

# Modeling Disease Spread

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MTH 443 Final Project

## Abstract

*This paper is an analysis to the SIR model regarding COVID-19. I will discuss the impact of changes in the basic reproductive number,  $R_0$ , to the outcomes of the SIR model, and use data from the pandemic to discuss how different interventions impact the value of  $R_0$ .*

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### • SIR Model & Basic Reproduction Number

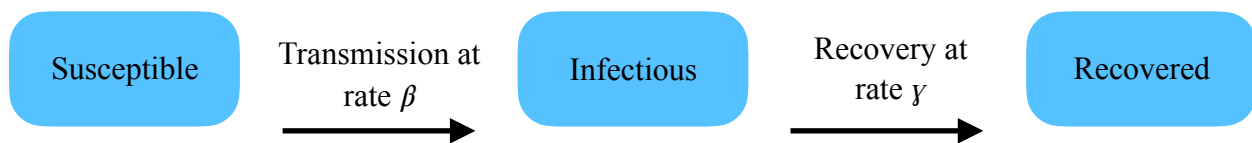
Compartmental models in epidemiology can be a powerful tool to assist animal health policy development and infectious diseases prevention and control<sup>[1]</sup>. The **SIR model** is one of the compartmental models. It was developed by Ronald Ross, William Hamer, and others in the early twentieth century<sup>[2]</sup>. The basic ideas of **SIR model** we use today are based on Kermack and McKendrick in 1927<sup>[3]</sup>. The **SIR model** computes the theoretical number of people infected with a contagious illness in a closed population over time<sup>[4]</sup>. It is particularly suitable when dealing with a large number of population<sup>[5]</sup>. The model contains three compartments.

**S** stands for the number of **susceptible** individuals. The notation is  $S(t)$ , meaning the individuals not yet infected with the disease at time  $t$ .

**I** stands for the number of **infectious** individuals. The notation is  $I(t)$ , meaning the individuals who have been infected and are capable of spreading the disease to susceptible individuals at time  $t$ .

**R** stands for the number of **recovered** individuals. The notation is  $R(t)$ , meaning the individuals who are recovered at time  $t$ . Individuals in this category are not able to be infected again or infect others<sup>[3]</sup>.

Suppose a fixed population  $N(t)$ , the **SIR model** follows that  $N(t) = S(t) + I(t) + R(t)$ .



