



SFI TRANSMISSION

COMPLEXITY SCIENCE FOR COVID-19

STRATEGIC INSIGHT: R_0 is just an average: the transmission rate varies widely, and outbreaks can be surprisingly large even when the epidemic is subcritical.

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Much of the coverage of COVID-19 talks about R_0 , the average number of people each sick person infects. If R_0 is bigger than 1, cases grow exponentially, and an epidemic spreads across the population. But if we can keep R_0 below 1, we can limit the disease to isolated outbreaks and keep it under control.

But R_0 is only an average. Your ability to practice social distancing depends on whether you are a first responder or healthcare worker, whether you have to work in close quarters, or whether you can work comfortably from home. (I'm one of the lucky few getting paid to work from my garden.) It depends on how seriously you take your government's warnings and how seriously your government takes the warnings of public health experts. And it depends on the structure of your family and your home.

As a result, R_0 varies wildly, not just from region to region, but across social space, as well. In New Mexico, Santa Fe has very few new cases, but there has been an explosion of cases in rural areas due to lack of running water, multi-generational homes, and other factors. As of April 26, 47 percent of our confirmed cases are in Native American communities, even though Native Americans make up only 11 percent of New Mexico's population. Clearly R_0 is larger in some parts of the state and of society than others.

Even if $R_0 < 1$, outbreaks can be surprisingly large. Suppose you meet 10 people while you are contagious, and you infect each one with a probability of 8 percent. The average number of people you infect is $10 \times 0.08 = 0.8$, less than 1. But those you infect may infect others in turn, and so on. If an outbreak starts with you, how many "descendants" will you have? A classic calculation shows that, if $R_0 = 0.8$, then the average number of people in this chain reaction is $1/(1 - 0.8) = 1/0.2 = 5$. But, like R_0 itself, this is only an average. Like earthquakes and forest fires, outbreaks have a "heavy tail" where large events are common.

Here is a visualization of 100 random outbreaks. The average size is indeed 5, and most outbreaks are small. But about 1 percent of those outbreaks have size 50 or more, ten times the average, and in this simulation the largest of these 100 outbreaks has size 82. This tail gets heavier if R_0 is just below the phase transition at $R_0 = 1$. If $R_0 = 0.9$, the average outbreak size is 10, but 1 percent have size 140 or more.

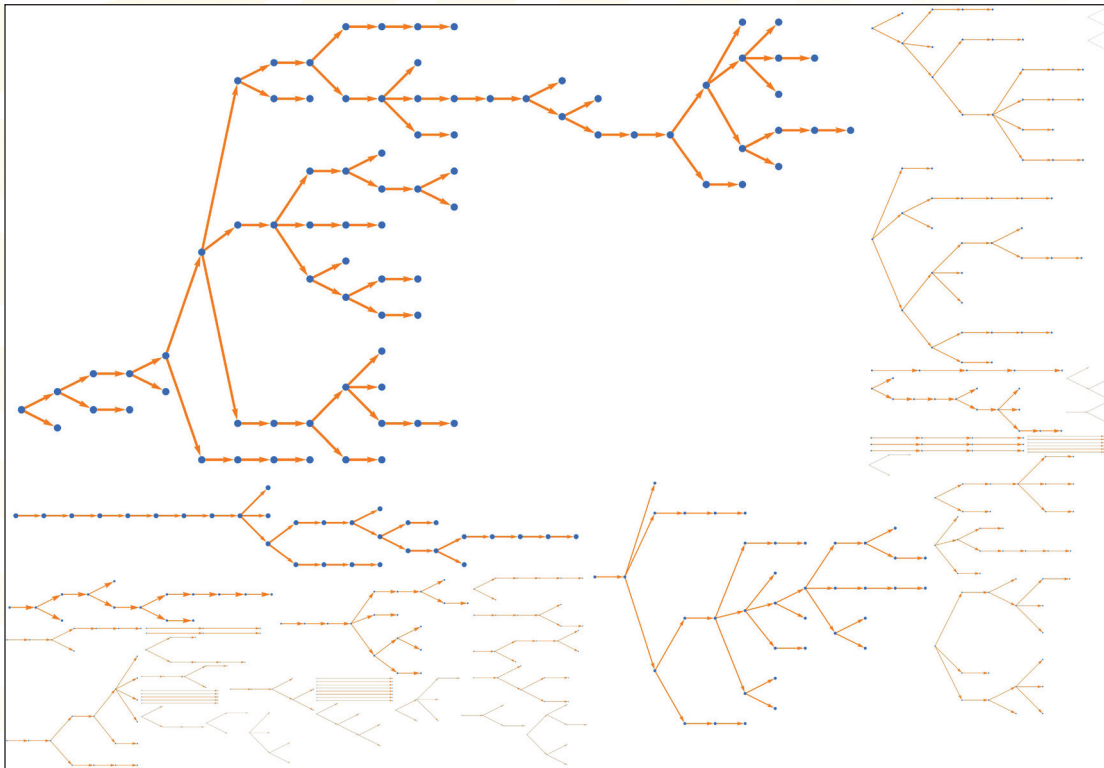


Figure 1. A hundred random outbreaks in a scenario where each sick person interacts with 10 others, and infects each one with probability 8 percent. Here $R_0 = 0.8$ and the average outbreak size is five, but 1 percent of the outbreaks have size 50 or larger, and in this run the largest has size 82.

This tail has real effects. Imagine 100 small towns, each with a hospital that can handle 10 cases. If every town has the average number of cases, they can all ride out the storm. But there's a good chance that one of them will have 50 or 100, creating a "hot spot" beyond their ability to respond.

