Faculty of Science and Engineering

School of Engineering, Computing and Mathematics

2022-04

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http://hdl.handle.net/10026.1/19118

10.1111/1740-9713.01628 Significance Wiley

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Covid lockdowns in the UK: Estimating their effects on transmission

UK citizens have lived through three lockdowns over the course of the Covid-19 pandemic. What effect have these restrictions had on the transmission of the virus? *Emily Prestige, Julian Stander* and *Yinghui Wei* investigate

The Covid-19 pandemic has impacted lives around the world and has led many countries to adopt large scale mitigation strategies – perhaps the largest of which are "lockdowns", in which the public are told to stay at home for all but a few exempt activities.

Many countries have implemented several lockdowns during the course of the pandemic – some lasting weeks, others lasting months. And while citizens generally have adhered to their government's stay-at-home orders, the question of whether lockdowns are a necessary and proportionate response to coronavirus has been frequently raised.

This investigation focuses on the effect of national lockdowns in the UK, in the hope of answering the question many have asked: "Do we need lockdowns?" While the debate goes deeper than simply whether they are effective, it is important for governments, and the public, to understand if and when lockdowns work.

In light of the Omicron variant, some countries may re-implement, or continue to have, mitigation strategies such as lockdowns. Therefore it is important that we have tools to investigate the influence of mitigation measures using data.

Why lock down?

Lockdowns have a simple purpose: to limit people's movements and interactions in order to break chains of viral transmission. Without restrictions, people infected with a virus have many opportunities to inadvertently infect others, leading to a rapid increase in new infections. With restrictions in place, opportunities to infect others are reduced, as are new infections.

Transmission models, such as the Susceptible-Infected-Removed (SIR) model (see box 1 and significancemagazine.com/648), allow officials to monitor a pandemic's progression, determine what mitigation measures are necessary, and assess how effective those measures have been.

Associated with the SIR model is the instantaneous reproduction number R_t , where t is time, which we measure in days. R_t – referred to more commonly as "the R number" – is the average number of susceptible people an infected individual would infect. The monitoring of R_t has been consistent throughout the pandemic, and was often quoted by officials as support for their policy decisions – even as early as April 2020 (youtu.be/GJZ_Q8RGZWg).

When R_t is less than 1, the pandemic is considered under control and will die out at some point in the future. When R_t is bigger than 1, the number of infected people can grow so fast as to be out of control, leading to a new or sustained outbreak. We

estimate R_t from the end of February 2020 to mid-July 2021 to investigate the impact of national lockdowns on the transmission of Covid-19 in the UK.

Data and assumptions

The data used in this investigation came from the UK government's official coronavirus dashboard (coronavirus.data.gov.uk). We work with the number of people who had tested positive for Covid-19 and the number of people who had died and had Covid-19 registered as one of the causes of death. The study period is from 30 January 2020 to 27 July 2021, including three UK-wide lockdowns:

- 23 March 2020 to 15 June 2020
- 5 November 2020 to 3 December 2020
- 5 January 2021 to 29 March 2021

We define the end of each lockdown as the point when non-essential businesses were allowed to re-open.

Estimation of R_t needs data on the number of people who were initially susceptible to Covid-19, and we used a mid-2019 population estimate from the Office for National Statistics as an approximation for this (bit.ly/3GiKc3B).

Estimation of R_t also needs data on the number of people who recover, and while the UK did not record this, it is possible to estimate recovery using information about infection and death. For Covid-19, researchers estimated that people can be infectious up to 10 days from the onset of their symptoms, which themselves develop up to 14 days after infection (bit.ly/3KYwK8x). Government guidance states that a person died of Covid-19 if death occurred within 28 days of their first positive test result (coronavirus.data.gov.uk/metrics). We therefore assumed that the time taken from infection to recovery was 28 days, during which the individual was classed as infected. It is for this reason we began our estimations of R_t 29 days from the first positive case. We also assumed that once recovered, individuals were immune to catching Covid-19 again. This is a simplifying assumption as the scientific community is still working to gain a full understanding of the immune response to the disease (bit.ly/3s6YtLI).

