

Modeling and Battling COVID-19

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The original version of this talk was given (virtually) at the Missouri University of Science & Technology on April 20, 2020. You can view a video of the original talk at <https://mst.hosted.panopto.com/Panopto/Pages/Viewer.aspx?id=5186e6c8-f050-4e54-8401-aba401089fa9> . An expanded version of that that talk was given virtually at Kennesaw State University on April 29, 2020. These set of notes are an expansion of the Kennesaw State talk.

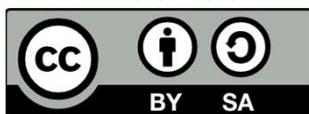
Abstract

This talk will describe a simple model that can be used to model epidemics and present its relevance to the COVID-19 Pandemic. The model is complex enough to describe some key strategies for managing a pandemic and can be easily used by anyone interested in understanding the dynamics of COVID-19. The relevance of the model to the developments in Georgia will be discussed.

Bio

Dr. George Markowsky is a Professor and former Chair of Computer Science at the Missouri University of Science and Technology, where he runs the Cyber Society Lab. He was Chair and Professor of Computer Science at the University of Maine, a Visiting Scholar at the Rochester Institute of Technology, a Visiting Professor at Rensselaer Polytechnic Institute, and Manager of Special Projects in the Computer Science Department at IBM's T. J. Watson Research Center. His research interests are theoretical methods in computer science and the impact of computers on society. He holds a Ph.D. in Mathematics from Harvard University and a B. A. in Mathematics from Columbia University. He is also the President of the US Chapter of the International Emergency Management Society.

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10. Where is the Exponential Growth?
11. Looking at Real Data
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14. Appendices
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 - A Python abc-Model
 - An Excel™ abc-Model
 - Looking at Real Data with Python & Excel™

The picture on the first slide comes from the CDC website (<https://www.cdc.gov/>) where it is on the home page on May 2, 2020. I am presuming, that like most US Government data and publications, this image is in the public domain.



Goal of this Talk

- The goal of this talk is to introduce you to a basic model used to model epidemics
- We will show how this model applies to the COVID-19 pandemic and how it leads to a strategy for dealing with the pandemic
- There are many important aspects of the COVID-19 pandemic that are not covered in this talk
- Our goal to achieve a qualitative understanding of the behavior of epidemics in general and apply this understanding to battling COVID-19
- The model we are discussing does not have the level of specificity to give predictions such as “on June 25, 2020 we will be all back to normal and can ignore the COVID-19 pandemic”
- We hope that this presentation will help you understand why accurate modeling is so challenging but that even rough models can still be very useful
- Understanding this model will help you to understand more complex and detailed models and highlight the important role that computer modeling plays in dealing with disasters

For many features of the COVID-19 Pandemic not covered in this talk, consult https://en.wikipedia.org/wiki/Coronavirus_disease_2019 and also websites such as <https://www.who.int/emergencies/diseases/novel-coronavirus-2019> and <https://www.cdc.gov/coronavirus/2019-nCoV/index.html>.

The following article talks about how a tabletop exercise using qualitative model in 2019 illustrated some of the difficulties that society would face from a real pandemic.

“The Good and Bad News from a Coronavirus Pandemic Model,” by Robert Bazell, March 19, 2020.

<http://nautil.us/issue/83/intelligence/the-good-and-bad-news-from-a-coronavirus-pandemic-model>

Modeling During a Pandemic

- One of the great difficulties in modeling during a pandemic such as COVID-19 is that there is still so much that we do not know about the virus and its spread
- For example, we do not know how many people are asymptomatic carriers, i. e., they have no symptoms but are able to spread the disease
- We don't know all the factors that affect susceptibility to the disease
- We don't know for sure how it spreads
- There are inconsistencies and deficiencies in testing
- etc., etc., etc.
- Nevertheless, we need to take action and do all we can to mitigate the damage

The article below addresses some of the issues raised in this slide.

“Why It’s So Freaking Hard To Make A Good COVID-19 Model” by Maggie Koerth, Laura Bronner, and Jasmine Mithani, March 31, 2020.

<https://fivethirtyeight.com/features/why-its-so-freaking-hard-to-make-a-good-covid-19-model/>.

This is a link to a video that shows how viruses might spread through the air.

<https://www.youtube.com/watch?v=EPNBHuu755E&feature=youtu.be&fbclid=IwAR3u1rnCNhC2d1ltzw0o80mX7rgguQLrFEWdSeydVAnOD64HvdZtdaL2Xd4&app=desktop>.

This link represents the best understanding that the CDC has for how COVID-19 spreads:

<https://www.cdc.gov/coronavirus/2019-ncov/prevent-getting-sick/how-covid-spreads.html>.

The following article discusses the asymptomatic spreaders of COVID-19:

<https://www.npr.org/sections/goatsandsoda/2020/04/13/831883560/can-a-coronavirus-patient-who-isnt-showing-symptoms-infect-others>.

Compartmental Models

- In a compartmental model, we partition the members of our group into compartments and establish rules on how individuals move from one compartment to another
- We assume that the behavior of all individuals in a given compartment is the same
- Usually, the more compartments we establish, the more accurate the model
- In principle, the most accurate model would be a model where each compartment consisted of a single individual
- Of course such a model is infeasible – we could never collect all the data that we would need for such a model and we would not have the computing power to run such a model even if we could collect all the data

A general discussion of compartmental models can be found at https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology.

