***Essential Workers*: Background epidemiological model**

On December 2019, the Chinese government informed the rest of the world that a new disease was spreading within its population. Shortly after, the disease spread to multiple countries and across continents. This disease known as COVID-19 is caused by the coronavirus SARS-CoV-2. The COVID-19 global pandemic has caused over 6.1 million recorded cases and over 373,000 deaths, as of June 1st, 2020.

An introduction to epidemiology and the SIR model

An epidemic occurs when a disease spreads over a short period of time affecting many people in a region. Meanwhile, a pandemic is an epidemic that has spread into multiple regions and/or countries. For centuries, scientists have worked in understanding and predicting epidemic's behavior as to control and prevent the spread of diseases.
The SIR model is one of the simplest models capable of capturing the dynamics of infection spread. In this model the population is divided in three groups: Susceptible, S; Infected, I; and Recovered (or Removed), R (see Figure 1). The number of individuals belonging to each group changes across time and is determined by a series of differential equations:

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

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

$$\frac{dR}{dt} = \gamma I \tag{1}$$

Where β is the infection rate and γ is the recovery rate (1/T_I, 1/days to recovery). Using these values, we can calculate R_0 which is the basic reproduction number of an infection, as β/γ. Although it does not describe the whole epidemic dynamics, R_0 is commonly used as an indicator of the epidemic's strength [1].
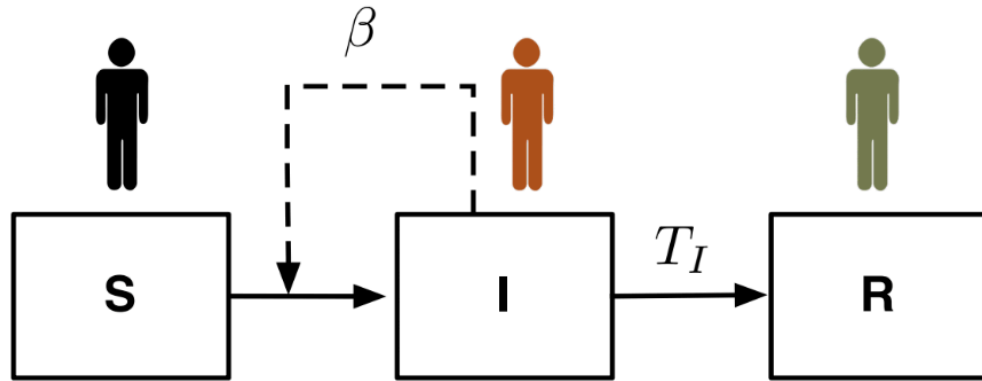
Figure 1: Depiction of an SIR model. Diagram by Joshua S. Weitz, 2019

Case study: SARS-CoV-2

Early estimates of the severity of the pandemic show a peak in infections around June for the US [2] (Figure 2a). Although calculated using individual-based models, the results are highly similar to predictions derived from SIR models. Furthermore, multiple studies regarding the global pandemic use modifications of the classic SIR model.

Surprisingly, we do not seem to observe this peak in the current US case data, but rather a slowly declining plateau [3] (Figure 2b). It's been hypothesized that the "lack of a peak" occurs as a side effect of averaging new cases in multiple locations in the country [4], that is, the US is not experiencing "one epidemic" but rather multiple ones. Overall, these epidemics do follow standard SIR curves.
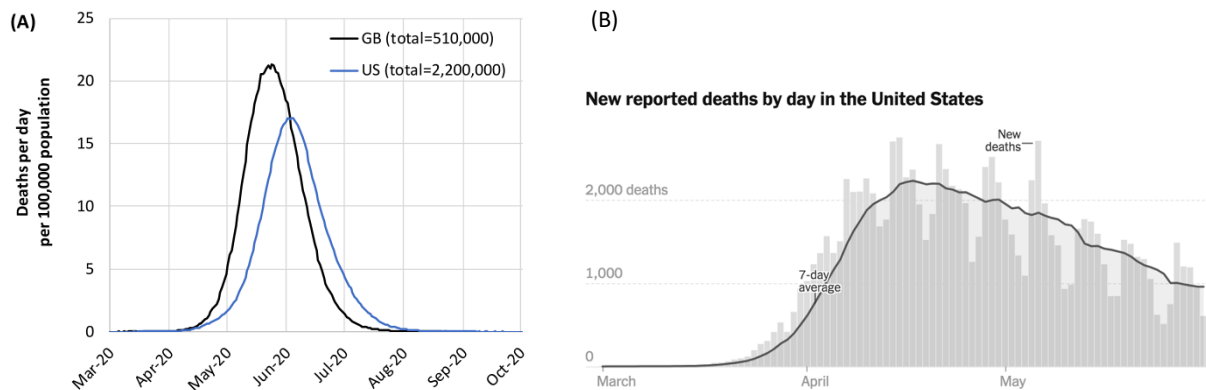

Figure 2: a) Early prediction of death toll for the US COVID-19 pandemic. B) New York Times COVID-19 tracking map, accessed on June 1st.