$$dS/dt = -\beta SI/N$$

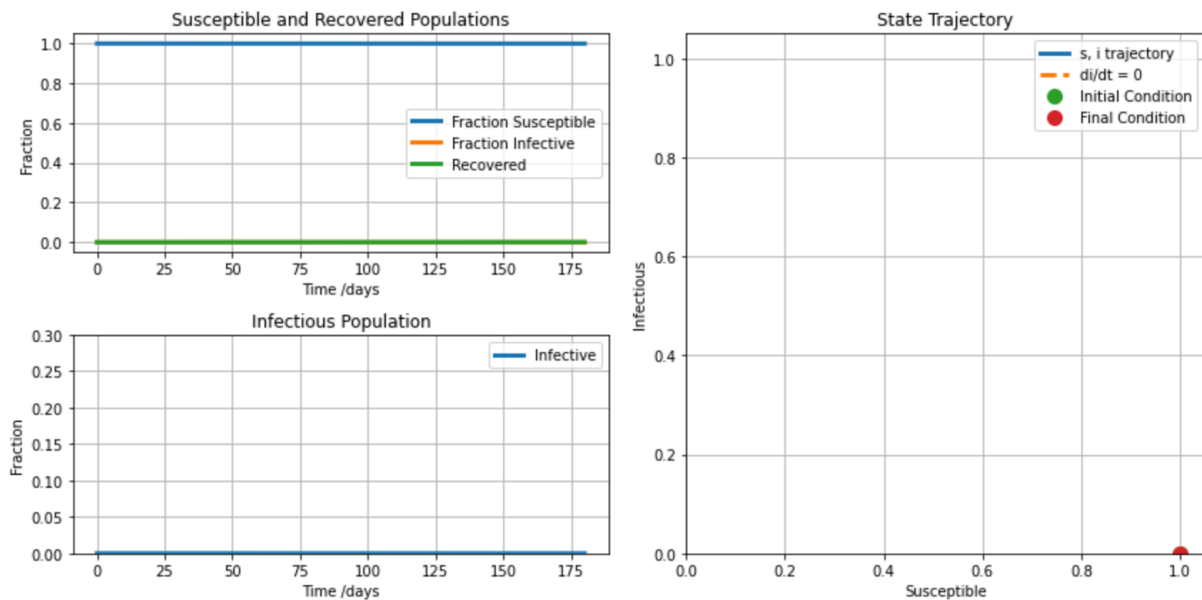
$$dI/dt = \beta SI/N - \gamma I$$

$$dR/dt = \gamma I$$

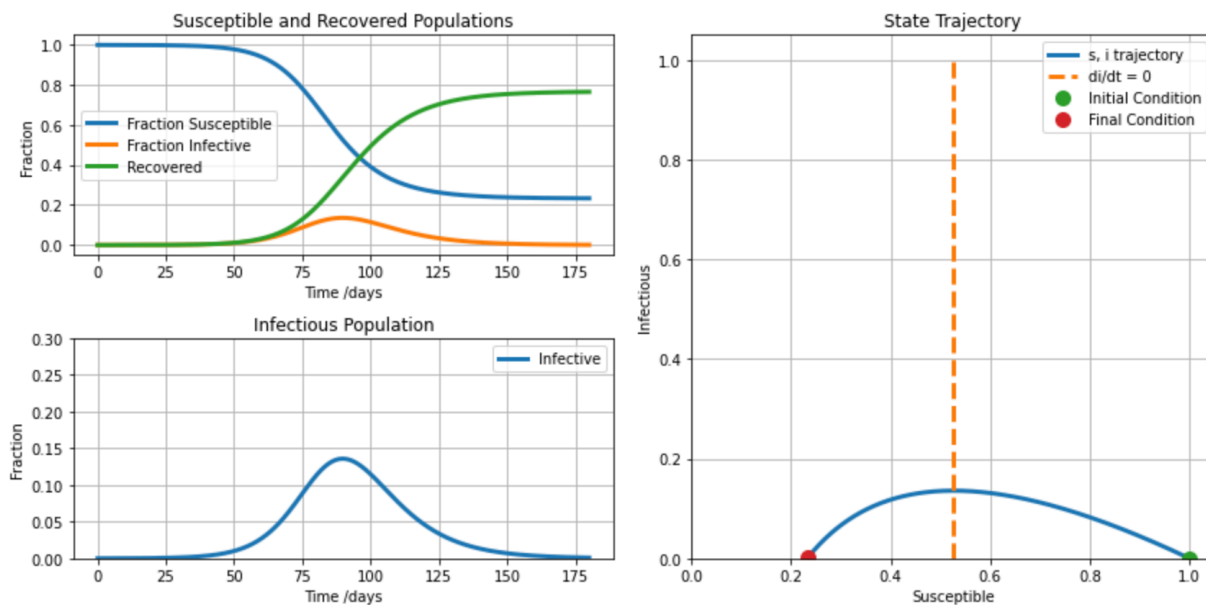
The **basic reproduction number**,  $R_0$ , is the expected number of cases produced by one case of infection in a susceptible population. Typically, when  $R_0 > 1$ , the infection start spreading in a population. The larger the  $R_0$ , the harder to control the epidemic. When  $R_0 < 1$ , the epidemic will start to disappear<sup>[6]</sup>.

$$R_0 \propto \left( \frac{\text{infection}}{\text{contact}} \right) \cdot \left( \frac{\text{contact}}{\text{time}} \right) \cdot \left( \frac{\text{time}}{\text{infection}} \right)$$

I modified the Python code from GitHub to find two plots with  $R_0$  less than 1 and  $R_0$  greater than 1 [7].  $R_0 = \frac{\beta}{\gamma}$



$R_0 = 0.9$



$R_0 = 1.9$

## • Flatten the Curve

December 31th, 2019, Wuhan Municipal Health Commission, China, reported a cluster of cases of pneumonia in Wuhan, Hubei Province. A novel coronavirus was identified<sup>[8]</sup>. According to the CDC (Centers of Disease Control and Prevention), this new coronavirus is similar to SARS-CoV, then it was named SARS-CoV-2. The disease caused by this virus was named COVID-19. The COVID-19 began spreading in Wuhan, China. The disease was growing fast, then it spread across several countries and affected large number of people. Finally, it became a pandemic<sup>[9]</sup>.

Researchers have modified the classic SIR model in several ways when describe the spread of COVID-19. For example, the susceptible-exposed-infectious-recovered (SEIR) model by Samuel Mwalili and others. The fourth and fifth order Runge-Kutta methods was using to solve the model equation. The result shown the pandemic will persist without strong control measures, and quarantine of contacts and isolation of cases can help stop the spread of virus<sup>[12]</sup>.