Statistical Assumptions

- The first assumption that we will make is that we want to create a short-term model
- In particular, we will ignore events such as births and immigration
- The second assumption is that we can use statistical arguments
- In 1663, John Graunt published a remarkable work called *Natural and Political Observations Made Upon the Bills of Mortality*, which was the first of what we would call a statistical analysis of mortality
- He found that while the cause of individual deaths might not be predictable (being kicked by a horse, being run over by a carriage, falling down a well, being bitten by a rabid dog) there was a remarkable consistency in the overall mortality rate barring things like plagues (pandemics)

An interesting article about John Graunt can be found at https://en.wikipedia.org/wiki/John_Graunt.

Statistical Assumptions

- Based on Graunt's work and that of his successors people have discovered that statistical principles often work surprisingly well and these days are often used without special remark
- How often have you heard things like the average student has a debt of \$x or that the life expectancy of the average 42 year old male is y years
- It may turn out that no one in the population actually has the average value
- Over the years, we have discovered the "Laws of Large Numbers" which basically state that the more random particles you have, the more predictable their behavior becomes
- The model I will discuss is at heart a probabilistic model that will look like a deterministic model

An article about the Law of Large Numbers can be found at https://en.wikipedia.org/wiki/Law_of_large_numbers.

The SIR Model

- The SIR model is one of the simplest of the compartmental models and gets its name from the three compartments (S, I, R) that it divides the entire population into
- The model was first proposed by William Kermack and Anderson McKendrick in a series of 3 papers written between 1927 and 1933
- The SIR model forms the basis for many of the models in use today
- It assumes that population does not change during the modeling period and that there are three compartments of people – Susceptible, Infectious, and Recovered

There are several references that you might want to consult related to this slide.

As noted earlier, a general discussion of compartmental models including the SIR model can be found at https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology.

A historically based discussion can also be found at https://en.wikipedia.org/wiki/Kermack%E2%80%93McKendrick_theory.

David Smith and Lang Moore have prepared materials that can be used to study the SIR model. These materials can be found at <https://www.maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-introduction>.

The S, I, and R Compartments

- You might think that you understand the nature of the S, I, and R compartments from their names and you would be mostly correct, but there are subtleties associated with these definitions
- One thing that might strike you as strange is that there do not seem to be any dead people in this model
- Actually, the dead people are in the Recovered compartment
- The term recovered is a bit misleading, since what we are really talking about is people who can no longer infect other people
- It might have been better to call this compartment U for uninfected

There are expanded versions of the SIR that treat people who die as a separate compartment. Since our goal to present the basic concepts we seek to minimize complications.

Infectious People

- Note also, that we refer to the compartment I as consisting of infectious people and not infected people
- For the sake of the model, we care primarily whether a person can infect other people and not whether they are infected or not
- For example, suppose a disease typically takes a person 15 days to recover from, but the person only produces particles that can infect other people on the first day of the disease, then we would put the person into the Recovered group after 1 day and not after 15 days
- Similarly, if a person is infectious for 15 days, but after day 5 the person goes into quarantine and can no longer infect other people they would go into the Recovered compartment as soon as they are quarantined even though they might still be sick
- Also, a person might get sick and end up with kidney failure but stop being infectious
- In this case, we classify that person as recovered but not everyone would apply the term "recovered" to this person

Recovered People

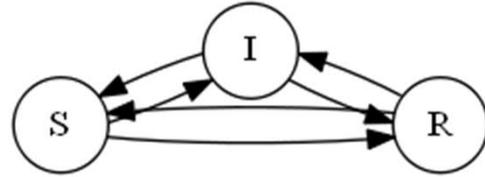
- The language is a bit tricky here
- Usually, when we say that someone recovered from the flu we mean that they are no longer sick and are back to “normal”
- If someone died from the flu, we would not normally say that “they recovered from the flu”
- The important thing to understand here is that recovered means that the people in question can no longer infect other people
- Another tricky instance is if a person had genetic immunity to the disease that person should be considered recovered even though that person was never infected
- Also, if an infectious person is quarantined so that they can no longer infect anyone, we would move them to the Recovered compartment even though they are still sick and could potentially infect people
- Because dead people are placed in the Recovered compartment we can say that the population does not change during the modeling

Susceptible People

- A susceptible person is a person who is not infected, but who could become infectious by exposure to infectious people
- Because of genetic variability there are usually some people who immune to a given disease
- Furthermore, certain genes run in families so you can have clusters of people who are super susceptible and clusters of immune people
- These details can only be worked out after painstaking research and ideally would be part of a more accurate model

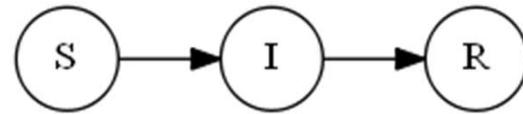
Relationships Between Compartments

- In modeling an epidemic, we want to understand how people move from one compartment to another
- In general, we can envisage a diagram such as the one to the right in which there are circumstances under which people can move directly from one compartment to any other compartment
- We want to simplify this picture to avoid analyzing 6 transitions



Simplifying the Diagram

- At this time, it is still not completely known whether “recovered” COVID-19 victims maintain any sort of residual immunity
- This is not an idle question since we know there is enough mutation among other Corona viruses (e.g., the common cold) so that people can get reinfected, even in the same cold season
- Needless to say, the more arrows we have in the model linking the compartments the more complex the model
- To simplify our discuss, we will assume that we have the diagram to the right which we will call the $S \rightarrow I \rightarrow R$ diagram
- We are now ready to start writing some equations!



