Virus Model

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1 Introduction

Recently, I took a class in mathematical modelling at my university, Math 142 at UCLA, and I thought one thing that made it a great class was that the instructor could choose

In particular, even though this was a pretty small unit, it really did catch my attention: epidemic modelling. At the beginning, I didn't really think that epidemic modelling could really be a thing because it was one of those fields where there's way too many variables to really get a good guess as to how a disease is going to spread. However, after even just our brief stint into the field, I was surprised on

More specifically, the one main model we explored was the very famous and popular SIR model. Some of the main points/assumptions of the model are:

- This is what's called a compartmental model. This basically just means that we're going to make the simplifying assumption that the whole population we're observing can be nicely compartmentalized into a few different categories.
- For this SIR model, the categories are:
  - **S**usceptible people who can still contract the disease
  - **I**nfected people
  - **R**ecovered from the disease. (You can also consider this to be people who are **R**emoved from the population after death if you want to be a bit more morbid).

1.1 Deriving a Basic Version of the SIR Model

In fact, one way you can think of this idea of organisms flowing among these compartments is actually borrowing ideas about rates of reactions from chemistry. So let's start thinking about what "flows" we would want to model with a basic SIR compartment system, and how we can translate those into "chemical reactions".

So first off, let's define three functions. If we let N be the number of total organisms in the population:

$$S(t) = \frac{\text{Number of Susceptible people}}{N}$$

$$I(t) = \frac{\text{Number of Infected people}}{N}$$

$$R(t) = \frac{\text{Number of Recovered people}}{N}$$

Sometimes it's more helpful sometimes to consider these $S(t)$, $I(t)$, and $R(t)$ functions to be represent *concentration* rather than absolute population numbers for normalization purposes. It also helps draw the parallel to these chemistry reaction rates a bit more easily, which often considers molarity as the functions in question.

Maybe the most obvious reaction to start with is the "disease spreading" reaction. This would be maybe where an infected person meets a susceptible person, and this happens to result in spreading the disease β times a day. So we'd be tempted to say that

$$\mathrm{S} + \mathrm{I} \xrightarrow{\alpha} \mathrm{I} + \mathrm{I}$$

If you remember how to turn chemical reactions with rates into differential equations, we get the purely mathematical form of our model:

$$\frac{dS}{dt} = -\alpha SI$$

$$\frac{dI}{dt} = \alpha SI$$

Now we of course want to model the second major interaction here, which is infected organisms recovering. In the simplest case, we can make another modelling assumption that a constant fraction β of the infected population recovers every unit of time.

$$\mathrm{I} \xrightarrow{\beta} \mathrm{R}$$

This turns into

$$\frac{dI}{dt} = -\beta I$$

$$\frac{dR}{dt} = \beta I$$

Adding these two sets of equations together, we get the full model.

$$\frac{dS}{dt} = -\alpha IS$$

$$\frac{dI}{dt} = \alpha IS - \beta I$$

$$\frac{dR}{dt} = \beta I$$

and that's it.

From this, we can actually notice that

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \implies S(t) + I(t) + R(t) \equiv N$$

This means that we have made another important assumption: notice also that the total population isn't changing here, we're considering birth and natural death rates as well as immigration rates to be negligible compared to the total population. In fact, a good way of saying this is that *no one leaves the Susceptible group except by getting infected*, and this translates to our modelling equations in the fact that the only term for $\frac{dS}{dt}$ is indeed that decrease as people flow from susceptible to infected.

I suppose one of the coolest ideas I saw as we explored this model was that if you got creative with it, even just these three compartments could allow you to model many different scenarios. Maybe mostly obviously from the previous discussion, you might want to consider the birth and death rates of the population as well, which is just as simple as adding another term to . To th Maybe you could add an extra flow from Recovered into Susceptible to represent an only temporary immunity gained after recovering for the first time. And maybe if you want some even more realism, you can add a **D**eceased term which with a flow from Infected to represent those unlucky people who didn't recover from the disease. There's lots of really interesting math you can do with some of these very basic additions, but to be honest, I haven't looked into them yet.

