Modelling Global Outbreaks and Proliferation of COVID-19

By Leon Tribe and Robert Smith?

M any of us are experiencing the effects of a pandemic for the first time. We may not be sick, but COVID-19 has disrupted our lives in some manner. From the trivial shortage of toilet paper to massive social and economic upheaval, a microscopic virus is affecting all of us in one way or another. A medical crisis has not affected the modern world this significantly since the 1918–1919 Spanish influenza pandemic, which was caused by an H1N1 virus.

While advanced models of diseases often employ differential equations to assess virulence, it is clear that SARS-CoV-2 has two distinct vectors of infection: community transmission and "recent arrivals." The discontinuous nature of recent arrivals introduces multiple sources of infection and makes analysis more difficult. Each new outbreak requires individual study. So, what other techniques can we apply to gain a level of certainty in uncertain times?

Determining a Threshold for Action

Although there is growing evidence that a strong national intervention—adopted as soon as possible—is key to economic recovery, we can utilize network theory to determine a threshold at which we personally choose to act. If we assume that an individual knows 100 unique people, each of whom has 100 friends, that makes 10,000 people within two degrees of separation from the original individual. Therefore, it makes sense to act before the ratio of confirmed cases of a disease reaches a level of 1 per 10,000 within a population.

Why is this so? Because at this level in our idealised network, you know someone who knows someone with the disease. When the density of disease victims exceeds this value, it generates an increased risk of direct exposure to an infected individual. Coincidentally, the threshold of 1 in 10,000 also corresponds to the point at which many countries began to introduce strong measures. For example, the day Italy crossed this threshold was the day the country effectively went into lockdown.

Unfortunately, it seems that this threshold is probably too late for adequate national intervention. For instance, Italy saw the density of cases increase to 1 in 1,000, which strained and broke down infrastructure. While beyond the scope of our current analysis, it would be interesting to consider national action before and after this 1 in 10,000 "line in the sand"—or even the 1 in 100,000 threshold as a predictor of rapid recovery.

Predicting the Threshold's Approach

Because a density of 1 in 10,000 provides a theoretical limit as to when effective action can commence at a national and personal level, we may want to predict the threshold's approach. Assuming that a disease initially spreads with minimal hindrance, we can rely on the properties of exponential growth to guide us.

A common property of exponential growth that researchers frequently use for analysis is the doubling rate of a disease. This rate is the exponential mirror image of the logarithmic half-life and tells us how long it takes for the number of infections to double. The growth of COVID-19 has been quite aggressive in some countries, with a doubling time of as little as 1–2 days. For many countries, however, it takes 3–5 days for the number of cases to double. It is relatively simple to consider the population of a country and-assuming consistent exponential growth—determine when that country will reach the critical density threshold of 1 confirmed case per 10,000 people.

The key assumption here is one of consistent exponential growth. In fact, few countries have exhibited a constant doubling time much past a week or two. Therefore, due to the sensitivity of exponential growth to initial conditions, we can only rely upon any prediction based on this technique for a week (or possibly two) ahead of the event.

Predicting a Slowing of Growth

Once we are in the midst of aggressive growth, what methods can we use to determine our progress? One common technique is to consider a log plot of the growth. If the curve is concave up, the doubling time is shortening and the disease is becoming more aggressive. If the curve is flat, the disease is exhibiting consistent exponential growth and will eventually overwhelm the region. If the curve is concave down, growth is slowing and—with time—may be brought under control.

An alternative option involves determining where a disease has progressed on its characteristic curve. We can split the typical sigmoidal curve of an illness' confirmed cases into three phases:

- 1. Exponential growth
- 2. Linear growth
- 3. Logarithmic flattening

By considering the best least-squares fit of these curves to the confirmed-cases data, we gain an understanding of our status in terms of disease progress (see Figure 1).

Utilizing this technique while accounting for the percentage of recovered cases allows us to define the moment when a country has recovered from disease. For example, with the slowing growth of new cases and the progressive increase in recoveries, the active cases (= confirmed cases – deaths – recoveries) follow a bell curve. By defining a percentage level of recovery, we can make predictions as to when this level is crossed.

Prediction in the Absence of Recovery Data

In March, the Johns Hopkins Coronavirus Resource Center temporarily stopped releasing the numbers of recovered cases for countries of the world; the data was simply too unreliable. In the absence of recovery data, how else can we gain insight into a country's recovery?