The $S \rightarrow I \rightarrow R$ Diagram

The question of reinfection has not been rigorously studied. There are, however, some news accounts that suggest reinfection is possible as you can see below. As of this writing, the jury is still out on this question.

“People can get the coronavirus more than once, experts warn — recovering does not necessarily make you immune,” Business Insider, February 27, 2020:

<https://www.businessinsider.com/wuhan-coronavirus-risk-of-reinfection-2020-2?op=1>

“Can You Get Coronavirus Again After Recovering Completely? ,” India.com, March 16, 2020:

<https://www.india.com/lifestyle/can-you-get-coronavirus-again-after-being-recovered-completely-3970598/>

Some Equations

- If the population we are studying has N people, the first equation we can write is $S + I + R = N$
- Notice we do not subtract people who were killed from the population for the purposes of the model – people who died are counted by R
- We are now going to reach into our bag of tricks and announce that we can differentiate the above equation
- You might object on the grounds that S , I , and R are not real numbers and it makes no sense to talk about 4.5 infected people, etc.
- However, there are two important counter arguments
 1. We want to primarily apply our model to large populations so the difference between 1,000,000 and 1,000,000.6 people is not significant
 2. These models work and we use them in many different situations

The approach discussed here is an example of the Stochastic Calculus. See https://en.wikipedia.org/wiki/Stochastic_calculus for a very brief introduction.

If you are unfamiliar with Calculus, do not worry about understanding the key parts of this presentation. We will soon introduce some straightforward numerical equations that do not require understanding Calculus. You can get a basic understanding of the derivative at <https://en.wikipedia.org/wiki/Derivative>.

There are a number of videos available on YouTube that discuss calculus from a visual perspective. You might sample some of these if you are interested.

https://www.youtube.com/watch?time_continue=2&v=WUvTyaaNkzM&feature=emb_logo

https://www.youtube.com/watch?v=WjJ-kpgps1c&feature=emb_rel_pause

A Differential Equation

- You might ask, why do we even want to differentiate the equation?
- The answer is, that we are interested in the movement between compartments, which suggests that we are interested in the rate of change of the numbers in all three compartments
- Note that we are dealing with functions $S(t)$, $I(t)$, and $R(t)$ but we will often suppress the t to reduce clutter
- If we differentiate both sides of $S + I + R = N$, we get
- $\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$
- This means that once we figure out how two of the compartments change, we will know how the third one changes
- In particular, the $S \rightarrow I \rightarrow R$ diagram shows that S has just one arrow leaving and R has just one arrow entering so we will begin our analysis with R and S

$$\frac{dR}{dt}$$

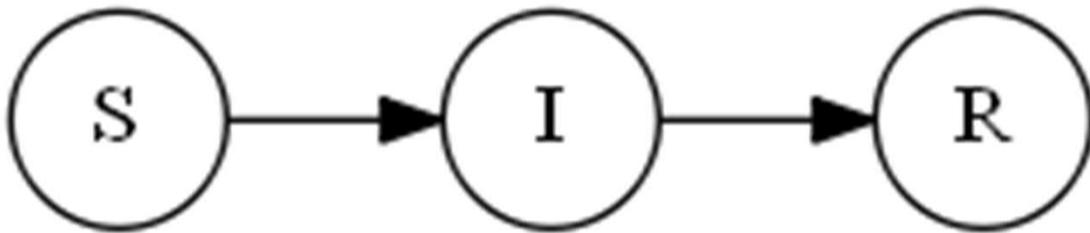
- We have shown the S→I→R diagram to the right
- Let's start with $\frac{dR}{dt}$
- It seems reasonable to assume that if a person "generally" is sick for d days, that every day 1/d of the infected people "recover"
- This leads to the equation $\frac{dR}{dt} = \frac{1}{d} I$
- To minimize fractions, let $a=1/d$ so we have the equation $\frac{dR}{dt} = aI$

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The S→I→R Diagram

The Constant a

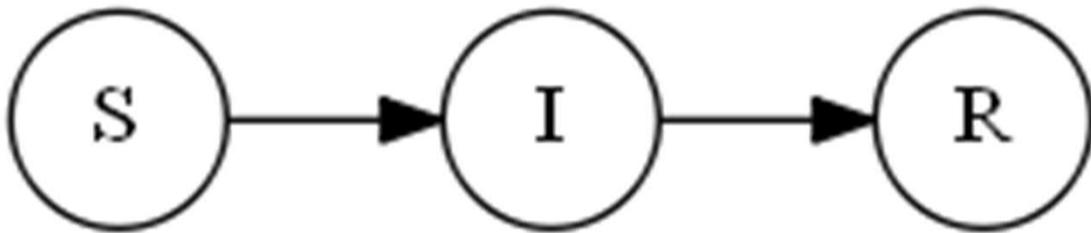
- Notice that we made an assumption that if a person is sick for d days on average, about $1/d$ of the infected people recover each day
- This might not be so simple since it looks like many people can be COVID-19 spreaders without being sick
- We do not know for sure what the constant a is so for the time being let's assume it is $1/d$
- Note that in our simple model $a \geq 0$ since we have no way for people to leave the Recovered compartment so $R(t)$ must be monotone increasing
- Note, having a large a is good because it means lots of people are leaving I , the set of infectious people!
- We will further discuss the constant a later in this talk
- Now let's turn to figuring out what $\frac{dS}{dt}$ should be