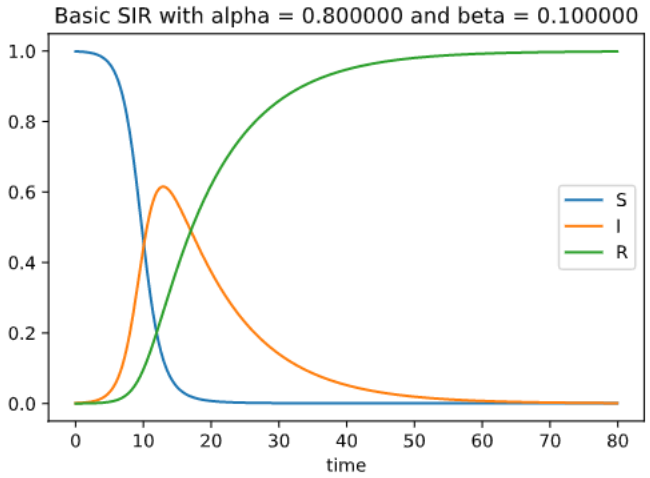
1.2 A Quick Diversion: What does Flattening the Curve Mean?

Based on the two main parameters that we have, α, the "transmission rate", and β, the "recovery rate". If you were trying to combat some kind of pandemic, how would you try to affect these two parameters? Well, just from common sense, it would just be to **increase** the recovery rate, and **decrease** the transmission rate.

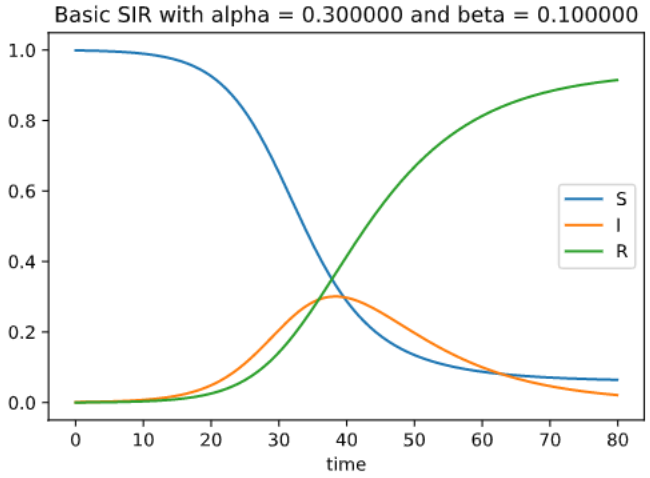
However, imagine you are in a scenario where there doesn't exist a vaccine or remedy for your virus. In this model, this means that we're imagining where it's not really easy to increase β, or decrease the time to recovery. Well in this case, all that's left that we can do is actually *decrease* α. And that just means **taking preventative measures (such as social distancing) to decrease transmission of the infection**.

In fact, let's take a look a look at what effect lowering the transmission rate alone could have on our model.

(While writing this PDF up, I've decided to make a complimentary Jupyter Notebook that explores some of this stuff with less pure math and more simulations and graphy stuff. It'll be in the same Github repository whenever this goes up.)



Compare this with lowering the transmission rate down to 0.3, without touching β, the recovery rate.



So all in all, just from a simple model like this, we can clearly see that lowering transmission rate corresponds with taking a longer time for the disease to completely disappear, but importantly lowers the peak below healthcare capacity, like number of beds available in dense cities.

2 Adapting the Model

So that basic version of the model is great and all; it's surprisingly simple to understand and come up with, and it alone gives very surprisingly complex epidemiological results. In particular, according to my professor, the general solution to this seemingly simply system of first order ODEs is currently unknown.

However, what's been interesting me a bit more as I've been reading the news over the past couple of weeks is this: if flights were to be closed between China and the US, might an outbreak still happen in the US even with quarantine? If so, how fast after cases become detected in America would the government have to react? The math actually turned out to be quite interesting and fun to mess with (which is why I'm writing this, also because I made some neat graphs).

2.1 Two City Assumption

Now of course, for this whole idea to work in this particular setting, we actually have to consider two cities here, each with SIR populations of their own. To simplify things one common trick I've seen is that we also assume that we are in the beginning stages of an outbreak. This is when S is very close to 1 and most of the population is not yet infected, sort of like there is an "infinite" pool of susceptible people to spread to, like most of a city or a country, and that there are no recovered people either. So basically, we're just trying to measure the infected populations.

But of course, now there are two infected populations, one in each city. Let's just call them I_C for China, and I_A for America. So now the normal rules for infected growth apply (α for the normal spreading rate, and β for the normal recovery rate).

2.2 Travel Assumption

As for the interaction between the cities, speaking in math, we're essentially adding a complicating factor to our model in that our rate of increase in the infected population is not just a product of the internal factors of the infected and susceptible population, but also of other infected individuals coming in from outside the original population. But then, that factor would have to disappear after the flights become closed.

In practice, this might look like

$$\frac{dI}{dt} = \alpha IS - \beta I + f(t)$$

where that $f(t)$ then some piecewise function that is positive when $t < t_0$, and 0 when $t \geq t_0$. You can maybe think of it like a faucet shutting off after a certain time.