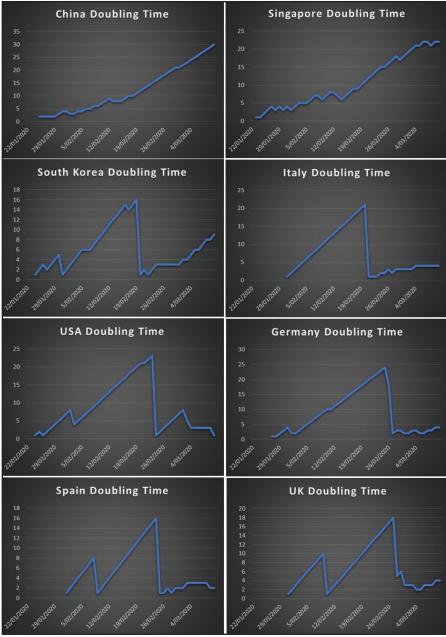


Figure 2. Doubling times of COVID-19 for a selection of countries. A higher (longer) doubling time is better. Figure courtesy of

One option is to reconsider the doubling time of COVID-19's growth. Examining the daily trend of the doubling time yields a "fingerprint" of the disease and its progress. Figure 2 identifies a selection of countries and their doubling times through March 11, 2020. Each plot has a unique fingerprint, but some share common characteristics. For example, China and Singapore showed an increasing doubling time—i.e., a move to recovery early on—although both countries experienced a setback in the middle of February before beginning to recover again.

South Korea and Italy both had their first COVID-19 outbreaks in January and began to recover quickly until around February 20, when strong resurgences occurred. The countries both began recovering again over the next two weeks, but their ultimate outcomes have been quite different. By March 25, South Korea's doubling time was over 20 days and the country was approaching a national recovery. Italy's doubling time was about one third of South Korea's, and the nation was far from recovering.

In contrast, the U.S. began recovering from its early outbreak but then saw a set-

back around the end of February. This new outbreak, presumably the one in the state of Washington, showed signs of an initial recovery but then grew out of control; the graph in Figure 2 dips again about a week later. Germany saw no strong recovery after its COVID-19 outbreak in late February, and the doubling times have remained flat, which indicates ongoing exponential growth.

Lastly, Spain and the U.K. faced an initial outbreak at the start of February from which there was recovery, only to experience a secondary outbreak in the middle of the month. There was again recovery until a third wave at the end of February, from which both countries struggled to recover as quickly.

With the absence of recovery data, our definition of national recovery uses the duration of infection as the doubling time, since this implies that COVID-19 is well-controlled. Once a country has a doubling time of this length, we can consider them recovered. In the case of China, for example, a doubling time of 30 days correlated with around 80 percent of all patients having recovered or died.

What Did We Learn?

In summary, understanding the growth patterns of a fast-moving disease in the early stages of a pandemic is a challenging task. One-size-fits-all models are not appropriate, and long-term predictions—such as equilibrium values of differential equations, which use infinite time as a proxy for the distant future—are likely to be futile. Instead, adapting models to short-term data enables a deeper understanding of the existing data while also allowing us to make predictions when data is absent.

Mathematics indicates that the fast-moving nature of COVID-19 necessitates fast-moving models. By determining crucial thresholds and adapting short-term "data fits," modelling offers us a glimpse into the future of the pandemic across the world and clearly indicates that we must act as early as possible to mitigate spread. Even if this information comes too late for the case of

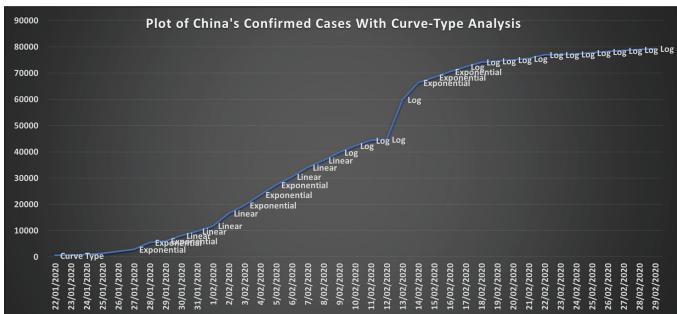


Figure 1. Time course of COVID-19 in China using linear, logarithmic, and exponential best fits. Figure courtesy of

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COVID-19, the lessons learned from this disease will apply to the next one. Infectious diseases will always be with us.

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