The $S \rightarrow I \rightarrow R$ Diagram

$$\frac{dS}{dt}$$

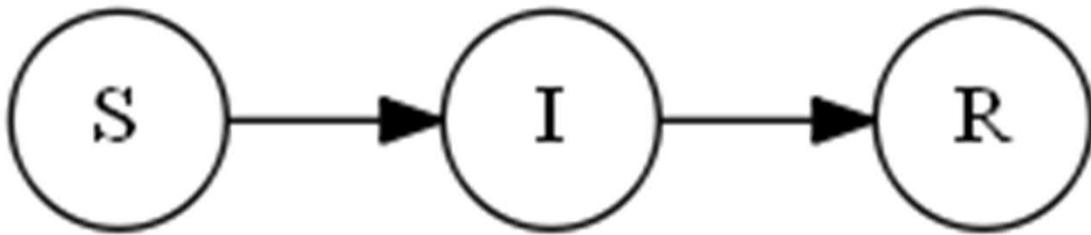
- Susceptible people become infected by interacting with infected people
- If we have twice as many susceptible people we would expect twice as many infections so roughly speaking $\frac{dS}{dt} = -kS$ for some k
- Notice that we have a minus sign because the number of susceptible people can only decrease through infection – we have no way in our model for infected or recovered people to become susceptible (research could change this)
- Now it seems reasonable to assume that $k = b\beta c$ where c is the number of “contacts” (interactions) that a person has per day, β is the percentage of the contacts who are infectious, and b is the probability that a person will become infected from a contact with an infected person
- Once again we are relying upon our “statistical” assumption



The $S \rightarrow I \rightarrow R$ Diagram

$$\frac{dS}{dt} \text{ (continued)}$$

- So far we have come to $\frac{dS}{dt} = -kS$ for $k = b\beta c$ where c is the number of “contacts” (interactions) that a person has per day, β is the percentage of the contacts who are infectious, and b is the probability that a person will become infected from a contact with an infected person (note that β is not a constant)
- The constant b (b for “bad”) is tricky, because clearly meeting an infected person outdoors at a distance of 50 feet is different from being in a crowded subway car containing 1 or even 10 infected people – again we use a statistical number for b
- We can argue that $\beta = I/N$, which is the proportion of infected people in the population
- This gives us the equation of $\frac{dS}{dt} = -bcIS/N$



The S→I→R Diagram

$$\frac{dI}{dt}$$

- Given that $\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$ we know that $\frac{dI}{dt} = bcIS/N - aI$
- Putting all our equations together and gives us the system displayed on the following slide

The Fundamental Equations

1. $\frac{dS}{dt} = \frac{-bcIS}{N}$
2. $\frac{dI}{dt} = \frac{bcIS}{N} - aI$
3. $\frac{dR}{dt} = aI$

- Notice the following: I appears in every term on the right-hand side of every equation
- Notice also that some terms involve N which suggests that we would have different equations for different populations – we would prefer to have a universal set of equations that works for any population
- Fortunately, there is a simple trick that we can use to make our equations “universal” so they will work for any population

The Simple Trick

- Derivatives are linear so if we replace S , I , and R by S/N , I/N , and R/N , we get what we want
- In particular, if we introduce the functions $s(t) = S(t)/N$, $i(t) = I(t)/N$, and $r(t) = R(t)/N$, we get
 1. $\frac{ds(t)}{dt} = -bci(t)s(t)$
 2. $\frac{di(t)}{dt} = bci(t)s(t) - ai(t)$
 3. $\frac{dr(t)}{dt} = ai(t)$
- Do not confuse i or $i(t)$ with $i = \sqrt{-1}$, the complex number!
- The beauty of the above system is that it is population independent – it just involves ratios!

“Flatten the Curve”

- You have undoubtedly heard the expression: “we have to flatten the curve”
- There are three curves here, which one do we need to flatten?
- The answer is we need to flatten $i(t)$ as you can see when we write the equations a bit differently
 1. $\frac{ds(t)}{dt} = -bci(t)s(t) = (-bcs(t))i(t)$
 2. $\frac{di(t)}{dt} = bci(t)s(t) - ai(t) = (bcs(t) - a)i(t)$
 3. $\frac{dr(t)}{dt} = ai(t)$
- We noted this earlier when we pointed out that $i(t)$ is a factor in every derivative – if you can keep $i(t)$ small you keep all the derivatives small!

For another view of “flattening the curve” see the article: “How to flatten the curve of coronavirus, a mathematician explains”, by Andrew Black, Dennis Liu and Lewis Mitchell, Medical Express, March 16, 2020: <https://medicalxpress.com/news/2020-03-flatten-coronavirus-mathematician.html>.

Dealing with the Equations

- Notice that the equations we derived are a non-linear system of differential equations because of the product $i(t)s(t)$
- Fortunately, we do not need to get bogged down in the theory of differential equations
- We can use the following approximation familiar from calculus
- $f(x + \Delta t) = f(x) + \frac{df(x)}{dt} \Delta t$
- If we make $\Delta t = 1$, we get the equation $f(x + 1) = f(x) + \frac{df(x)}{dt}$
- This transforms our equations as shown on the following slide

For more information on this process see: <https://medicalxpress.com/news/2020-03-flatten-coronavirus-mathematician.html>.