2.3 Quarantining Assumption

Finally, I discovered that things actually get a lot more interesting when you throw in a "quarantining" rate k/I that gets smaller as the infected population grows. This models another idea I've been seeing, that it is harder to quarantine and treat infected individuals the more there are in the population due to strained healthcare resources.

2.4 Final Model

Combining these three ideas, this is the model I'll be using going forward:

$$\frac{dI_C}{dt} = \alpha I_C - \left(\beta + \frac{k}{I_C}\right) I_C$$

$$\frac{dI_A}{dt} = \alpha I_A - \left(\beta + \frac{k}{I_A}\right) I_A + \mu I_C$$

where μ represents the rate at which people moving from the China to America. I suppose there movement from America to China as well, but we're interested in the time before an outbreak happens in America. I'm also assuming that America and China have the exact same k quarantining efficiency.

3 Simplifying the Model

Now the model we have is in a state where is term's purpose and each coefficient's meaning is pretty clear, but there's a good amount of simplifying we can do through something fancy I actually learned in my Math 134 class (which focuses on systems of differential equations and dynamics): nondimentionalization. This is where we sort of "rescale" our variables so that the model is nicer to deal with at the end of the day. At the end, the goal is that instead of having many different parameters like α and β and μ for which we might not care about/have control over the particular values, we want scale to eliminate them, or at least condense them down into single coefficients.

3.1 Nondimentionalization

Out first move is to set

$$x = \frac{I_C}{I_0}, y = \frac{I_A}{I_0}, \tau = \frac{t}{t_0}$$

where you can already see we are scaling the populations and our time to some scaling with constants I_0 and t_0 determined by our coefficients.

To create our new scaled differential equations, we can differentiate now with respect to τ and use the chain rule:

$$\dot{x} = \frac{dx}{d\tau} = \frac{dI_C}{dt}\frac{t_0}{I_0} \implies \frac{dI_C}{dt} = \dot{x}\frac{I_0}{t_0}$$

$$\dot{y} = \frac{dy}{d\tau} = \frac{dI_A}{dt}\frac{t_0}{I_0} \implies \frac{dI_A}{dt} = \dot{y}\frac{I_0}{t_0}$$

Note that the dot notation for derivatives now should represent not t-derivatives, but rather τ-derivatives.

Now if we substitute into our original modelling equations:

$$\dot{x}\frac{I_0}{t_0} = \alpha I_C - \left(\beta + \frac{k}{I_C}\right) I_C = \alpha x I_0 - \beta x I_0 - k$$

$$\dot{y}\frac{I_0}{t_0} = \alpha I_A - \left(\beta + \frac{k}{I_A}\right) I_A + \mu I_C = \alpha x I_0 - \beta x I_0 - k$$

Then isolating the derivative terms,

$$\dot{x} = (\alpha - \beta) x t_0 - k\frac{t_0}{I_0}$$

$$\dot{y} = (\alpha - \beta) y t_0 - k\frac{t_0}{I_0} + \mu x t_0$$

So now that we have these scaled equations, we need to "choose judiciously the definition of the characteristic unit for each variable so that the coefficients of as many terms as possible become 1" as Wikipedia tells us. To achieve that, it looks like a good first move is to set

$$\boxed{t_0 = \frac{1}{\alpha - \beta}}$$

so that the first terms of both equations have their coefficients cancel. With that choice, to cancel out the second terms, we want then to set

$$\boxed{I_0 = k t_0 = \frac{k}{\alpha - \beta}}$$

and then the second terms will just become 1. And that's all we need to set. Substituting back in then, this is our nondimentionalized model:

$$\dot{x} = x - 1 \tag{1}$$

$$\dot{y} = y - 1 + cx \tag{2}$$

and while we have that funny looking term at the end there with all the coefficients, this is actually a bit of a good thing that all the coefficients are grouped up. We can just set another variable $c = \frac{\mu}{\alpha - \beta}$ and we're basically down to a system with just one parameter, which is pretty good.

3.2 Nondimentionalization Observations

Now as I looked at these equations, I got a bit confused for a second why there was no $-cx$ term for the $\dot{x}$ equation. Then I realized what this term actually represents: it would technically represent the drop in infected people due to the chance that an infected person leaves China's population and flies to America. However, when you consider this is becomes pretty obvious what's going on: I didn't consider this term in the original model simply because I thought that it would have basically no impact on the overall infected population of China.