Implementation in R

The SIR model is defined by the three states which an individual can be in, and describes how the number of susceptible S(t), infected I(t), and removed R(t) changes over time *t*. An individual begins as susceptible, in which state they can remain, or they can go on to be infected and subsequently removed – via recovery or death. Movement between the three states is characterised by a positive infection rate β and a positive removal rate γ .

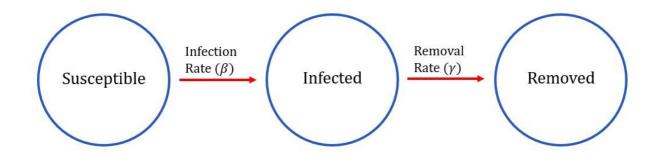
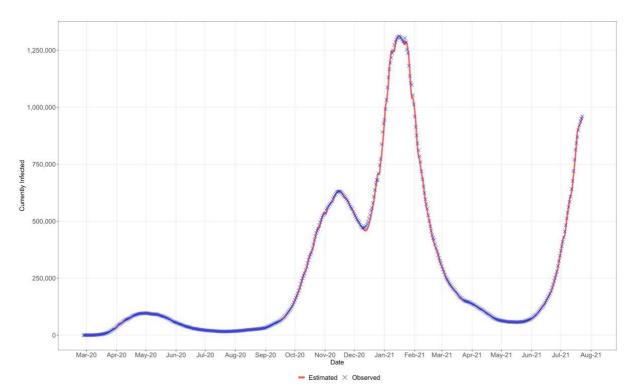


Figure 1: Representation of the SIR model.

Figure 1 shows us that a higher value of β would increase the speed at which people become infected, and a higher value of γ would increase the speed at which people are removed.

We used the modFit function (bit.ly/3ri5MRt) from the FME package (bit.ly/3L1aLxB) in the statistical software R to estimate the parameters β and γ of the SIR model. As part of this we employed the ode (bit.ly/3gbKgaR) function from the deSolve (bit.ly/3GdmBkM) package to solve three ordinary differential equations (ODEs; see box 1) using initial values obtained from the data and various combinations of values of β and γ . The process minimised the residual sum of squares, which is based on the difference between the observed number of infections and the values predicted by the SIR model. We then used the optimal β and γ over moving eight-day windows of data (initial value, followed by a week's data) to estimate the instantaneous reproduction number R_t (as defined by the equation in box 1). We obtained similar results using R's optim function (bit.ly/3uiNIOC).



Results

Figure 2: The observed number of infections and the number predicted by the SIR model.

Figure 2 shows that the number of people infected with Covid-19 is in good agreement with one day ahead predictions from the moving SIR model. We believe that the overall high quality of fit justifies the use of the SIR model to estimate R_t .

Another way we can visualise these infections is by using a logarithmic scale on the vertical axis, as shown in Figure 3. This simply changes the way in which we look at our data, so that smaller data points are not flattened at the bottom of the graph.

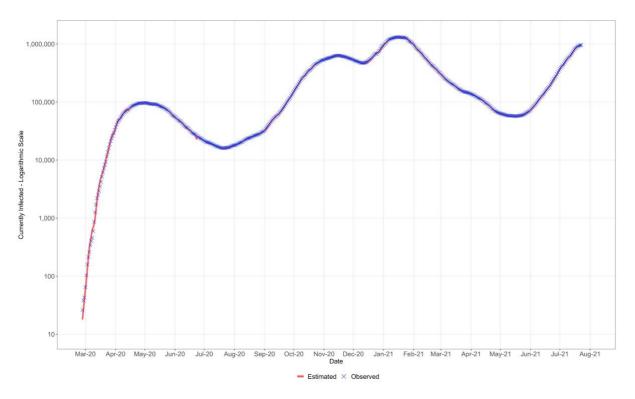


Figure 3: The observed number of infections and the number predicted by the SIR model, using a logarithmic scale for the number of infections.

