Estimating the COVID-19 R number: a bargain with the devil?



The deeper understanding Faust sought Could not from the Devil be bought. But now we are told By theorists bold All we need know is R_n.¹

Robert May, 1936-2020

Bob May's limerick alludes to both the promises and dangers of characterising epidemic control by a single number. The basic reproduction number (R_0) is the average number of infections produced by a single infectious person in a population with no immunity. R_0 has a close relative named the effective reproduction number (R), which is the average number of infections produced by a single infected person in a population with partial immunity. In *The Lancet Infectious Diseases*, You Li and colleagues² estimate how the imposition and lifting of non-pharmaceutical interventions (NPIs) changed the R number for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in 131 countries in the first half of 2020.

If the *R* value is less than 1, an epidemic eventually dies out because each infected person generates less than one new infection. Ending an epidemic by keeping the *R* value below 1 could take a long time if there are currently many infections, like the proverbial small rudder on a big ship. However, when the *R* value is higher than 1, the epidemic could continue to grow. *R* can also change over time: NPIs such as closing schools, physical distancing, and mask use can reduce *R*. Hence, *R* is often used to gauge whether pandemic mitigation is working.

Li and colleagues compared daily estimates of *R* at the country level against a database describing which NPIs each country applied and when. Generally, they found that imposing NPIs reduced *R*, and lifting them later on increased *R*. School closure, a public events ban, requirements to stay at home, and internal movement limits—both when being imposed and when lifted—had the biggest individual effects, changing *R* between 3% and 25%.

NPIs in combination were even more effective. The combined effect of school and workplace closure, a ban on public events and gatherings of more than ten people, internal movement limits, and a stay at home requirements reduced R by 52% (95% CI 29–68) 28 days after they were introduced. The R_0 value for

SARS-CoV-2 lies somewhere between 2 and $3.^3$ Hence, early pandemic interventions must reduce R by between 50% and 67% to bring it below 1. Li and colleagues' estimates do not include the effects of contact tracing and isolation. Despite this omission, the estimate suggests that it might have been exceedingly difficult to flatten the curve in spring, 2020, had the R_{\circ} for SARS-CoV-2 been a little higher.

But R is not without shortcomings. Just as our body-mass index does not tell us everything about our state of health, a single number cannot provide a complete picture of the state of a pandemic. National-level estimates can hide local heterogeneity. Seasonal differences in contact patterns from spring to autumn are not captured by the short time windows used in many epidemiological studies. Reporting delays, stochastic effects, and superspreading can also bias R. Moreover, R does not tell us what proportion of infections are caused by an infected individual before symptom onset. This crucial distinction for infection control might explain why severe acute respiratory syndrome coronavirus did not cause a pandemic, whereas SARS-CoV-2 did, despite their comparable R_o values.4,5

Li and colleagues discuss some of these limitations and also raise the issue of behavioural inertia. Timelines of decision making lend the perception that governments can turn NPIs on and off like a switch. But in fact, populations can take weeks to adjust their mobility patterns in response to imposition of NPIs.^{2,6} This effect probably contributes to the authors' finding that NPIs did not exhibit their maximal effect on *R* until up to 28 days later.

R promises crystal clarity in a time when there are no crystal balls. Hence, the allusion to R_{\circ} as a bargain with the devil. Statistician George Box has been widely paraphrased as writing "All models are wrong, but some are useful." I like to re-paraphrase this as some models are useful precisely because they are wrong. A model including all the real-world details of a study system would no longer be a model, because it would be the system itself.

Despite R's imperfections, the findings of Li and colleagues tell us that NPIs work and which ones work best. This information is crucial, given that some NPIs

Lancet Infect Dis 2020

Published Online October 22, 2020 https://doi.org/10.1016/ 51473-3099(20)30840-9 See Online/Articles https://doi.org/10.1016/ 51473-3099(20)30785-4 have massive socioeconomic effects. In a similar vein, transmission models that project COVID-19 cases and deaths under different NPI scenarios could be highly valuable for optimising a country's portfolio of NPIs.⁸⁻¹⁰ Moreover, I think *R* provides a social utility that epidemiologists can easily overlook. The success of large-scale NPIs requires population adherence. *R* can stimulate populations to act and gives them useful feedback on the fruits of their labour. Perhaps this is one reason that *R* has entered our vernacular in 2020.

I declare no competing interests.

Chris T Bauch

cbauch@uwaterloo.ca

Department of Applied Mathematics, University of Waterloo, Waterloo, ON N2L 3G1, Canada

1 Anderson RM, May RM, eds. Population biology of infectious diseases. Report of the Dahlem workshop on population biology of infectious disease agents Berlin 1982, March 14–19, vol 25. Berlin: Springer Science & Business Media. 2012.

- 2 Li Y, Campbell H, Kulkarni D, et al. The temporal association of introducing and lifting non-pharmaceutical interventions with the time-varying reproduction number (R) of SARS-CoV-2: a modelling study across 131 countries. Lancet Infect Dis 2020; published online Oct 22. https://doi.org/10.1016/S1473-3099(20)30785-4.
- Hilton J, Keeling MJ. Estimation of country-level basic reproductive ratios for novel coronavirus (SARS-CoV-2/COVID-19) using synthetic contact matrices. PLoS Comput Biol 2020; 16: e1008031.
- 4 Bauch CT, Lloyd-Smith JO, Coffee MP, Galvani AP. Dynamically modeling SARS and other newly emerging respiratory illnesses: past, present, and future. Epidemiology 2005; 16: 791–801.
- 5 Moghadas SM, Fitzpatrick MC, Sah P, et al. The implications of silent transmission for the control of COVID-19 outbreaks. *Proc Natl Acad Sci USA* 2020; 117: 17513-15.
- 6 Google. COVID-19 Community Mobility Reports. https://www.google.com/covid19/mobility (accessed Sept 5, 2020).
- 7 Box GEP. Science and statistics. J Am Stat Assoc 1976: 71: 791–99.
- 8 Karatayev VA, Anand M, Bauch CT. Local lockdowns outperform global lockdown on the far side of the COVID-19 epidemic curve. Proc Natl Acad Sci USA 2020; 117: 24575-80.
- 9 Tuite AR, Fisman DN, Greer AL. Mathematical modelling of COVID-19 transmission and mitigation strategies in the population of Ontario, Canada. CMAJ 2020; 192: e497–505.
- 10 Firth JA, Hellewell J, Klepac P, et al. Using a real-world network to model localized COVID-19 control strategies. Nat Med 2020; 26: 1616–22.