Majumder, a researcher at Harvard Medical School and Boston Children's Hospital who had previously helped predict the spread of Saudi Arabia's MERS epidemic of 2014 and the West African Ebola outbreak shortly thereafter, agreed with that statement—at that point, it wasn’t clear whether the culprit was an infectious pathogen capable of jumping from one person to the next. But when murmurs of possible human-to-human transmission started to circulate a few weeks later, she and her Harvard colleague Kenneth Mandl set out to calculate a metric—the pathogen’s basic reproductive number (R0)—that would hint whether it could cause an epidemic.

Simply explained, R0 represents the average number of people infected by one infectious individual. If R0 is larger than 1, the number of infected people will likely increase exponentially, and an epidemic could ensue. If R0 is less than 1, the outbreak is likely to peter out on its own. R0 alone cannot definitively forecast an outbreak, but “it’s like an early warning system, in a lot of ways, for the possibility of an epidemic or pandemic,” Majumder says.

To estimate R0 for the coronavirus now known to the world as SARS-CoV-2, Majumder and Mandl picked a simple mathematical model that can infer the R0 from the curve of rising, case numbers as well as another metric that describes how quickly an infection spreads from one person to the next, based on previous studies of MERS, another coronavirus infection. On January 23, they published one of the first estimates for the R0 for SARS-CoV-2 infection: 2.5, significantly higher than on previous studies of MERS, another coronavirus infection.

Defining R0

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—Nelly Yatich, epidemiologist in Nairobi, Kenya

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To estimate R0, epidemiologists use the reproductive number R0, which describes the initial spread of a pathogen to a human host. R0 is defined as the average number of secondary infections caused by a single infectious individual in a fully susceptible population. It is a key metric in understanding the potential for an epidemic to occur. A basic reproductive number R0 of 1 indicates that each infectious individual will transmit the infection to exactly one other individual, on average. If R0 is greater than 1, the disease will spread; if R0 is less than 1, the disease will die out. R0 can be calculated using a mathematical model or estimated from data on the growth of the outbreak.


Fast forward a month, and the world did have a pandemic on its hands. Models around the world scurried to forecast the spread of SARS-CoV-2 and the COVID-19 disease it causes in their own country or region. Some models assumed that R0 was fixed, while others were more flexible, allowing R0 to change depending on factors such as public health interventions and population mobility. The challenge was to make assumptions about the factors that determine human movement, which can limit the precision of their models and the accuracy of the predictions they generate.

R0 is a metric that is, first of all, poorly measured. And second, it’s informing models that result in public health action, says Juan B. Gutierrez, a mathematician at the University of Texas at San Antonio. “If we get it wrong, the public health action will be misplaced.”

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Defining R0

WHAT IS R?

The reproductive number R describes the average number of individuals a person infected with a particular pathogen infects. It depends on how that pathogen is transmitted as well as how often people come into contact with each other—factors that could vary depending on a pathogen’s strain and on the time and location of an outbreak. Scientists typically distinguish between R0, the basic reproductive number that describes disease transmission at the beginning of an outbreak in a fully susceptible population, and Re, the effective reproductive number that describes transmission once measures such as social distancing or vaccination campaigns have been introduced. Re is typically much lower than R0.

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