Numerical Approximations

- Taking great liberties, which I will not try to justify here, we end up with the following equations written in computer-friendly style
 1. $s(t+1) = s(t) - b*c*i(t)*s(t)$
 2. $i(t+1) = i(t) + b*c*i(t)*s(t) - a*i(t)$
 3. $r(t+1) = r(t) + a*i(t)$
- The previous 3 equations are easy to implement in Python and in a spreadsheet like Excel
- I am preparing an expanded version of this talk that will have both working Python code and a working Excel version that I will distribute soon on my website DrGM.us

These implementations will be discussed later in this presentation to avoid disrupting the development of the SIR model.

Let's Run Some Examples

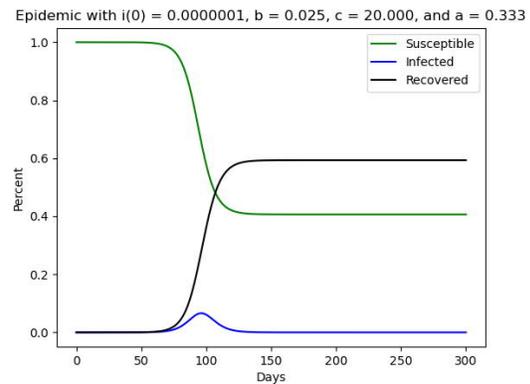
- When we run examples, we need to pick some values for $s(0)$, $i(0)$, and $r(0)$ along with coefficients a , b , and c
- If we pick $i(0) = 0$, then nothing happens in the model because all derivatives are 0
- It is simple to assume that $r(0) = 0$ since we are assuming that no one has recovered yet since no one got infected – we are ignoring genetic immunity
- Thus we need $i(0) = \epsilon$ and $s(0) = 1 - \epsilon$
- We will investigate the choice of ϵ soon
- We then need to pick a , b , and c

Picking a, b, and c

- Let's start off with a disease, something like a cold, during which people are infectious for 3 days
- We will assume that $a = 1/3$
- What about b and c?
- Just to get started, let's suppose that a person has 20 contacts a day and that the chance of getting infected from meeting an infected person is 2.5% = .025
- Let's run the program and see what we get

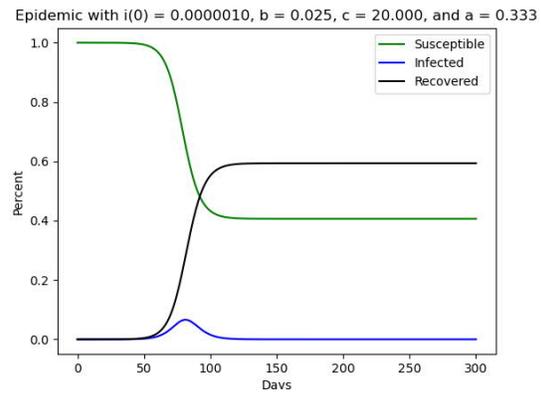
Our Starting Scenario

- With the parameters set up top, we get the graph shown to the right
- What does $i[0] = .0000001$ mean?
- It means that there is only 1 infection for every 10,000,000 people – this is the equivalent of about 35 infected people in the entire USA
- Why did the graph stabilize? Shouldn't everyone get infected?
- The reason the graph stabilized is that $I(t)$ became 0, so all changes stop
- The peak for $i(t)$ happens about 100 days out while the peak for $r(t)$ is maybe 115 days out with that being around the maximum of deaths if $dead(t)$ is counted in $r(t)$



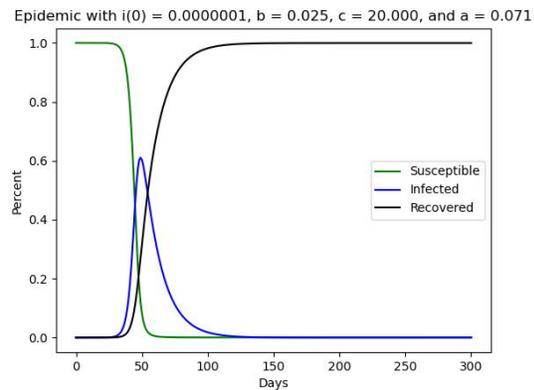
Starting With More Infected People

- Let's change $i[0]$ to 1 in a million instead of 1 in 10 million
- We then get the graph to the right
- We got pretty much the same curve except that the peaks happened earlier which make sense
- About 60% of the population ends up in the recovered category and about 40% never get infectious



Extending Days of Infectiousness

- Let's change $i[0]$ back to 1 in 10 million
- Let's assume that people are infectious for 14 days instead of 3 so that $a = 1/14$
- With these parameters, we get the graph to the right
- The graph to the right is much scarier than the graph on the previous slides!
- Remember that this graph is population independent
- Clearly, we did not flatten the $I(t)$ curve enough