Another example is a modified SIR model with characteristics by Ian Copper and others. The researchers thought the classic SIR model is rather simplistic and cannot take into consideration. *“In particular, one of the major assumptions of the classic SIR model is that there is a homogeneous mixing of the infected  $I$  and susceptible  $S$  populations and that the total population  $N$  is constant in time. Also, in the SIR model, the susceptible population  $S$  decreases monotonically towards zero.(Copper<sup>[13]</sup>)”* They thought these assumptions are not valid in the case of COVID-19, since it spread around globe at different time. They developed a new SIR model that does not consider the total population  $N$ , but take the susceptible population  $S$  as a variable which can be adjusted at different times<sup>[13]</sup>. *“Thus, our model is able to accommodate surges in the number of susceptible individuals in time, whenever these occur and as evidenced by published data, such as those in that we consider here.(Copper<sup>[13]</sup>)”*

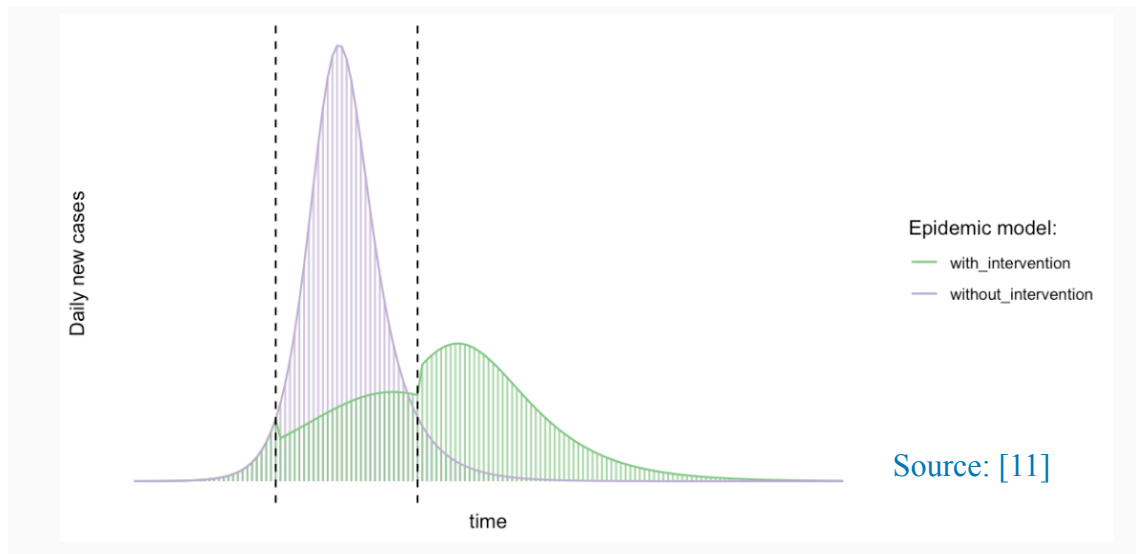
Flattening the curve is a public health strategy to slow down the spread of coronavirus during the COVID-19 pandemic. The curve that being flattened is the epidemic curve. The health care system has a limited capability, the infected individuals may exceeds that capability during a pandemic. Flattening the curve means to slow down the spread of virus, then infected individuals at a time reduced. The total number of infections will stay the same and the period time of the pandemic will be longer. Therefore, the health care department can treat more infected people<sup>[10]</sup>. It can also win time to find better treatment forms and develop the vaccine<sup>[11]</sup>.

One research study by Höhle showed two ways of reduce  $R_0$  in order to fallen the curve. In his paper, he calculated  $R_0$  as  $N\beta/\gamma$ , so the first way is to reduce the number of contacts person have with each other which is make  $\beta$  smaller. The second way is to reduce the duration for how long people are effectively spreading the disease, for example by quarantine which is make  $\gamma$  larger. He construct the following equations:

$$\beta(t) = \begin{cases} \beta_0 & \text{if } t \leq t_1, \\ \beta_1 & \text{if } t_1 < t \leq t_2, \\ \beta_2 & \text{if } t_2 < t \end{cases}$$

where  $\beta_0$  is the ordinary  $\beta$  value of the disease.