The tail of large events gets even heavier if we add superspreading. We often talk of "superspreaders" as individuals with higher viral loads, or who by choice or necessity interact with many others. But it's more accurate to talk about superspreading events and situations — like the Biogen meeting, the chorus rehearsal, or the pork processing plant, as well as prisons and nursing homes — where the virus may have infected many of those present.

Suppose that 20 percent of cases generate one new case, 10 percent generate 2, 4 percent generate 5, and 1 percent “superspread” and generate 20 (and the remaining 65 percent infect no one). The average number of new cases is again $R_0 = 0.8$. Let's generate 100 random outbreaks with this new scenario.

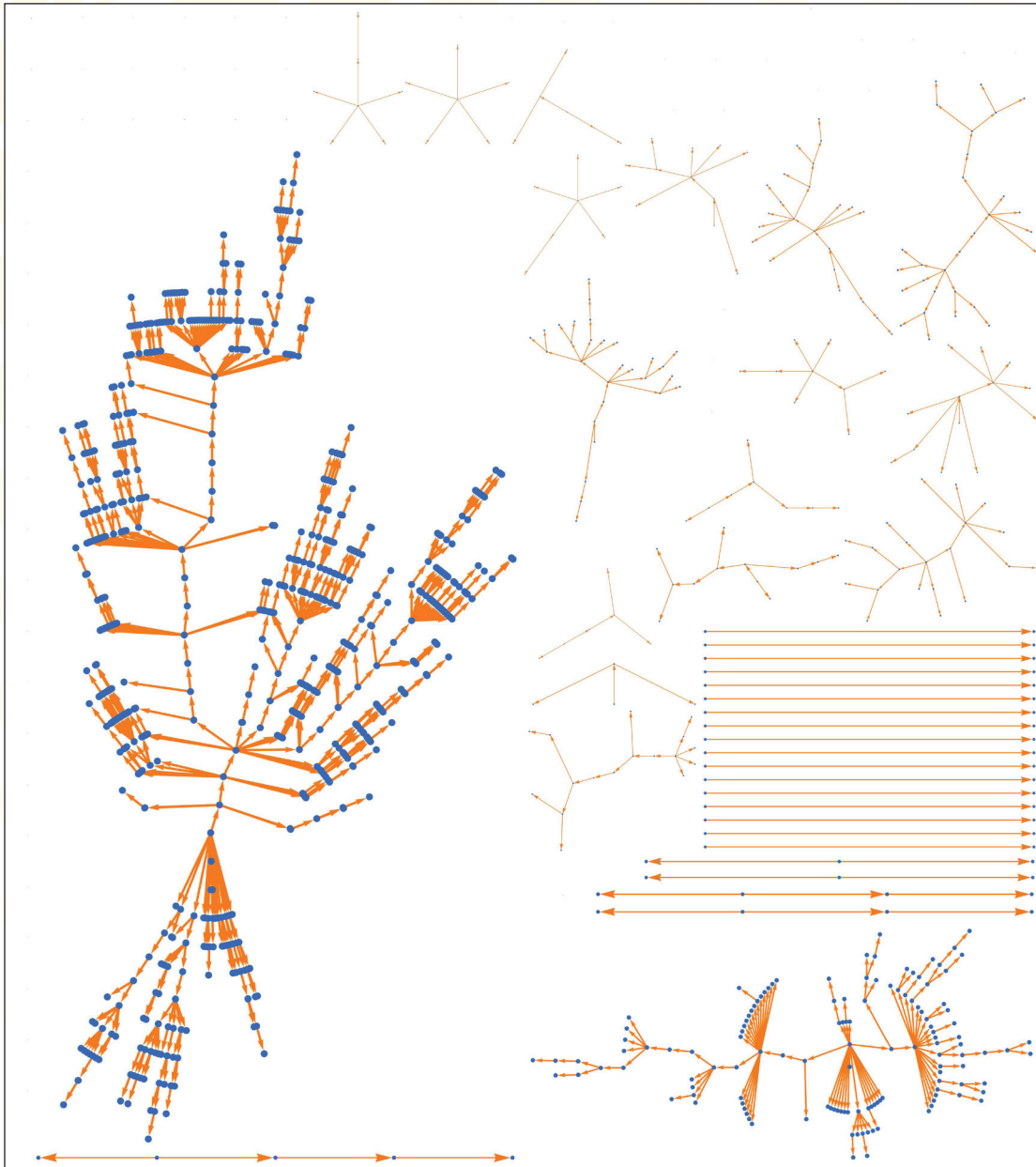


Figure 2. A hundred random outbreaks in a scenario with superspreading, where 1 percent of the cases infect 20 others. As in Figure 1, we have $R_0 = 0.8$ and the average outbreak size is 5, but now the heavy tail of outbreaks is much heavier. In this run the largest outbreak has size 663.

The average outbreak size is still 5, but now the tail is much heavier. If just one of the 100 original cases is involved in superspreading, we get a large outbreak. If there are several generations of superspreading, the size multiplies. As a result, large outbreaks are quite common, and the largest one in this simulation has 663 people in it.

What does all this mean? First, it can be misleading to look at statewide or national averages and celebrate if R_0 seems to be falling below 1. The epidemic could still be raging in particular places or among particular groups.

Second, even if R_0 is below 1, we need to prepare for hot spots. Even if the average outbreak is small, large outbreaks will occur due to superspreading or simply by chance. If we do a fantastic job at testing and contact tracing — using both technology and human effort — we will get this pandemic under control, but for the foreseeable future there will be times and places where it flares up and strains local resources. And through those flare-ups, we have to do our best to help each other, and hope that intelligent, generous voices prevail.

REFERENCES

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