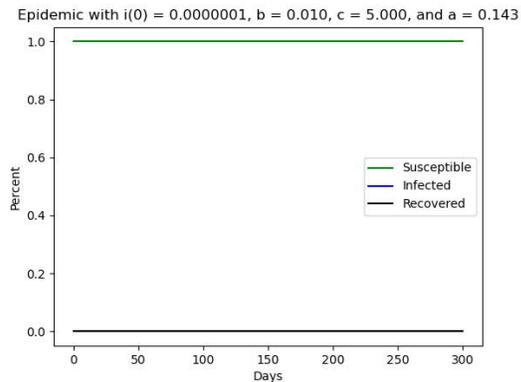


The abc-Attack on COVID-19

- The model we have come up with depends on 3 parameters: a, b, and c
- To control the pandemic we need to increase a ($a = 1/d$, so decrease d), decrease b, and decrease c
- The simplest and fastest way to decrease d (increase a) is to find infectious individuals and quarantine them until they stop being infectious
- The role of testing is crucial here!
- If we test only sick people, we will never find the asymptomatic carriers!
- Ideally, we should test everyone
- We must quarantine infectious people!
- We can decrease b by creating greater distances between people, having people wear masks, and washing your hands and not touching your face (distancing, mask wearing, washing your hands and not touching your face)
- We can decrease c by people seeing fewer people (social isolation)
- An abc-attack can also be called a lockdown

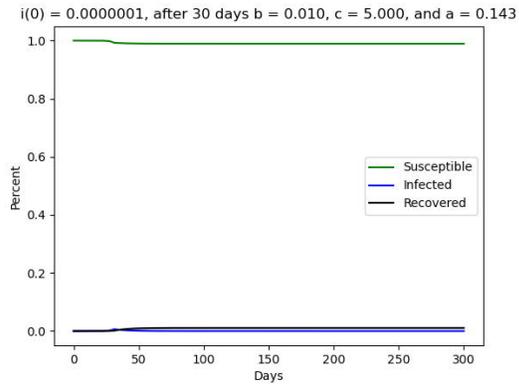
An Effective abc-Attack

- Let's keep $i[0]$ at 1 in 10 million
- Let's assume that people are infectious for 7 days instead of 14 so that $a = 1/7$
- Let's assume we knock b down from .025 to .010 and c from 20 to 5
- This abc-attack generates the graph to the right
- The graph to the right is much more pleasant to look at than the earlier graphs
- Remember that this graph is population independent
- We have really "flattened the curve"!



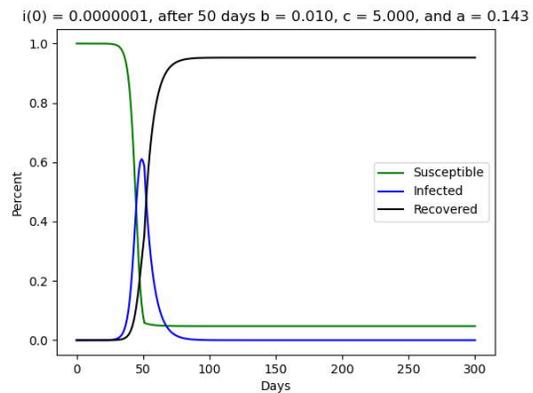
“Normal” and then an abc-Attack

- Suppose that we start out with the “normal” parameters with $a = 1/14$, $b = .025$, and $c = 20$ for 30 days
- After 30 days, we switch to $a = 1/7$, $b = .010$, and $c = 5$
- This scenario generates the graph to the right!
- What a difference!
- What if we wait for 50 days before we switch to the new a , b , and c ?



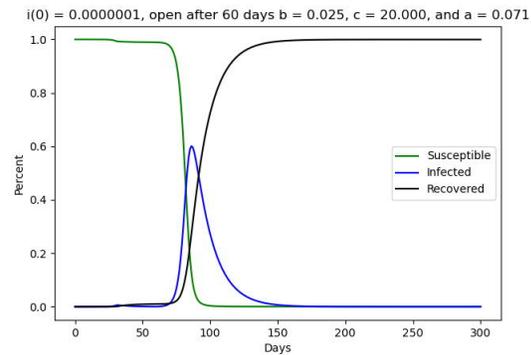
A "Small" Delay

- The graph to the right shows what happens if we just delay 20 days before applying a lockdown
- The graph on the right demonstrates vividly the importance of implementing your abc-attack as quickly as you can
- We've gone from a not-so-bad scenario to a very bad scenario with nearly everyone getting infected just by delaying for 20 days
- LACK OF SPEED, KILLS



Reopening

- Let's consider the following scenario: we start out with our "normal" scenario with $a = 1/14$, $b = .025$, and $c = 20$ for 30 days
- After 30 days we lockdown to $a = 1/7$, $b = .010$, and $c = 5$
- After 60 days we decide to go back to "normal" with $a = 1/14$, $b = .025$, and $c = 20$
- The graph you get is shown to the right
- It is clear that reopening must be done carefully!



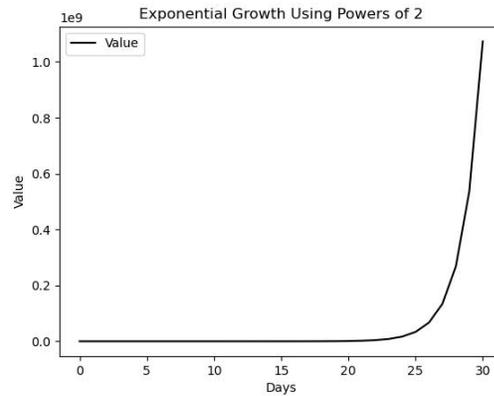
An interesting approach to reopening can be found in the article "10-4: How to Reopen the Economy by Exploiting the Coronavirus's Weak Spot" by Uri Alon, Ron Milo, and Eran Yashiv that can be found at <https://www.nytimes.com/2020/05/11/opinion/coronavirus-reopen.html>.