With large reduction of the contacts within the interval  $[t_1, t_2]$  and then  $\beta_1 < \beta_2$ . With  $\beta_1 = r_1\beta_0$  and  $\beta_2 = r_2\beta_0$  such that  $r_1$  is less than or equal to  $r_2$ . The two epidemic curves are as follows<sup>[11]</sup>:



### • Expectations in Different Types of Interventions

There are different types of interventions might affect the actual value of  $R_0$ . For example, social distancing, masking and lockdowns. All three ways can reduce  $R_0$ , but I expect that they do not have the same effect size. In my expectations, the lockdown is the most powerful way to reduce the spread of the virus. Stores and restaurants closed by the government's order can largely reduced the contact with each other. People are forced stay home is more controllable than the other two interventions. The other two interventions can also reduce  $R_0$ , but much more slower than the lockdown. It is hard to keep social distancing in high population area. At the beginning of the pandemic, masks were not produced enough. People did not wearing masks because there was nowhere to buy masks or wearing masks made from loosely woven fabric or only one layer which cannot protect them from coronavirus according to CDC<sup>[14]</sup>. The other two interventions also involve consciousness of individuals. Not all people are willing to keep social distancing or masking.

### • Data Examine for $R_0$

Here, I am going to examine the data for  $R_0$  for different states from <https://rt.live> to see if my assumption was right. I chose the top four population states: California, Texas, Florida and New York. At this website,  $R_0$  is referred to as  $R_t$ .

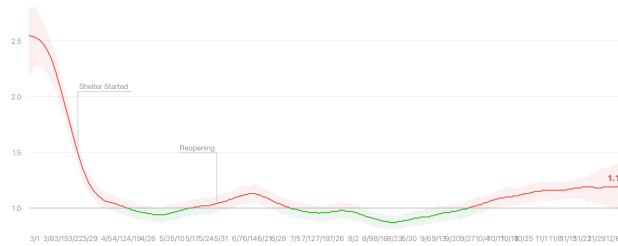
## California

Tweet Share

Current  $R_t$  **1.19** Cases **1,418,370** Tests **26,041,556**

### Effective Reproduction Rate - $R_t$

$R_t$  is the average number of people who become infected by an infectious person. If it's above 1.0, COVID-19 will spread quickly. If it's below 1.0, infections will slow. [Learn More](#)



Here is a screenshot of  $R_0$  in California. At the shelter started,  $R_0$  was 1.53, it started drop to the lowest  $R_0$  0.94 then increased. At reopening,  $R_0$  was 1.04, then increased to 1.13 then drop.

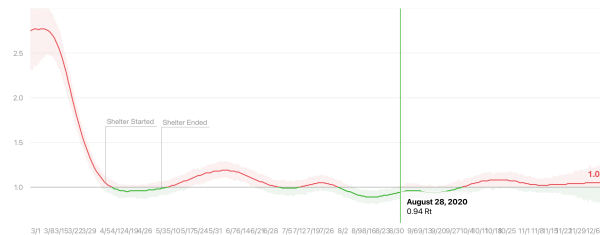
## Texas

Tweet Share

Current  $R_t$  **1.05** Cases **1,252,885** Tests **11,621,180**

### Effective Reproduction Rate - $R_t$

$R_t$  is the average number of people who become infected by an infectious person. If it's above 1.0, COVID-19 will spread quickly. If it's below 1.0, infections will slow. [Learn More](#)



Here is a screenshot of  $R_0$  in Texas. At the shelter started,  $R_0$  was 1.06, it started drop to the lowest  $R_0$  0.95 then increased. At shelter ended,  $R_0$  was 0.98, then increased to 1.19 then drop.

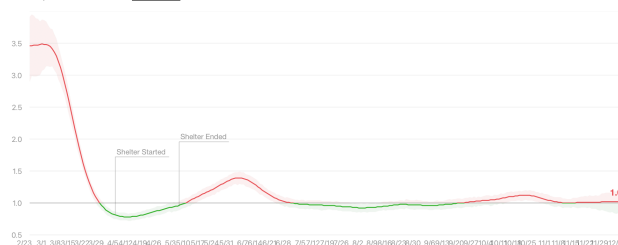
## Florida

Tweet Share

Current  $R_t$  **1.02** Cases **1,057,987** Tests **13,363,418**

### Effective Reproduction Rate - $R_t$

$R_t$  is the average number of people who become infected by an infectious person. If it's above 1.0, COVID-19 will spread quickly. If it's below 1.0, infections will slow. [Learn More](#)



Here is a screenshot of  $R_0$  in Florida. At the shelter started,  $R_0$  was 0.82, it started drop to the lowest  $R_0$  0.78 then increased. At shelter ended,  $R_0$  was 0.95, then increased to 1.39 then drop.

