Optimizing the Spread of Disease through Evolutionary Game Theory

Kiran Dsouza
Dept. of Engineering, Dartmouth College, Hanover, NH 03755

Abstract

The COVID-19 pandemic is unprecedented and it demands novel approaches for understanding and mitigating the virus's spread. Evolutionary Game Theory (EGT) provides an interdisciplinary tool in biology, mathematics, and social science to optimize strategies against the pandemic. Employing the SEIR model, we simulate disease dynamics, considering factors such as transmission rates, recovery rates, and societal responses. Our study explores a best-response function between implementing public health measures and preserving mental well-being, illustrating the challenges and trade-offs faced in combatting the pandemic. We also evaluate a simple textbook model of infection biology to see if it corresponds well enough to actual US covid data to be useful as a basis to study the behavior of covid variants.

Introduction

The COVID-19 pandemic has presented an unprecedented global challenge, requiring innovative approaches to understand and control the spread of the virus. As nations grapple with implementing public health measures, an emerging field of study, Evolutionary Game Theory (EGT), offers a unique lens through which we can analyze and optimize strategies to combat the transmission of the virus while also keeping people happy. Social distancing helped in stopping the spread at Covid, but this isolation came at a cost. Over half of Americans reported being anxious or depressed during the lockdown. Opioids related deaths increased by 32% and alcohol related deaths [1]. In this paper we explore simulations to keep the death count as low as possible, from Covid and substance abuse, but also trying to maximize people's happiness. We also explore whether a simple model can be used to explain US Covid infections. This would motivate us to extend it to analyzing the behavior of Covid variants using EGT.

Methods

The SEIR model is a mathematical model used in epidemiology to describe the spread of infectious diseases within a population. The acronym SEIR stands for Susceptible, Exposed, Infectious, and Recovered, which represent the different stages individuals go through during the course of the disease [2].

Susceptible (S): This group represents individuals who are not infected and are susceptible to the disease.

Exposed (E): Individuals in this group have been exposed to the infectious agent but are not yet infectious themselves. This accounts for the incubation period during which the individual is infected but not yet capable of transmitting the disease.
Infectious (I): This group includes individuals who are currently infected and can transmit the disease to others.
Recovered (R): Individuals in this group have recovered from the infection and are assumed to have acquired immunity, making them no longer susceptible to the disease.

The transitions between these compartments are governed by a set of differential equations that take into account parameters such as the transmission rate, recovery rate, and the duration of the incubation period. The SEIR model provides a framework for understanding how infectious diseases spread through a population over time.

For this simulation we will assume the death rate is equal to the birth rate when there is no disease present, so the population loss is a consequence solely from the disease. The SEIR model uses differentiations to capture each category. The following differential equations will be used to get the populations of each stage with respect to time [3]:

1. dS = (-T*S*I/N+delta*R)
2. dE = (T*I*S/N - E*Ei)
3. dI = (E*Ei - R*I + delta*R+NSD*(E))
4. dR = (R*I + delta*R)

where the variables represent the following:

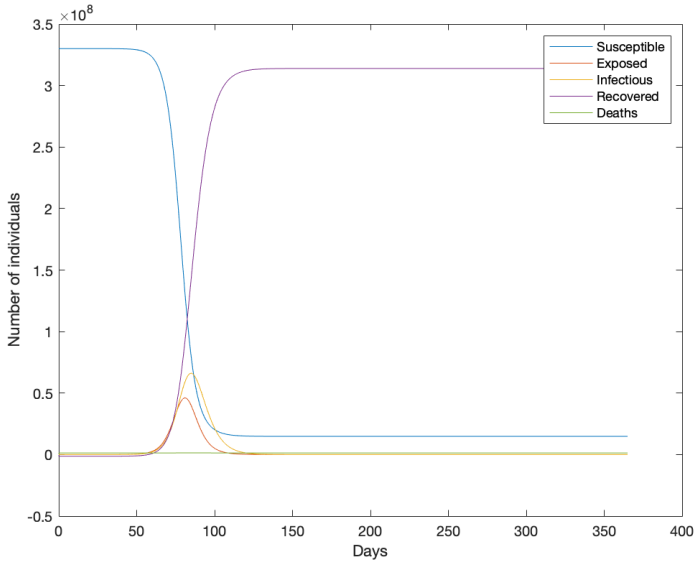
T: The transmission rate of the virus
S: The population of people who are susceptible to the virus
I: The population of people who are infected by the virus
N: Starting population (for the US its 330 million people)_
Delta: Chance of someone who recovered from the virus getting the virus again
R: The recovery rate of the virus
E: The rate at which people are exposed to the virus
Ei: Initial people exposed to the virus
NSD: How many people are not practicing social distancing