The Troll Trap

- Fighting COVID-19 is taking place in the political arena
- If we succeed in controlling COVID-19, we need to be wary of trolls arising and saying that because the worst case did not happen the entire pandemic was “overblown” and even a hoax
- This model illustrates that we must be very careful in dealing with epidemics since we can quickly lose control
- The human race must move beyond requiring disasters to take place before it acts
- The role of computer models is critical in combating COVID-19

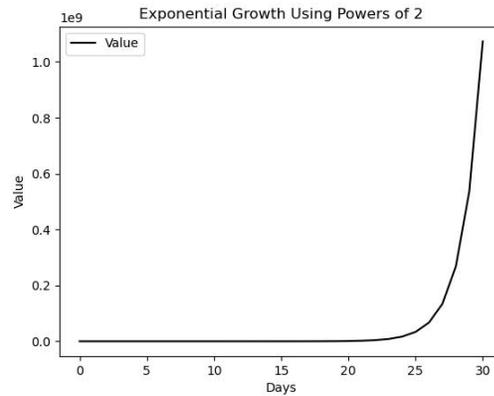
Where is the Exponential Growth?

- You have probably read or heard the term “exponential growth” when discussing the COVID-19 pandemic
- It is not immediately clear where that exponential growth is visible in the curves we have seen so far – after all a pure exponential curve looks something like the curve to the right



Where is the Exponential Growth?

- The chart on the right needs some explanation
- The 1e9 in the top left represents the scale, $1e9 = 10^9 = 1$ billion
- The last value is $2^{30} = 1,073,741,824$
- Note that the curve looks like it is almost at 0 for the first 20 days and then it rapidly (almost vertically) shoots up to 1 billion
- This is why people fear exponential growth because you can manage for a while, but then you are overwhelmed
- Clearly, we do not have pure exponential growth since there are limits on the various curves



Where is the Exponential Growth?

- So let's return to our equations and see where there exponential growth is lurking
- In particular, I want to focus on the following equation
- $\frac{di(t)}{dt} = bci(t)s(t) - ai(t) = (bcs(t) - a)i(t)$
- Using the standard manipulations used in differential equations we can rewrite this equation as follows
- $\frac{di(t)}{i(t)} = (bcs(t) - a)dt$
- If we integrate both sides we get
- $\ln(i(t))|_{t_0}^{t_1} = \int_{t_0}^{t_1} (bcs(t) - a)dt$
- With some standard algebraic manipulation we get
- $\ln\left(\frac{i(t_1)}{i(t_0)}\right) = \int_{t_0}^{t_1} (bcs(t) - a)dt$
- Which after more manipulation yields
- $i(t_1) = i(t_0)e^{\int_{t_0}^{t_1} (bcs(t) - a)dt}$

Where is the Exponential Growth?

- So now we have $i(t_1) = i(t_0)e^{\int_{t_0}^{t_1}(bcs(t)-a)dt}$ so at least you are seeing powers of the constant e
- We now note that in the early stages of the pandemic $s(t)$ is roughly 1 and b , c , and a are constants so $\int_{t_0}^{t_1}(bcs(t) - a)dt \cong (bc-a)t$
- This gives us the equation $i(t_1) \cong i(t_0)e^{(bc-a)t}$, i.e., $i(t)$ grows exponentially in the early part of an epidemic
- This is why people devote so much effort to minimize the possibility of the explosive growth shown in the Powers of 2 graph

Looking at Real Data

- Once you have a model, regardless of how crude it might be, there is an overwhelming temptation to apply it to real data
- There is some preliminary work that must be done since the data does not directly measure the functions that appear in our SIR model
- In particular, the number most commonly cited is the number of people who got infected over the course of the epidemic, let's call this number X since we haven't quite figured out how to interpret this number
- This number never goes down so it clearly cannot be $i(t)$ which goes up and eventually goes down
- Another problem is that when people recover, they are never removed from the count

Looking at Real Data

- There are a bunch of other problems
- For example, people are added to X when they have received a positive result on a test for COVID-19
- However, we do not know where in the cycle of infectiousness the tested person was
- In particular, we do not know the following
- Is the tested person infected but not infectious?
- If the tested person is infectious, how much longer will they be infectious?
- Will the tested person be prevented from infecting other people?

Looking at Real Data

- As mentioned at the beginning of this talk, there are many problems with creating models with the lack of information that we face
- COVID-19, however, will just do its thing and not care whether we understand it or not
- In short, we need to make our best assumptions and move on
- Note that $X(t)$ is given in terms of individuals so we need to use the function $I(t)$ rather than $i(t)$ since $I(t)$ counts individuals and $i(t)$ is a ratio
- At this point the simplest thing we can do is to assume that $X(t+1) = X(t) + I(t)$, so if we want to estimate $I(t)$ we should use the equation $I(t) = X(t+1) - X(t)$
- Because of asymptomatic carriers we really don't know $I(t)$, but this is the best that we can under the circumstances

Looking at Real Data

- Let's return to our differential equation for $I(t)$
- $\frac{dI}{dt} = \frac{bcIS}{N} - aI$
- Let's also use $I(t+1) = I(t) + \frac{dI(t)}{dt} = I(t) + (bcS(t)/N - a)I(t)$ so
- $(I(t+1)/I(t)) = 1 + bcS(t)/N - a$ which is not quite a constant because of the term $S(t)/N$
- However, when the pandemic starts out almost nobody is infectious so $S(t)/N$ is essentially 1
- So after all this work, we have come up with $\frac{I(t+1)}{I(t)} \approx (1 + bc - a)$
- Now we are ready to look at some data and see how it matches up with this analysis