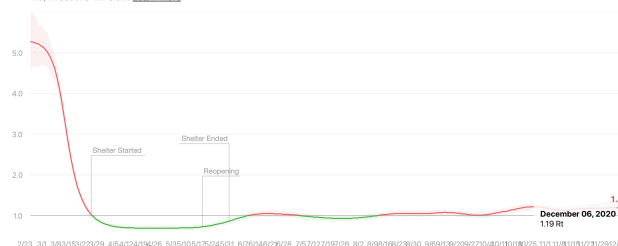
## New York

Tweet Share

Current  $R_t$  **1.19** Cases **733,064** Tests **21,104,040**

### Effective Reproduction Rate - $R_t$

$R_t$  is the average number of people who become infected by an infectious person. If it's above 1.0, COVID-19 will spread quickly. If it's below 1.0, infections will slow. [Learn More](#)

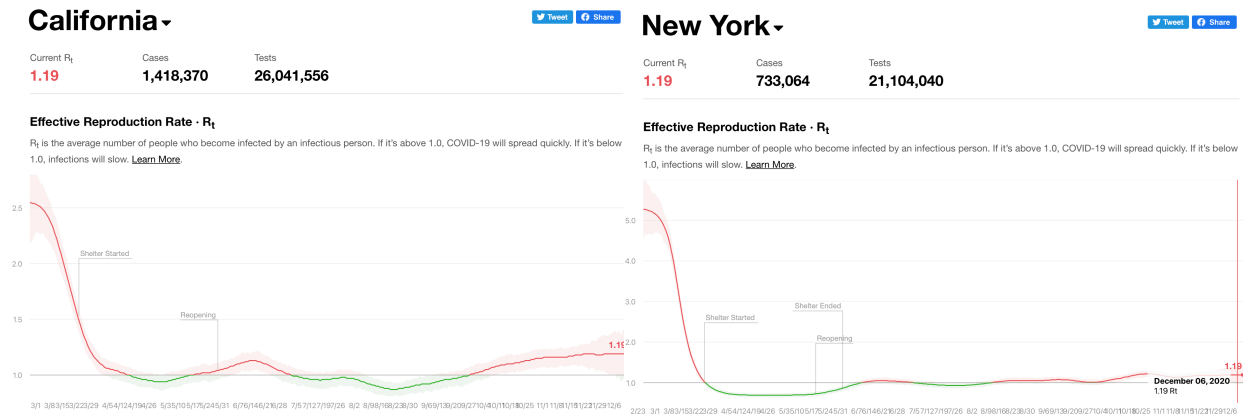


Here is a screenshot of  $R_0$  in New York. At the shelter started,  $R_0$  was 1.06, it started drop to the lowest  $R_0$  0.69 then increased. At reopening,  $R_0$  was 0.72. At shelter ended,  $R_0$  was 0.85. then increased to 1.05 then drop.

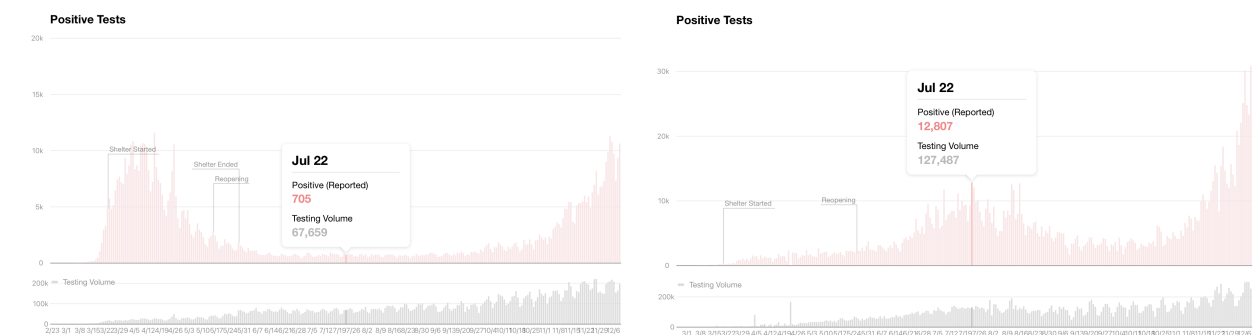
After the shelter ended (reopening for California), four states averaged a 25% increased  $R_0$  before drop. Hence, the data match my expectation, lockdown can largely reduce  $R_0$ .