Figure 3 shows that a drastic increase in the number of infected people occurred between March and April 2020, which does not appear in such an obvious way in Figure 2. When we use a logarithmic scale, a straight line increase corresponds to exponential growth. Exponential growth in the number of people infected with Covid-19 is a worrying situation for governments as it means that health services can quickly become overwhelmed.

We used the parameter estimates from the SIR model to compute the instantaneous reproduction number R_t , as shown in Figure 4.

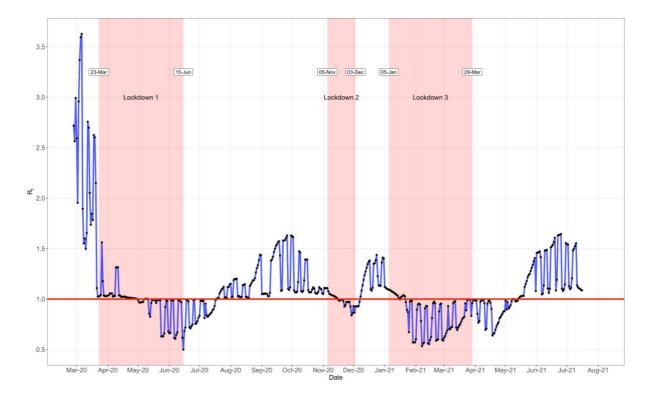


Figure 4: The instantaneous reproduction number R_t . A red horizontal line has been added at $R_t = 1$ to show whether the pandemic was growing quickly ($R_t > 1$) or was under control ($R_t < 1$).

Figure 4 shows that R_t significantly decreased during national lockdowns. For example, the first national lockdown caused R_t to fall from large values before the lockdown to values considerably below 1. We observe that R_t was around or below 1 through some of the warmer summer months of 2020, during which there were some interim measures, and then increased to reach high values at the end of August 2020.

During the second lockdown, R_t fell from around 1.1 to around 0.95 just as the lockdown was lifted. After this lockdown, the value of R_t started to increase rapidly. This suggests that the length of the lockdown may influence the effect it has on reducing transmission – implying that a short lockdown may only delay the inevitable.

During the third lockdown, R_t fell from around 1.15 to values around 0.6. The value of R_t subsequently remained at or below 1 for at least a month from mid-April 2021, after which it started to rise. There were still some measures in place during this time until 19 July 2021 when most restrictions were removed (bit.ly/3Gn7qWa).

Limitations

The quality of statistical estimates depends on the quality of the data on which they are based. Covid-19 detection and recording procedures have generally improved over time, meaning that we have greater trust in our estimations as time proceeds. We are more confident in our results towards the end of the time period than we are at the beginning. However, as the UK does not record data on those who recover from Covid-19, we had to estimate the number of people who recovered and so we may be limited in the accuracy of our estimations of R_t .

In this article we have made some simplifying assumptions, one of which was that the chance of reinfection was negligible. This assumption means that our estimates of R_t may be lower than the true reproduction number. Another simplification made was in the use of a SIR model, as opposed to a SEIR – Susceptible-Exposed-Infected-Removed – model. We know that transmission can occur before people become symptomatic, so the use of an SEIR model may provide better estimates of R_t .

Quantifying the uncertainty associated with estimates of R_t cannot be obtained through the method of estimation employed in this article in a straightforward and reliable way. However, it is possible to quantify uncertainty through the use of alternative methods, such as Bayesian inference. Maruotti, Ciccozzi and Divino have recently articulated, in the context of Italy, why R_t should be used with care.¹ They discuss issues associated with testing procedures, the length of the window of the data used and other assumptions that can have a considerable effect on estimations. These authors also point out that some modelling assumptions may not hold consistently across different regions of a country.

Discussion

We have used the SIR model to estimate the instantaneous reproduction number R_t for the Covid-19 pandemic in the UK from the end of February 2020 to mid-July 2021. These estimates have provided us with interesting and useful insights into the effects of national lockdowns in the UK.

