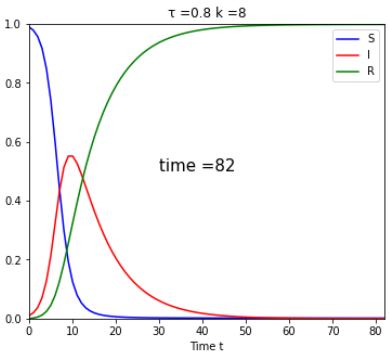


Image 1: when $\tau = 0.8, k = 4$ *Image 2: when* $\tau = 0.4, k = 4$ *Image 3: when* $\tau = 0.8, k = 8$

For part 1.2, we've used python to run the simulation for three different pairs of parameters (τ , k) with the following values: (0.8, 4), (0.4, 4), (0.8, 8). Utilizing numpy and scipy functions, we were able to solve the differential equation. We ran a simulation until $I(t) < 10^{-4}$, which was defined as the stopping condition. The stopping condition, in this case, is when barely any more infection occurs and the epidemic is nearly over (technically $10^{-4} \neq 0$, however we can assume it's a very small number). We then observed the time t when this condition occurs. For the first scenario, we got $t = 51$, for the second scenario we got $t = 95$, and finally, for the third scenario, we got $t = 82$. This indicates in the first scenario took the shortest to meet the conditional conditions, while the second scenario took the longest. The second scenario has both the lowest τ and k value, which means infected people will relatively recover quicker and the virus is spreading at a relatively slower rate. Looking at image 2, the red curve that represents I(s), has a lower peak and it takes more time to get the peak than the

other two scenarios. This correlates to the blue curve which remains relatively higher than others, and the green curve whose peak is also relatively lower than the other two scenarios. In other words, there were fewer people who got infected, however, it took a while to actually get rid of the virus as it wasn't exposed to enough people and spread slowly. Overall it had less infection and yet took the longest to end the epidemic. Image 3 is quite the opposite of image 2, as both τ, k values are higher than the other two models. We can see this in image 3, which has the highest red curve peak and the blue curve hits the lowest faster than the other two scenarios. This means that the virus spread quickly and it took longer to recover, but it took slightly less time to meet the stopping condition compared to the second scenario. This is because more people were exposed to the virus and although their recovery took a while, eventually most people were exposed to the virus (as shown in the blue curve that nearly hits 0.0) and were able to recover. This is possible because our assumption was everyone eventually recovers from the disease, and no one will die. So in this hypothetical scenario, if we wanted to end the epidemic, it'd be better to expose the virus to the mass population as quickly as possible and let people recover (well, at least we thought at first. Turns out this isn't exactly the case; we'll discuss more in #1.3). The first scenario is similar to the third scenario in the sense that the virus is spreading quickly (τ = *0.8),* and also similar to the second scenario in the sense that people are recovering quickly as well (k = *4)*. This is the best scenario to meet the stopping condition as the disease is spreading quickly and people are also recovering quickly. The red curve's peak is somewhere in between scenario 1's red curve and scenario 3's red curve, while the blue and green curves are similar to scenario 3. In scenario 1, slightly fewer people are infected compared to scenario 3, but still, the majority of people got infected (which is shown through the blue curve's lowest point around 0.08) and yet were able to get recovered quickly, which resulted in the shortest amount of time to end the epidemic. Our initial intuition was that under our basic assumption of all the people who got infected will eventually recover from the virus, the ideal situation will be when τ value is maximized and k value is minimized. However, this has been proven only partially correct later on when we plotted various ranges of τ, k values. We'll discuss this more in detail in section 1.3

#1.3 - various range plots

In section 1.2, we initially thought in order to minimize time to meet the stopping condition, one strategic approach was to maximize τ value and minimize k value. However, this isn't necessarily true when we plot various ranges of τ, k. Below are 2-D contour plots showing when $0 < \tau \leq 4,\ 1 \leq k \leq 5$.