## • Data Compare for NY and CA

Below, I will compare the data between NY and CA and discuss differences in the value of  $R_0$  over time and compare that with differences in the total number of cases over time and intervention strategies taken by each state. Data source: <https://rt.live>.



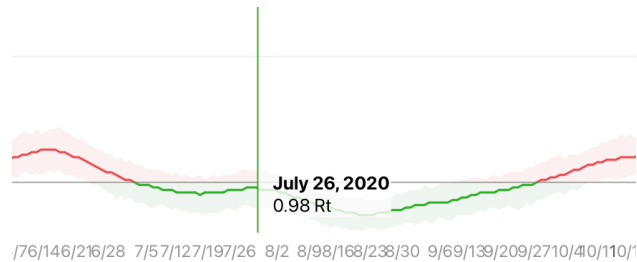
Until December 10th, 2020. The total tests for California is 26,041,556, and 21,104,040 in New York. The total cases for California is 1,418,370, and 733,064 in New York. The total tests in NY are 23% less than CA but the total cases in NY are 93% less than CA. In CA the shelter started three days earlier than NY. In NY, when the shelter started  $R_0$  was close to one, but in CA  $R_0$  was 1.53. The reopening in NY was nine days earlier than CA with a 0.32 lower  $R_0$ . However, the average positive tests during shelter to reopening was around 6,000 in New York but around 2,000 in CA. With the  $R_0$  increasing in both NY and CA after reopening, NY has a large decreasing in positive tests compare with the large increasing in CA. The figure below is the positive tests in NY (left) and CA (right).



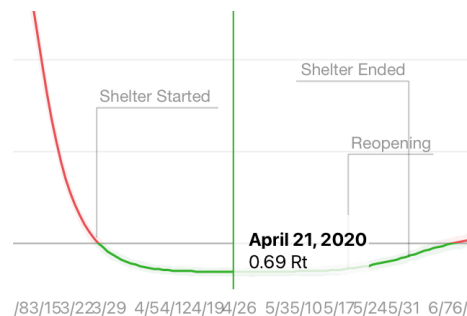
A recent large increase in total positive tests in both states are from November 10th which is around Thanksgiving. More people are traveling can be the cause of this increase.

According to Andy Markowitz: “New York has had a mask requirement since April 17. Gov. Andrew Cuomo's order applies to anyone over age 2 who can “medically tolerate a face covering” when in a public place and unable to maintain social distancing.”, and “Californians have been required since June 18 to mask up in ‘most settings outside the home.’ The policy was updated June 29 to exempt children under age 2.”<sup>[16]</sup>”

Below is a plot of  $R_0$  in CA. We can see there is a drop starting July. According to the Office of Governor Gavin Newsom: “The state launched ‘Wear A Mask’ public awareness campaign encouraging Californians to use face coverings – one of the best ways people can protect themselves and others from the virus. (7/2/2020)<sup>[15]</sup>”



Below is a plot of  $R_0$  in NY, after New York started the mask mandates, the state had their lowest  $R_0$  ever, 0.69.



With the increasing of positive tests,  $R_0$  still dropped. As a result, masking is a good way of interventions to reduce  $R_0$ .

## • Disease Spreads in Different Geographical Locations

Although COVID-19 became a pandemic, but there are still some diseases found only in focal geographic regions or in isolated populations. There are some factors could affect that. According to Mary E. Wilson’s study on Geography of infectious diseases: lack of interaction with the outside world could be one factor that allow an infection become geographically isolated. “For example, the fungus *Coccidioides immitis*, which causes coccidioidomycosis, thrives in surface soil in arid and semiarid areas with alkaline soil, hot summers and short, moist winters; it is endemic in parts of south-western USA, Mexico and Central and South America. People become infected when they inhale arthroconidia from soil.”<sup>[17]</sup>”

## • Why is the Total Number of Cases Important

Just examining the basic reproduction number alone doesn't give the full story about what is happening. It is also important to take into account the total number of cases as well. Take California and New York as an example.



In July 22,  $R_0$  in CA was 0.97 but the positive tested individuals were 12,807. In April 15, NY had low  $R_0$  of 0.69, but also had a very high positive tested number of 11,571. Even with a lower  $R_0$  value alone does not mean the total positive tested number is also low. Behind a lower  $R_0$  value of could be a higher positive tested number. Combining both number can help us better understanding the pandemic.

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