The results of this investigation suggest that lockdowns reduce transmission rates after around two or three weeks, but this is likely to be a delay in the data. Other studies support this range of values, including one from Sebastiani, Stander, and Cortina Borja (bit.ly/3Ge40VD). The results also suggest that lockdowns continue to have an effect on transmission rates after they are lifted. However, this effect may be difficult to maintain if the lockdown led to a value of R_t that was under 1 for only a short time. Indeed, the value of R_t was still falling at the end of the second lockdown after which an increase soon occurred. This is in contrast to R_t being low for over a month towards the end of the first lockdown, with similar long-lasting low R_t values for over two months of the third lockdown. Following both the first and third lockdown, R_t remained below 1 for a further month. Therefore we may conclude that if lockdowns are lifted too quickly, their benefits are diminished.

Other studies, including work that the first author completed in their undergraduate dissertation, compare different approaches to estimating R_t and find that, whilst estimates vary across methods, the underlying trends (and related conclusions) are similar. Such studies have included the use of the Bayesian framework to learn about the SIR model parameters β and γ . One way that the Bayesian approach could be implemented in this case is through the use of Stan (mc-stan.org). Similar to the approach that we used, Stan provides us with a helpful function (bit.ly/3IUzTo5) that solves the ODEs for S(t), I(t), and R(t). The Bayesian approach allows us to incorporate our beliefs about the model parameters before seeing new data, and we can do this in a more and more precise way as our knowledge about Covid-19 increases.

The decision-making processes of policy makers has been influenced by a range of considerations including R_t , the number of hospitalisations, doubling rates, and

economic factors. We believe that policy makers should continue to make use of quantities such as R_t in their decision making processes as it is important to control spikes in cases caused by highly infectious variants of the virus, whilst energising and maintaining the economy going forward.

We know it is important that other factors associated with lockdowns should also be taken into consideration. While lockdowns may reduce transmission, we have seen that they can negatively impact a population's mental health.² Additionally, there are serious economic consequences to long-term protective measures – for example, each time a national lockdown has been implemented, there has been a fall in GDP (bit.ly/3APWHT8).

About the authors

Emily Prestige is a graduate of the BSc (Hons) Mathematics and Statistics degree at the University of Plymouth, and this article is based on their final year undergraduate project. They are currently undertaking an MSc in Medical Statistics at The London School of Hygiene & Tropical Medicine.

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Disclosure statement

YW is supported by a fellowship grant from the UK Medical Research Council (MR/W021358/1), which supports her secondment to the COVID-19 Longitudinal Health and Wellbeing National Core Study (MC_PC_20059).

Box 1: The SIR model and the R number

The SIR model is constructed using the following system of ordinary differential equations (ODEs):³

$$\frac{dS(t)}{dt} = -\beta \frac{I(t)S(t)}{N} \tag{1}$$

$$\frac{dI(t)}{dt} = \beta \frac{I(t)S(t)}{N} - \gamma I(t)$$
(2)

$$\frac{dR(t)}{dt} = \gamma I(t) \tag{3}$$

Here *N* is the total number of people who are susceptible to Covid-19 at the start of the epidemic, which we assume is the entire population, and we know that S(t) + I(t) + R(t) = N.

- Equation (1) describes the rate at which the number of susceptible individuals changes. This rate is always negative because susceptible individuals are becoming infected, and hence their number is constantly decreasing.
- Equation (2) describes the rate at which the number of infected individuals changes.
- Equation (3) describes the rate at which the number of removed individuals changes. This rate is always positive as an individual cannot leave the removed category and so *R*(*t*) can only grow.

The basic reproduction number R – which does not relate to time – is defined as the ratio of the infection rate to the removal rate:

$$R = \frac{\beta}{\gamma}.$$

We can then calculate the instantaneous reproduction number, R_t , using estimates of β and γ over time *t* measured in days.

References

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