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An explicit formula for minimizing the infected peak in an SIR epidemic model when using a fixed number of complete lockdowns

Eduardo D. Sontag[1,2]

[1]Departments of Electrical and Computer Engineering and Bioengineering, and affiliate of Departments of Mathematics and Chemical Engineering, Northeastern University, Boston, Massachusetts, USA

[2]Laboratory of Systems Pharmacology, Harvard Medical School, Boston, Massachusetts, USA

Correspondence
Eduardo D. Sontag, Departments of Electrical and Computer Engineering and Bioengineering, and affiliate of Departments of Mathematics and Chemical Engineering, Northeastern University, Boston, MA, USA.
Email: sontag@sontaglab.org

Abstract
Careful timing of nonpharmaceutical interventions such as social distancing may avoid high "second waves" of infections of COVID-19. This article asks what should be the timing of a set of K complete-lockdowns of prespecified lengths (such as two weeks) so as to minimize the peak of the infective compartment. Perhaps surprisingly, it is possible to give an explicit and easily computable rule for when each lockdown should commence. Simulations are used to show that the rule remains fairly accurate even if lockdowns are not perfect.

KEYWORDS
COVID-19, epidemics, lockdowns, mathematical epidemiology, SIR model

1 | INTRODUCTION

The year 2020 will be remembered for the COVID-19 (coronavirus disease 2019) pandemic, which is an individual-to-individual infection by SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2). An immediate way to stop transmissibility is to establish total lockdowns, as China and Northern Italy did early on in the outbreak.[1] Lockdowns and other NPIs (nonpharmaceutical interventions) such as quarantine and social distancing were soon implemented around the world. On the other hand, frustration with isolation rules and economic costs mean that, in most countries, long lockdowns are not feasible, nor is it easy to enforce even milder forms of NPIs.[2-4] However, relaxation of NPIs could lead to "second waves" of infections when the NPIs are relaxed. This motivates the search for optimally timing the start of multiple short NPIs so as to minimize the maximum peak of infective individuals. This article deals with that problem.

To be precise, we consider an SIR model with strict (no-contact) lockdowns, and assume that policymakers want to decide when to start each one of K of lockdowns, with respective lengths T_k, $k = 1, \ldots, K$. For example, the T_k's may all be equal, say two weeks. We provide an exact and very simple rule, which says that lockdowns should commence

whenever the number of infectious individuals reaches a certain level, namely, $I_{start} = (1 + K - (e^{-vT_1} + \ldots + e^{-vT_K}))^{-1}V_0$, where V_0 is a number that can be easily computed from the infectivity rate, recovery rate (v), and the initial populations of susceptible and infected individuals. The formula for I_{start} simplifies in the case in which all T_k's are equal, $T_k = T$, to just $(1 + K - Ke^{-vT})^{-1}V_0$. In addition, we show that there will be exactly K peaks of infected populations, all equal to this value. Observe that as the lockdown intervals become larger, $T \to \infty$, the best possible maximum peak is $V_0/(1 + K)$. (Using a larger value of T will lengthen the duration of the pandemic but, asymptotically, not change the peak value. If there is a hope for a quick cure or vaccines, this is not necessarily a good strategy.) Obviously, a perfect or near-perfect lockdown is not practical, except in jurisdictions where complete obedience can be strongly enforced, but this theoretical problem is nonetheless of interest. Moreover, studying this case also helps understand the problem with nonstrict lockdowns, as we will discuss.

1.1 | Infections and mathematical modeling

Infectious agents have critically influenced the history of mankind, with disease-causing pathogens constantly emerging or evolving. From the Plague of Athens (430–428 BC), to the fourteenth century Black Death that killed about a third of Europe's population, to the Yellow Fever epidemic in Philadelphia in 1793, in which a tenth of the population of the city perished, to the 1918 "Spanish flu" pandemic (which did not originate in Spain) that resulted in about 3%–5% of the world population dying, to the COVID-19 2020–2021 pandemic, infectious diseases have had major impacts on health, psychological and social well-being, medical advances (mRNA vaccines, for example), economics, politics, military history, and religious and racial persecution. Different types of pathogens are involved in infectious diseases. Viruses cause the common cold, influenza, measles, West Nile, and COVID-19, while anthrax, salmonella, chlamydia, and cholera are caused by bacteria, and protozoa give rise to malaria and trypanosomiasis (sleeping sickness). There are many mechanisms for transmission, including respiratory droplets (influenza, colds), body secretions (chlamydia), flies (trypanosomiasis), mosquitoes (malaria), and food or water (cholera). Control strategies include behavioral and sanitation changes (NPIs), vaccines, antibiotics, antiviral drugs. Notwithstanding this variety, there is a common mathematical structure.