Data for the US

- Here's our plan of attack
- We first collect our best data for X
- Then we determine that $I(t) = X(t+1) - X(t)$
- Then we look at the ratios of $I(t+1)/I(t)$ and see whether we get a constant
- For the first test run we used data for the entire USA from the New York Times data repository (<https://github.com/nytimes/covid-19-data>)
- The sequence of values that we calculated is shown to the right and show our estimates of $1 + bc - a$
- While the results are not constant, they are not super bad and come in somewhere in the neighborhood of 1

| | | |
|-------|-------|-------|
| 0.889 | 1.308 | 0.947 |
| 1.312 | 1.223 | 0.855 |
| 1.714 | 0.998 | 0.948 |
| 1.861 | 1.402 | 1.035 |
| 1.239 | 1.165 | 1.126 |
| 1.410 | 1.013 | 1.057 |
| 1.017 | 1.210 | 0.995 |
| 1.689 | 0.893 | 0.902 |
| 1.343 | 1.149 | 0.893 |
| 0.907 | 1.143 | 1.076 |
| 1.653 | 1.090 | 0.933 |
| 1.373 | 1.100 | 1.128 |
| 1.212 | 1.107 | 1.179 |
| 1.042 | 1.079 | 1.086 |
| 1.292 | 0.720 | 0.933 |
| 1.541 | 1.167 | 0.775 |
| 1.745 | 1.071 | 0.871 |
| 1.655 | 1.001 | |
| 1.388 | 1.089 | |
| 1.163 | 0.967 | |

Avg = 1.159, SD = 0.249
a = 0.071, bc = 0.231

Data from Georgia

- For the second test run we used data for the state of Georgia supplied by Dr. Ian Ferguson of Kennesaw State University
- The sequence of values that we calculated is shown to the right and show our estimates of $1 + bc - a$
- As you can see, there is a lot more variability in the results which is not surprising because we are dealing with a smaller population

| | |
|-------|-------|
| 1.478 | 0.674 |
| 0.654 | 1.399 |
| 1.069 | 0.413 |
| 1.849 | 0.719 |
| 1.477 | 3.706 |
| 0.870 | 0.894 |
| 1.258 | 0.713 |
| 2.421 | 1.651 |
| 0.368 | 0.929 |
| 0.956 | 0.391 |
| 1.473 | 1.584 |
| 3.109 | 1.404 |
| 0.582 | 0.843 |
| 1.103 | 1.220 |
| 0.751 | 0.834 |
| 0.795 | 0.778 |
| 0.863 | 1.192 |
| 2.273 | 0.366 |
| 1.958 | 2.811 |
| 0.646 | 0.843 |

Avg = 1.233, SD = 0.852
 a = 0.071, bc = 0.304

Conclusions

- This simple model shows very graphically that in the absence of a “cure” or a vaccine, controlling the constants a , b , and c is extremely important
- This model is not detailed enough for precise planning, but it offers strong evidence that controlling a , b , and c can be an effective way to limit the damage done by COVID-19
- The model very clearly illustrates the value of testing and quarantining, distancing, social isolation, and washing your hands and not touching your face
- It also illustrates that keeping $i(t)$ as low as possible – “flattening the curve”, is extremely important!
- Also, we have shown that LACK OF SPEED, KILLS!
- It makes clear that pandemics like COVID-19 are exponential processes that can explode if we are not very careful in managing reopening
- When we compare the output of the program to real data, we see some promising results that suggest that our modeling is useful and reflects some aspects of reality

Experimenting with the Model

- There are several experiments that you might want to do with the model
 1. You can add more compartments – it is well known that different ages have different infection rates and mortality rates
 2. You can have a separate compartment for people who died or suffered some complications
 3. You can start the model assuming that r is at a certain value and see how the pandemic develops under these circumstances
 4. You can see what happens if people can become infectious or susceptible after recovering

Programs

- The Python and Excel Programs will be released separately on the same website.
- The programs will have their own documentation and licenses rather than try to put everything into one document
- They will be available within a week of this document becoming available

In Memoriam

- While I have been focusing on mathematical analysis, it is important to bear in mind that we are talking about people and their lives in an ongoing tragedy
- As of 9:48 pm, May 11, 2020, there were 1.3+ million confirmed cases of COVID-19 with 80,542 deaths in the USA
- The USA death rate is 6.2% of the confirmed cases, this is not very good
- Globally, there were 4.1+ million confirmed cases with 285,329 deaths
- The global death rate is 7.0% of the confirmed cases which is slightly worse than the USA ratio
- I want everyone to appreciate the scale of this tragedy and think about all the suffering that is going on in the world because of COVID-19
- I ask for a minute of silence during this presentation to commemorate all the victims and the victims-to-be of COVID-19
- Among the victims of COVID-19 is someone of special interest to computer scientists: John Conway – the inventor of the game of “Life”

The number of cases and deaths continues to increase. You can get the updated numbers from <https://www.nytimes.com/interactive/2020/world/coronavirus-maps.html>. For the USA, you can get updated numbers from <https://www.nytimes.com/interactive/2020/us/coronavirus-us-cases.html>.