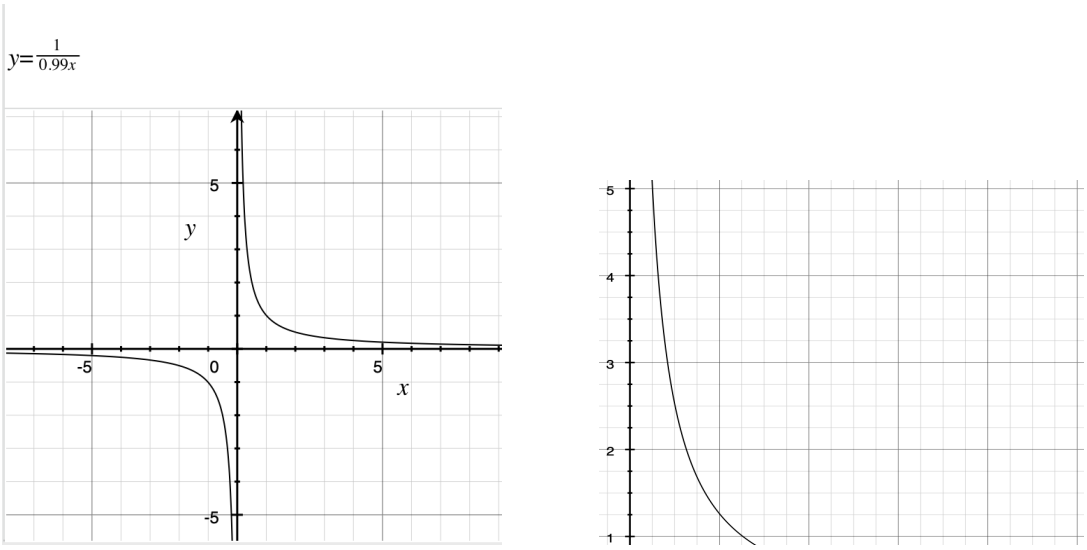


Image 4: y = 1/(0.99x)

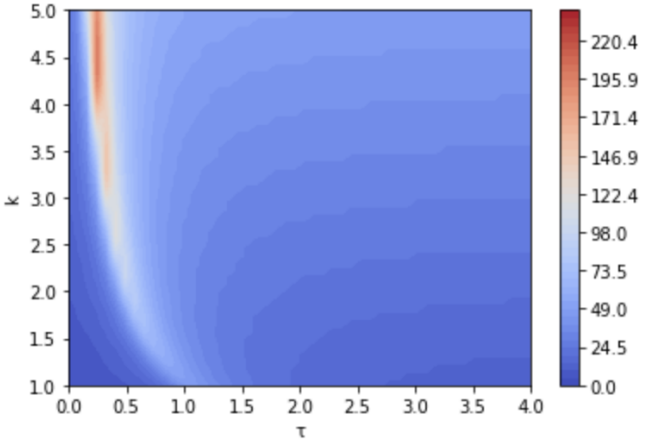


Image 5: 2-D contour plots

The red represents a higher t value, while the blue represents a lower t value. We were somewhat right about minimizing k value and maximizing τ value, but not entirely. In fact, when τ is nearly 0, the 2-D contour plot shows dark blue, and although a lower k value is heavily correlated to darker blue, it does not necessarily show the same effect in a certain τ range. Under the assumption that recovered people won't get infected again, a quicker recovery can guarantee the sooner end of the epidemic in most cases. One interesting thing to point out is

that we can separate the trend among line 1 = $\frac{1}{\tau kS0}$. That's the curve that's composed of red and white, which determines the stability of the system. While 1 > $\frac{1}{\tau kS0}$, all the fixed points are unstable, and when 1 <= $\frac{1}{\tau kS0}$, all the fixed points are stable. Another thing we can observe is whenever $tkS0$ > 1, an outbreak occurs, while when tkS0 <= 1, an outbreak doesn't occur. Looking carefully at the line $\frac{1}{\tau kS0}$, we can see that in the left part of the line $\frac{1}{\tau kS0}$ is dark blue, and the outbreak doesn't occur (the disease is spreading really slowly) as the value of τ is too small. In this case, an outbreak won't occur and therefore (fixed points are stable), it'll take a short time to meet the stopping condition. When an outbreak does occur, (whenever $\tau kS0$ > 1; in this case portions that are right to $\frac{1}{\tau kS0}$ line) it's impossible to determine the ideal scenario even though we can find some sort of general trend. In general, the lower the k value and the higher the τ value, it will meet the stopping condition sooner. This is because once the outbreak occurs, there's no way to go back to the phase where the outbreak didn't occur as those fixed points are unstable. In general, when an outbreak occurs, the way to meet the stopping condition as soon as possible is to spread the disease and people recover as fast as they could. All three scenarios from #1.2 had an outbreak occur. However, this doesn't apply every time when an outbreak occurs. For example, comparing the time for (τ, κ) values such as (1.5, 1.5) and (1.5, 1), it actually turns out (1.5, 1.5) -> t = 25 took less time than (1.5, 1) -> t = 27. This is partially due to unstable points that make the prediction unexpected. Therefore, we can find a general approach to minimize the time for stopping conditions, but it's impossible to guarantee that it works due to instability.

#1.4

For vaccination, we introduced a new state Variable V(t) such that S(t) + I(t) + R(t) + V(t) = 1 still holds. Some of the basic assumptions for this new state variable include vaccines only working for people who are susceptible, and not everyone can get vaccinated as there is a cost for vaccination. We've decided to adapt the formula from the textbook but modify the parameter v, such that $dV = v * R(t) * I(t) / (R(t) + I(t))$, $v = \frac{1}{\tau kS0}$.