The modeling of infectious diseases and their spread is an important part of mathematical biology, specifically mathematical epidemiology. Modeling is an important tool for gauging the impact of NPIs such as social distancing, masking, lock-downs, or school closings, as well as predicting/attenuating magnitude of peak infections ("flattening the curve" so as not to overwhelm ICU capacities), predicting/delaying peak infections (until vaccine/treatments available), and devising strategies for vaccination, control, or eradication of diseases. The social and political use of epidemic models must take into account their degree of realism. Good models do not incorporate all possible effects, but rather focus on the basic mechanisms in their simplest possible fashion. Not only it is difficult to model every detail, but the more details the more the likelihood of making the model sensitive to parameters and assumptions, and the more difficult it is to *understand and interpret* the model as well as to play "*what-if*" scenarios to compare alternative containment policies. It turns out that even simple models help pose important questions about the underlying mechanisms of infection spread and possible means of control of an epidemic.

Most mathematical epidemiology models incorporate some version of the classical SIR model proposed by Kermack and McKendrick.[5] We will restrict attention to this core model, which is suitable for describing initial stages of an infection in a single city, and also for modeling later stages when community spread becomes dominant. Mathematical models have long played a central role in epidemiology, and this has been especially true with the COVID-19 pandemic.[6-14] This includes control-theoretic aspects, especially optimal control.[15-18]

Mathematical models had a major impact on the political response to the COVID-19 pandemic. To quote from "Behind the virus report that jarred the U.S. and the U.K. to action" (*New York Times*, March 17, 2020):

> *The report [from Imperial College London], which warned that an uncontrolled spread of the disease could cause as many as 510,000 deaths in Britain, triggered a sudden shift in the government's comparatively relaxed response to the virus. American officials said the report, which projected up to 2.2 million deaths in the United States from such a spread, also influenced the White House to strengthen its measures to isolate members of the public.*

Of course, one should always keep in mind as well the following quote from Dr. Anthony Fauci, Director, National Institute of Allergy and Infectious Diseases, United States (*CNN*, May 05, 2020):

I have skepticism about models [of COVID-19], and they are only as good as the assumptions you put into them, but they are not completely misleading. They are telling you something that is a reality, that when you have miti- gation that is containing something, and unless it is down, in the right direction, and you pull back prematurely, you are going to get a rebound of cases.

2 | FORMULATION OF PROBLEM

We consider a standard SIR model for epidemics, which consists of three groups of individuals: those who are *susceptible* and can be passed on the pathogen by the *infectious* individuals, and the *removed* individuals, who are have either devel- oped immunity after infection or who have died. In SIR models, one does not include a flow back from individuals into the susceptible compartment. On longer time-scales, one may also allow for the fact those individuals in the removed group who are immune may eventually return to the susceptible population, which would happen if immunity is only temporary or if a pathogen has evolved substantially. The numbers of individuals in the three classes will be denoted by S, I, and R, respectively, and hence the name "SIR" model. See Figure 1, where we use the symbol "$\otimes$" to indicate that the number of new infected will depend both on the number of susceptibles and infectious (specifically, it will be a product in the classical SIR model to be discussed next, with a proportionality constant β), and ν denotes the flow to the recovered compartment. Observe that the "feedback" term implicit in the $\otimes$ effect means that this is not exactly a compartmental system, because for those, *the flow into* a compartment does not depend on the number of individuals in that compartment.