For the deaths the following equation will be used where 0.011 [5] is the covid mortality rate and 100,000 is the number of people who die per year from overdose of opioids or alcohol, which saw a 35% increase during the shutdown :

5. D = .011*I + 1000000*1.35*(N-NSD)/N))

Model

Assuming everyone practices social distancing, we get the following SEIR model during the time where covid was at its peak:



Where the total number of deaths is 1.32 million. Here we can see the number of people sustainable drops rapidly as many people get infected since it was a very contagious virus. However the mortality rate was quite low, so there were not many deaths in the simulation.

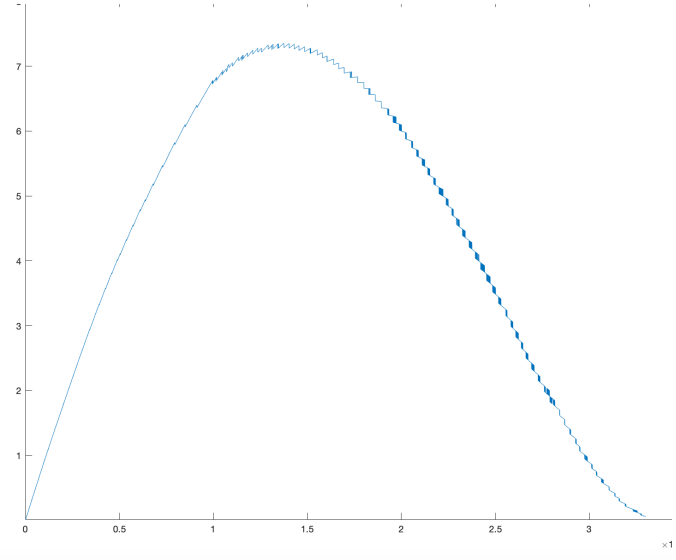
We will continue using this model but change the amount of people who follow stay at home orders. We will maximize the best response equation:

6. BR = NSD*(Alive)^2

This equation is used because many people in the US were not happy during lockdown. Over 50% of people reported being depressed [4], so by increasing the amount of people who do not social distance, we increase a person's happiness and decrease the number of deaths from overdoses. This comes at a cost of increasing the amount of deaths from the virus though because more people are exposing themselves.

Results

Running the simulation on the US population, which took a hour on my laptop, we obtained the following graph:



NSD vs Best Response

To get the maximum best response, 140 million people don't have to follow the social distancing guidelines.

Discussions

The best response function is a subjective function. With 140 million people not socially distant, about 10 million people are predicted to die from the virus. There needs to be a balance between people socializing for their mental health and to prevent substance abuse, and also social distancing to stop the spreading of the virus. People are going to disagree on how much those factors should be weighed. For example, a college student who wants to have the "college experience" might value socializing over containing the virus. On the other hand, a person who is at "high risk" might define the best response as minimizing the total deaths at all costs.

With only a portion of the country being able to not follow social distancing guidelines, this brings up a prisoner dilemma sort of problem of who should follow the rules and who shouldn't. If everyone doesn't follow the rules that leads to the most people getting infected; however if everyone follows the rules, that leads to the decline of mental health as a whole and an increase in substance abuse.

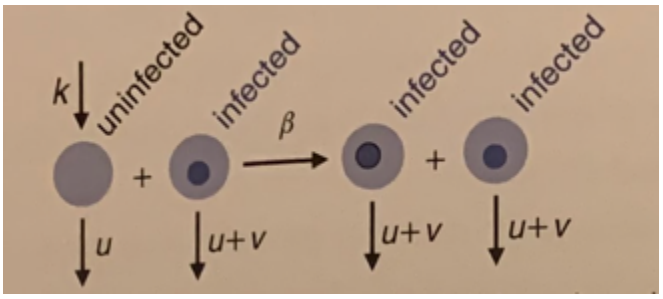
Virus Viewpoint

So far, we have considered the human response to the Covid virus. Looking at future simulations we can look at the virus's viewpoint. In this simulation we looked at human behavior's response to the virus using data from a pandemic that already happened. We can use these models to predict Covid virulence and predict superinfection behavior.