But now that we have properly scaled, we can give that a bit more justification. We now know what "basically no impact" means at least a little more concretely; when something is much less than one. In particular, examining that same assumption mathwise now that we have this model, we can see that in the limit where $c \to 0$, we have that $cx \ll x$, and we can safely then ignore that term. And again, this checks out because $c = \frac{\mu}{\alpha - \beta}$ should be very small because the chance that an infected individual travels to America (μ) is much smaller than the chance that they infect someone else in China ($\alpha - \beta$)

Also notice that we can't do the same comparison with the $\dot{y}$ America equation, because we don't know how to compare cx with y. In fact, for a while, the main source of infected individuals *should* be the those travelling from China, which is exactly that cx term.

3.3 Solving the First Equation

Notice that the first equation for $\dot{x}$ only depends on x, and so it's really easy to solve in isolation. If the initial condition is $x(0) = C$, then our solution is

$$x(\tau) = (C - 1)e^{\tau} + 1 \tag{3}$$

And so another nice result of our scaling reveals itself here: when the initial infected population C is greater than 1, we have exponential growth of our infection, which is what we expect of an outbreak. However, if $C \leq 1$, we actually have exponential decrease as our quarantine term quickly handles the outbreak. This means that a population such that $C = 1$, which is when the population exactly matches I_0, is actually **the minimum starting infected population needed where the quarantine capacity is overrun and an outbreak (exponential growth) starts happening**. And when we see that we defined $I_0 = \frac{k}{\alpha - \beta}$ which is sort of like the ratio between how fact the virus can be contained vs how fast it spreads, this again check out. Pretty neat.

Either way, for the sake then of making our model actually interesting, let's assume from here on out that $C > 1$ so that an outbreak actually occurs in China.

4 The Interesting Part

Now is where we are finally ready to start answering the question I asked at the beginning about how long

But then I realized over the course of thinking about all of this, if we really want to measure "reaction time" of how fast flights would have to be shut down, we actually need that starting "stimulus" which would trigger a response, or when the pandemic "arrives" at America. This would of course have to be when the situation gets so bad in China that number of infected people arriving in America starts exceeding exceeding quarantine capacity, and politicians/governments start having to seriously consider the economic consequences of shutting down travel. Let's call this τ_{start}.

4.1 Calculating τ_{start}

To do this, we of course have to start using the $\dot{y}$ differential equation which defines the infection spread in America. Substituting in our solution for x,

$$\dot{y} = y - 1 + c\left[(C-1)e^{\tau} + 1\right]$$

However, notice that we don't actually have to solve this equation outright.

Instead we can afford to be a bit more clever here with a pretty important observation here.

τ_{start} = time until infected overwhelm quarantine capacity = time when $\dot{y}$ is first non negative

Now why is this true? Well, $\dot{y}$ starts negative as quarantining allows the small amount of infected arriving to be treated. Since the negative impact on spread quarantining has remains constant while the infection monotonically grows, eventually $\dot{y}$ will become positive. When that happens, we will see the infected population in America y start to grow, and the infection will start to increase not just because of incoming infected people, but from those infected people not being quarantined enough and spreading the infection on their own. You can almost think of it like overcoming friction, with the spreading "acceleration" set to 0 until you push your object hard enough to overcome the coefficient of friction.

I wanted to spend a tiny bit more time hammering this point home a little more because I've realized this is a pretty darn important modeling concept and requirement: *some qualitative change in the system need to be related to a calculable quantitative aspect of the math/model.* Now that I

Since $\dot{y}$ is an increasing function, we actually then just need to find τ_{start} such that we hit breakpoint where $\dot{y} = 0$.

Notice that this also means that we can ignore any natural spread as all the infected individuals are able to be quarantined at this stage. In math, that means we can just set $y = 0$. Putting these facts together, our problem reduces to solving this equation for τ

$$-1 + c\left[(C-1)e^{\tau} + 1\right] = 0$$

$$(C-1)e^{\tau} + 1 = \frac{1}{c}$$

$$\tau_{start} = \ln\left(\frac{1-c}{c(C-1)}\right)$$

4.2 Calculating Time to Outbreak

We know from our nondimentionalization that we will be too late when we hit that critical $y = 1$ population in America when, where the infection can become self sustaining even when no additional infected people enter. Now is the time where we'll actually have solve equation (2). After again substituting in (3),

$$y' = y - 1 + c\left((C-1)\,e^t + 1\right)$$

Since this equation is first order and linear, we can just solve it with integrating factor.

But that's a lot of work that I don't feel like writing out, so just trust me or Wolfram Alpha that the answer is

$$y(\tau) = 1 - c + c\,(C-1)\,e^\tau\tau - (1-c)e^\tau = 1$$

But, there's no easy way to isolate τ, as this is a transcendental equation with no closed-form solution.