Mathematically, assuming that new infections are due to contacts between S and I individuals, and that the rate at which this happens is proportional to the numbers of such individuals, there results a system of three coupled ordinary differential equations as follows:

$$\dot{S} = -\beta SI \tag{1}$$

$$\dot{I} = \beta SI - \nu I \tag{2}$$

$$\dot{R} = \nu I. \tag{3}$$

From now on we will ignore the last equation since it does not affect the number of infectives. The initial state satisfies $S(0) = S_0 > 0, I(0) = I_0 > 0$. The positive parameter β (infectivity/contact rate) quantifies the transmission rate between the susceptible S and infected I individuals in a well-mixed population, and ν (recovery/death rate) is the rate of flow into the removed R compartment. We will assume that $\mathcal{R}_0 := \beta S_0/\nu > 1$; otherwise, the problem to be discussed is not interesting, as I decreases monotonically to zero if the condition does not hold. (This and other well-known facts about SIR systems are reviewed in Section 5; see also, for example, Reference 19.)

In the SIR model, NPIs are viewed as reducing the contact rate β. (More sophisticated models of social distancing have been widely studied, see, for example, References 20-26.) The reduction of β is modeled by a time-varying $\beta(t)$ where

$$\beta(t) = \begin{cases} \beta_0 & t \in J \\ \beta & t \notin J \end{cases}, \tag{4}$$

where $0 \leq \beta_0 < \beta$ are two fixed values, and $J \subseteq [0, \infty)$. In our work, J will be the union of a number K of intervals

$$J_k = [t_k, t_k + T_k], \quad k \in K$$

and *we will be taking $\beta_0 = 0$*, representing a strict or full lockdown. The lengths T_k of the respective intervals will be allowed to be arbitrary (but fixed) in our theory, though the most elegant formulas are obtained when they are all equal
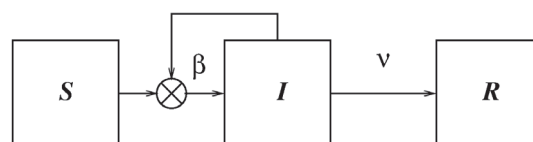

FIGURE 1   Diagram of standard SIR system

(we might have $T_k = 14$ or 28 days for all k, for instance). The objective will be to minimize the maximum of $I(t)$ for $t \geq 0$ ("flatten the curve") by appropriately choosing the start times t_k.

As discussed in the introduction, even if perfect lockdowns are not completely realistic, studying this case helps understand the case $\beta_0 > 0$. Indeed, we show via simulations that the conclusions for $\beta_0 = 0$ are very relevant to the case of a small but nonzero β_0, even one that is about 20% of the value of β.

Previous work on this and related problems includes,[27] which treats an optimal schedule minimizing a combination of the total number of deaths and the peak of the infected compartment,[17] which shows that a single interval ($K = 1$) is optimal if the objective is to minimize the total number of susceptible individuals at the end of the epidemic,[15] with numerical studies of optimally timing fixed-duration "one-shot" strategies, and the very nice theoretical paper[16] which showed that the optimal strategy for minimizing peak infection is a combination of a strict lockdown ("full suppression") with a feedback strategy which keeps $\mathcal{R}_0 = 1$. Also closely related to this work is Reference 28, which studies timing of lockdowns, including periodic strategies, through a combination of theoretical and numerical methods. Periodic strategies are also studied in References 25,29-31 as well as other references.

2.1 | Main result

Let

$$r := \nu/\beta$$

and consider the "virtual peak" of $I(t)$ if no lockdown were imposed:

$$V_0 := \max_{t \geq 0} I(t) = I_0 + S_0 - r(1 - \ln(r/S_0))$$

(cf. Section 5). Define this expression:

$$I_{\text{start}} := \frac{V_0}{1 + K - (e^{-\nu T_1} + \ldots + e^{-\nu T_K})}$$

The main result is as follows. It considers the optimization problem in which the number of lockdowns is fixed (K) as well as their respective lengths (T_k's). The parameters to be optimized over are the times at which the each lockdown should commence.

Theorem 1. *Suppose that $I(0) < I_{\text{start}}$. Then, in order to minimize the maximum of $I(t)$, $t \geq 0$, lockdowns should start whenever*

$$I(t_k) = I_{\text{start}}.$$

Moreover, under this policy, the maximum $I_{\max}$ of $I(t)$ will equal I_{start}.