We decided to start with a simpler model than SEIR that would be easier to extend to multiple Covid variants. However, we would have to validate the basic model against actual Covid data before extending it to analyzing multiple Covid variants. The model we chose was

the Basic Model of Biological Infection [6]. It has many limitations but due to its simplicity we decided to compare it to actual Covid data to see if it was good enough to extend.

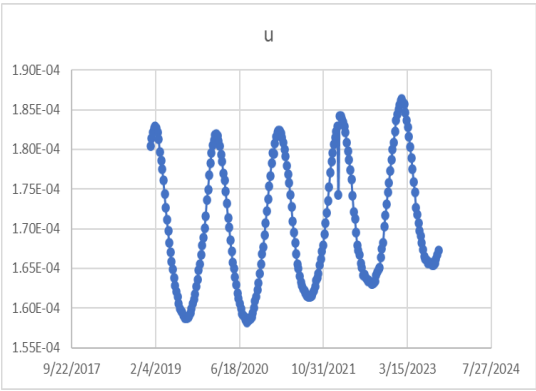
The Basic Model is shown in the figure below from [6]. The system starts with uninfected and infected people, with a death rate *u* and an increase in the death rate *v* based on infection. There are *k* new arrivals in the population, due to births and immigration. Based on an infectivity factor β, uninfected people may get infected and are subject to the higher death rate of *u*+*v*.

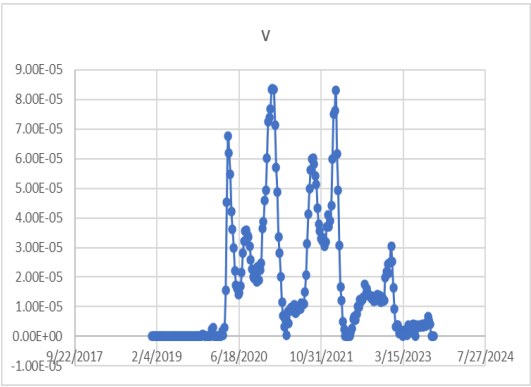


This model can be expressed in the differential equations in the figure below, also from [6]. Here, the additional variables are *x,* the number of uninfected people, and *y,* the number of infected people.

7. $\dot{x} = k - ux - \beta xy$
8. $\dot{y} = y(\beta x - u - v)$

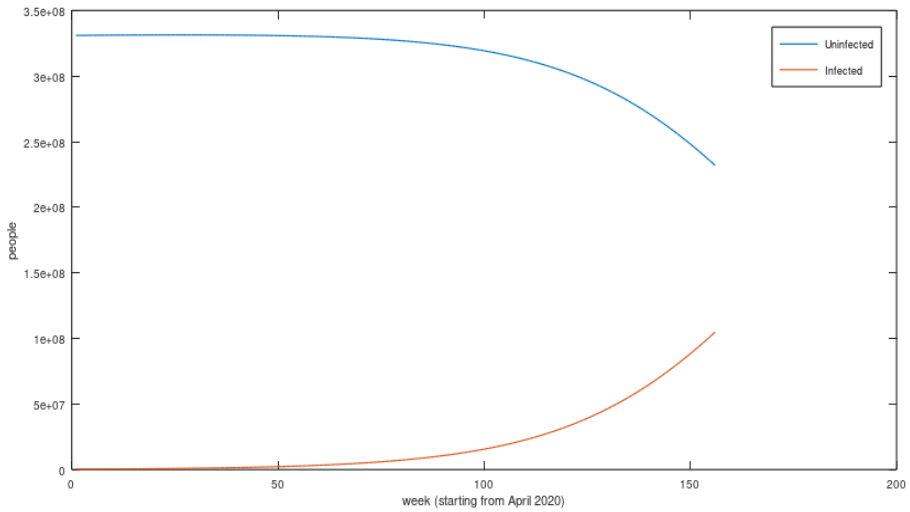
We obtained data on the expected number of deaths in the absence of Covid and the actual number of deaths from Covid on a weekly basis. This allowed us to compute *u* and *v* values for each week. For our model, we computed the *u* and *v* values, using raw data gathered from the CDC website [7].