Based on our heatmap, we thought It is the most effective to vaccinate more people when τ and k are close to the line of $1 = \frac{1}{\tau k S0}$, so we set the v = 1/(τ*k*0.99)to maximize the v when τ and k are on the line of $1 = \frac{1}{\tau k S0}$. The further away (τ, k) values are from the line, we'll let people recover without using too much of the vaccine as it's relatively blue. It is true for those scenarios that are already blue, it'll help if we vaccinate more people, however, it may not always result in an efficient solution. Therefore, we primarily focused our vaccination policy on the line involving red and white and modified parameters v in order to vaccinate accordingly. We used R(t) and I(t) to multiply by v as we discussed earlier, we have to consider how many people have gotten infected and recovered. When more and more people are getting infected, whether at a slower or faster rate, we'll need more vaccines as the likelihood of susceptible people getting infected rises as well. Therefore we'll multiply v by I. However, infection will eventually go down even without a vaccine as recovered people increase as well, so we'll have to take that into consideration as well. This is why we're multiplying R by v and I. By having R(t) into the equation, we're able to sort of upper bound the vaccination number as at some point enough people have recovered and vaccines won't be highly needed anymore. Then we divide those by I+R as there's no point in vaccinating people who are either infected or recovered. We'll have to vaccinate fewer people overall as we have a higher I+R value, which makes sense as I+R is in the denominator.

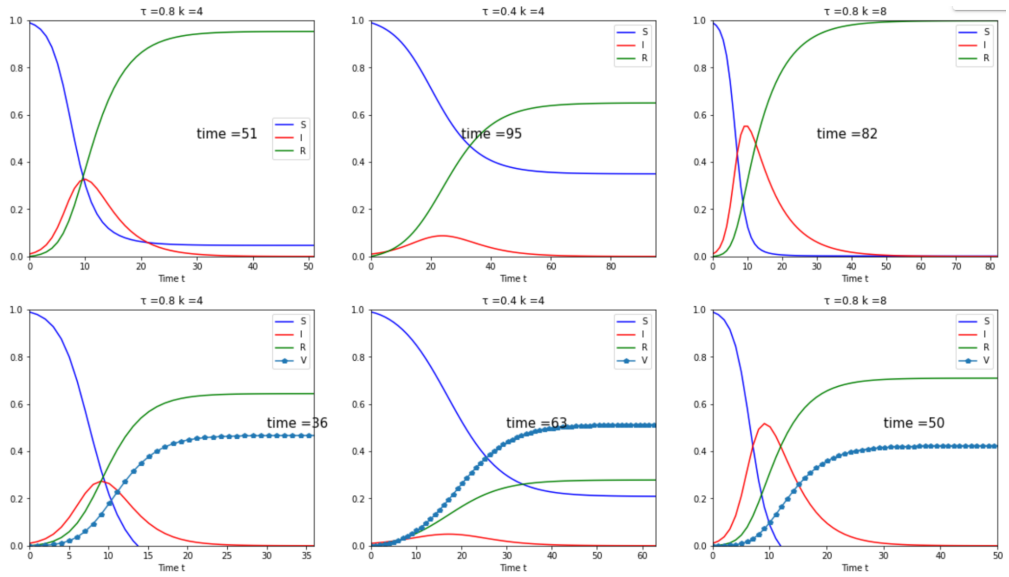


Image 5: Comparison between three scenarios from #1.2 before (above three) and after (bottom three) vaccination policy

As shown above in image 5, we can see a reduced amount of people who got infected and significant improvements over time. Although we've had a few other functions that reduced the number of infections a lot more than this model, we chose this function as we're not vaccinating too many people and yet reduce the time to meet the stopping condition quite a lot.

#1.5

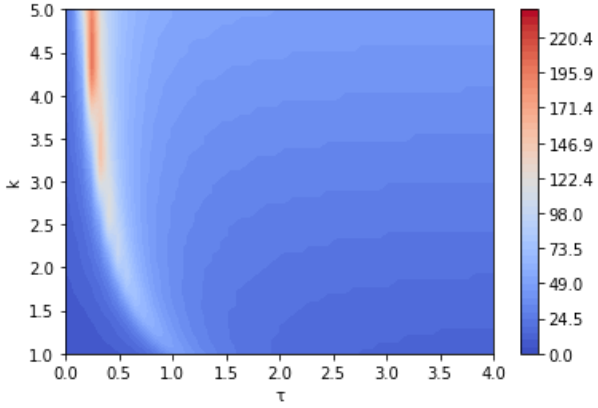


Image 6: heatmap from #1.3

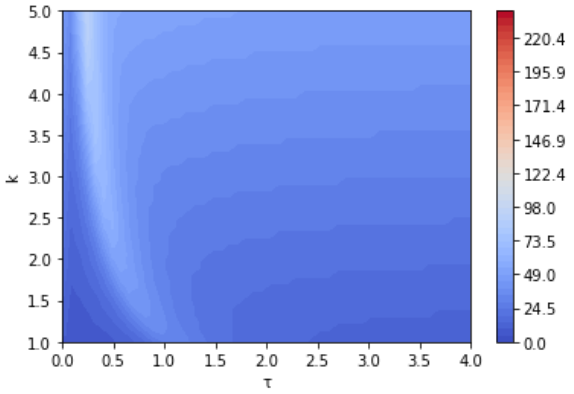


Image 7: heatmap with new vaccination policy

This is the comparison of the heatmap before and after our vaccination policy. As we discussed earlier, one of our main goals was to focus on the line where it's red. We can see a significant improvement as most of the red is gone, and instead, we see a white line. Outside of the red zone, we also see overall blue has been darker as well. Although our model doesn't focus on reducing the amount of infection, we have shown a great improvement in time replacement.