In other words, any time that the infective population level reaches the value I_{start}, the next time-T_k lockdown interval I_k should start.

For example, if $T_k = T$ for $i = 1, \ldots, K$ then the formula is

$$I_{\max} = \frac{V_0}{1 + K - Ke^{-\nu T}}.$$

Note that as $T \to \infty$ the best possible maximum peak is

$$\frac{V_0}{1 + K}.$$

Proof. Proof of Theorem 1: For mathematical elegance, we will include the theoretical possibility of a lockdown starting at time exactly $t_0 = 0$ (and later make $T_0 = 0$, so that there is in effect no initial lockdown).

For any initial population (σ, ι), we introduce the following function:

$$\mathcal{V}(\sigma, \iota) := \iota + \sigma - r + r \ln r - r \ln \sigma$$

which gives the peak value of $I(t)$ if we start at the initial population (σ, ι) and there would be no further lockdowns, and let:

$$t_k := \text{time when } k\text{th lockdown starts}$$
$$I_k := I(t_k)$$
$$S_k := S(t_k)$$
$$V_k := \mathcal{V}(S(t_k + T_k), I(t_k + T_k))$$
$$T_k := \text{length of } k\text{th lockdown}$$
$$p_k := e^{-\nu T_k}$$
$$a_k := 1 - p_k.$$

(so $t_0 = 0$ and (S_0, I_0) is the state at the start of the epidemic). Observe that, for all k,

$$I(t_k + T_k) = p_k I_k$$
$$S(t_k + T_k) = S_k.$$

Consider these equalities:

$$V_k + r - r \ln r = p_k I_k + S_k - r \ln S_k \tag{5}$$
$$V_{k-1} + r - r \ln r = p_{k-1} I_{k-1} + S_{k-1} - r \ln S_{k-1} \tag{6}$$
$$I_k + S_k - r \ln S_k = p_{k-1} I_{k-1} + S_{k-1} - r \ln S_{k-1}, \tag{7}$$

where the last equality follows from the conservation law $I(t) + S(t) - r \ln S(t) \equiv \text{constant}$, applied to a solution that starts at $\iota = p_k I_k$ and $\sigma = S_k$. Adding (5)–(7) and subtracting (6), we obtain:

$$V_k + I_k + S_k - r \ln S_k - V_{k-1} == p_k I_k + S_k - r \ln S_k$$

from which we conclude the following recursion:

$$V_k = -a_k I_k + V_{k-1}.$$

Applying this formula recursively, we conclude:

$$V_K = V_0 - (a_0 I_0 + \dots + a_K I_K). \tag{8}$$

The largest value of $I(t)$ will occur at the maximum of the peaks occurring at the start of each kth lockdown, or the last "virtual peak" (which is then a real local maximum). In other words, the maximum of I is

$$I_{\max} = \max \{I_0, I_1, \dots, I_K, V_K\}.$$

Under the epidemic assumption $\mathcal{R}_0 > 1$, $\dot{I}(0) > 0$, so we can drop I_0 from the list. We replace the value for V_K from formula (8). Letting $T_0 = 0$ means that $a_0 = 1 - p_0 = 0$, so we conclude that

$$I_{\max} = \max \{I_1, \dots, I_K, V_0 - (a_1 I_1 + \dots + a_K I_K)\}. \tag{9}$$

To minimize the peak, we need to pick nonnegative $I_1, \dots, I_K$ in such a way that this expression is minimized. This is achieved at a unique global minimum, at which

$$I_{\max} = I_1 = \cdots = I_K = V_0 - (a_1 I_1 + \ldots + a_K I_K) \qquad \text{for all } k$$

(see Lemma 1 below), namely

$$I_k = \frac{V_0}{1 + (a_1 + \ldots + a_K)} = \frac{V_0}{1 + K - (e^{-vT_1} + \ldots + e^{-vT_K})} \qquad \text{for all } k.$$

This completes the proof of Theorem 1. ∎

Lemma 1. *For any $a_1 \geq 0, \ldots, a_K \geq 0$ and $b > 0$, define*

$$\xi := \frac{b}{1 + \sum_{k=1}^{K} a_k}.$$

Consider the following function, defined on $(x_1, \ldots, x_K) \in \mathbb{R}_{\geq 0}^K$:

$$g(x_1, \ldots, x_K) := \max \left\{ x_1, \ldots, x_K, \; b - \sum_{k=1}^{K} a_k x_k \right\}.$$

Then, the minimum value of g is ξ, and it is achieved at the unique point where all $x_k = \xi$.