Essential Workers: A toy model

The Essential Workers Game simulates the life of different essential workers in the spam of three weeks. Although not actively playing, there is a background town population whose infection state may change overtime and affect the lives of the essential workers.

To represent the evolving population, we use a classic SIR model where non-players can be either Susceptible, Infected, or Recovered. We use equations (1) to describe the change in the population with parameters biologically relevant to the COVID-19 pandemic (See Table 1).

Parameter	Value	Reference
β (Infection rate)	0.4/days	[2]
γ (Recovery rate)	1/10 days	[2]
Infectiousness time	10 days	[5]
Infection probability	0.05	[6]
$R_0 = \beta / \gamma$	0.4/0.1 = 4	-

Table 1: Parameter values for *Essential Workers*, representing the 2020 COVID-19 pandemic. Predicted R_0 of 0.4/0.1 = 4. Which is within the expected range for SARS-CoV-2 [10].

To start the model, we use a set of initial conditions that mock those of New York City on April 15th, 2020, when the case growth rate was at its highest (Table 2). Using real-life data from the New York Times tracking service we estimate that on April 15th about 6% of the NYC population was actively infectious (assuming an average infectiousness period of 10 days [5], and assuming 10 unrecorded cases for every recorded case [7,8]). We assume the cumulative number of cases on April 5th as an estimate of recovered/removed individuals by April 15th (in line with the 10 days infectiousness estimates), which results in 0.05% of the population being recovered at the beginning of the game. We run the model for 21 days (42 game shifts), which gives of an estimate of the expected proportion of susceptible, infected and recovered people we would expect at those times if shelter in place and other policies were not implemented (Figure 3).

	Total	Proportion in an 8 million population
Susceptible (S)	7,426,210	~93%
Infected (I)	529,270	~6%
Recovered / Removed (R)	44,520	~1%

Table 2: Initial population state mocking NYC on April 15th 2020, estimated from NYT tracking data (https://www.nytimes.com/interactive/2020/us/coronavirus-us-cases.html).
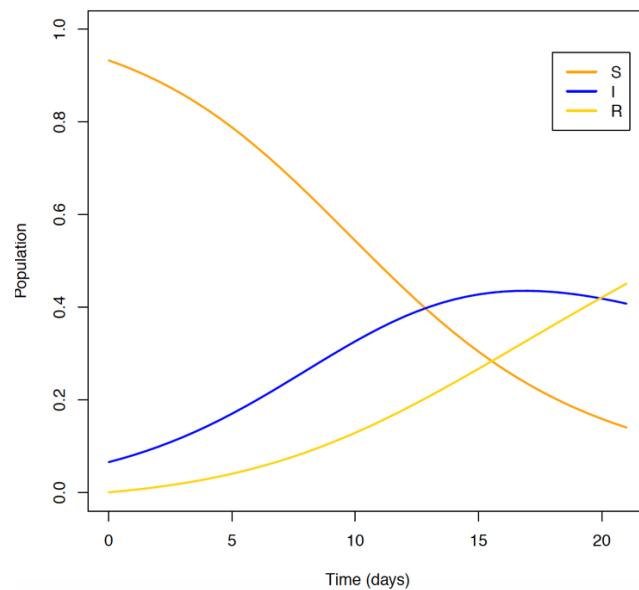
Figure 3: Background population evolution for the game using discussed parameters and initial conditions, simulated over the span of 3 weeks.

To describe the probability of a player being infected when going out, we model the probability of getting infected in one place as a function of the current state of the background population, the number of individuals in the place, and the mixing (number of contacts that occur). As we have discussed, the SIR model calculates the number of susceptible, infected and recovered individuals in the background population at any given time. Using this information and the number of people in one place we can calculate the expected number of infected individuals in a given place at any given time. For example: if we there are 100 people in a restaurant, and 10% of the population is infected, we would expect a number of 10 infected people in the restaurant in that moment in time. Next, if we know that in a restaurant you get in contact with a 50% of the people present, we would expect that you will run into 5 infected people. Now, if we know the probability of being infected given contact with one infected person, we can calculate the probability of getting infected given the number of infected contacts you had. To simulate these probabilities, we use a random number generator for a binomial distribution that with tell us at any given event whether you "get infected" or not.

Scientists have estimated a household infection rate that ranges between 57% and 15% percent [6,9]. Nonetheless, contact and time spent is way higher within household members than in random interactions. To account for this, we have decided on an infection probability upon contact of 5% (10 times and 3 times lower than the highest and lowest household estimate, respectively), see Table 2.

Corollary: Models have a bunch of assumptions, man. Here, we have made our best to capture real data from the COVID-19 pandemic and shape it into an educationally useful system.

References

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