Next we used the *u* and *v* values from the first week of April 2020 as the pandemic was really taking off in the US, and beta=1.195e-10, in the Basic Model and simulated it for 3 years (156 weeks). The results are shown below. At the end of 3 years, we have a predicted number of infections of 1.0495e8, which is close to the actual number of infections of 1.03e8, as reported

in [9]. The basic reproductive ratio from this model is 5.27, a bit on the high side but within the range of estimates of actual Covid studies[10]. The predicted number after 1 year and 2 years is a bit lower than actual but overall it is surprisingly reasonable even though it ignores many factors like vaccination. To improve the model, β, *v*, and *u* should really all be functions of *t*.



Running this model longer would show that almost everyone would be infected, but that actually may be true in real life. This is also shown by computing the equilibrium for the model, where we get $x^* = \beta/(u+v) = 1.83M$ and $y^* = (\beta k - u(u+v))/(\beta(u+v)) = 391M$.

These results are sufficiently encouraging that we will extend our analysis to the model for multiple variants to see how well it matches what was observed during this 3-year period of the Covid pandemic. We will rank the variants 1..n in order of increasing virulence, obtain v and beta values for each variant, and use the following model from [6] over periods where they were active.

9. $\dot{x} = k - ux - x^*(\beta_1 y_1 + \ldots + \beta_n y)$
10. $\dot{y}_i = y_i(\beta_i x - u - v_i + x\beta_i(y_1 + \ldots + y_n) - x(\beta_1 y_1 + \ldots + \beta_n y_n))$ $\quad i=1,\ldots,n$

Conclusion

In navigating the COVID-19 pandemic, Evolutionary Game Theory (EGT) emerges as a valuable tool for strategy analysis. By incorporating the SEIR model, we simulated the impact of social distancing on virus spread and population well-being. Striking a balance between minimizing virus transmission and preserving mental health proves challenging, as the best response is subjective. The model highlights the need for nuanced approaches, recognizing diverse perspectives and weighing the impact of interventions on both health and well-being.

References

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Appendix

```
%Matlab code
%Kiran Dsouza
[deaths,y,t] = simulation(.65, .2, .331, 20/100, 0);
deaths
plot(t,y);
xlabel('Days');
ylabel('Number of individuals');
legend('Susceptible','Exposed','Infectious','Recovered','Deaths');

trial =[];
happy = 0;
for i = 1:3300
  [deaths,y,t] = simulation(.65, .2, .331, 1/60, happy);
   happy = happy+1000;
   trial(i) = happy*(N-deaths)^2;
end

plot(trial)
indexmax = find(max(trial) == trial);
maxvalx = happy(indexmax)

function [deaths,y,t] = simulation(transmission, recover, exposed, delta, happy)
   N = 330000000;
   I0 = 20;
   E0 = 0;
   S0 = N;
   T = 365;
   R0= transmission/recover;
   y0 = [S0; E0; I0; R0];
   tspan = [0 T];
   [t,y] = ode45(@(t,y) seir_model(t,y,transmission,exposed,recover,N, delta,happy),tspan,y0);
   deaths = 0;
   for i = 1:length(y(:,3))
      deaths = .5*floor(((deaths + .001*y(i,3) + 1000000*1.32*(N-happy)/N))) ;
      y(i,4) = y(i,4) - deaths;
      y(i,5) = deaths;
   end
   %plot(t,y);
   %xlabel('Days');
```

```
    %ylabel('Number of individuals');
    %legend('Susceptible','Infectious','Exposed','Recovered','Deaths');
end

function dydt = seir_model(t,y,transmission,exposed,recover,N,delta,happy)
    S = y(1);
    E = y(2);
    I = y(3);
    % Equations of the model described above
    dS = (-transmission*S*I/N+delta*recover);
    dE = (transmission*I*S/N - exposed*E);
    dI = (exposed*E - recover*I + delta*recover+happy*(exposed));
    dR = (recover*I + delta*recover);
    dydt = [dS;dE;dI;dR];
end



% Matlab code for Nowak Basic Model
function xdot = f (x, t)
  % beta = 1e-11;
  beta = 1.195e-10;
  k = 93571;
  u = 1.73e-4;
  v = 4.53e-5;

  xdot (1) = k - u * x (1) - beta * x (1) * x (2);
  xdot (2) = x (2) * (beta * x (1) - u - v);
endfunction
% used ode45
% US population and infected propulation starting Apr 2020
initState = [331e6, 324339];
% 3 years simulation
t=1:1:156
```