Proof. Proof of Lemma 1: Define $A := \sum_{k=1}^{K} a_k$, so that $\xi = \frac{b}{1+A}$, and note these properties:

1. $g(\xi, \ldots, \xi) = \xi$.
    To prove this, note that, when all $x_k = \xi$,

$$b - \sum_{k=1}^{K} a_k x_k = b - \left(\sum_{k=1}^{K} a_k \right) \xi = b - A\xi = b - A\frac{b}{1+A} = \xi,$$

    so all terms in the max are the same.
2. If $g(x_1, \ldots, x_K) \leq \xi$ then $x_k = \xi$ for all k.
    Notice first that $x_k \leq \max\{x_1, \ldots, x_K\} \leq g(x_1, \ldots, x_K) \leq \xi$ for all k.
    If for some k this inequality were strict, then $-x_k \geq -\xi$ for all k, and $-x_k > -\xi$ for some k, so

$$b - \sum_{k=1}^{K} a_k x_k > b - \left(\sum_{k=1}^{K} a_k \right) \xi = b - A\xi = b - A\frac{b}{1+A} = \xi$$

    but and this would contradict $b - \sum_{k=1}^{K} a_k x_k \leq g(x_1, \ldots, x_K) \leq \xi$.

    Property 2 shows that $g(x_1, \ldots, x_K) > \xi$ unless all $x_k = \xi$, and Property 1 shows that the minimum is achieved when all $x_k = \xi$. ∎

We next show some illustrations of the use of the formula for several lengths of lockdowns as well as simulations for various scenarios of 1, 2, 3, or 4 lockdowns. We use reasonable parameters in each case. Finally, we will show computationally that a small positive β_0 does not change conclusions much, at least for the case of a single lockdown.

2.2 | Equal lengths are optimal

The formula derived in this article allows one to prove the following result. Suppose that we are given a total "lockdown time budget" $T > 0$, and wish to find K lockdown times T_k, such that $\sum_{k=1}^{K} T_k = T$ so as to minimize $I_{\max} = (1 + K - (e^{-vT_1} + \ldots + e^{-vT_K}))^{-1} V_0$. Minimizing $I_{\max}$ over the T_k's is equivalent to minimizing

$$e^{-vT_1} + \ldots + e^{-vT_K}$$

subject to

$$\sum_{k=1}^{K} T_k = T.$$

The functions e^{-vT_k} are strictly convex, the objective function is separable, and the constraint is affine, so it follows that there is a unique solution to this optimization problem (see example 5.4 in Reference 32). Consider the Lagrangian:

$$L(T_1, \ldots, T_K, \lambda) := e^{-vT_1} + \ldots + e^{-vT_K} + \lambda \left(\sum_{k=1}^{K} T_k - T \right)$$

and set the K partial derivatives with respect to the T_k's to zero. This gives:

$$e^{-vT_k} = \frac{\lambda}{v}, \quad k = 1, \ldots, K$$

which implies $T_1 = \cdots = T_K$. From $\sum_{k=1}^{K} T_k = T$ it follows that

$$T_k = \frac{T}{K},$$

that is, equal lengths are optimal.

We now prove that *the more intervals, the better*. Indeed, suppose that we compare the optimal solution with K intervals to the optimal solution with $K + 1$ intervals. Let us think of the optimal solution with K intervals as a particular solution with $K + 1$ intervals, in which the last interval is zero (and the first K are equal to T/K). Clearly, this last solution is not optimal, since the (unique) optimal solution to the problem with $K + 1$ intervals has all intervals nonzero (and equal to $T/(K + 1)$). In other words, *having one more interval is always better*. Of course, this ignores the social, economic, and psychological problems of imposing multiple lockdowns.

A variation of the "total budget" problem is as follows. Suppose that the "cost" of a second lockdown is different from (and presumably larger than) the cost of the first lockdown. This may represent "lockdown fatigue" or lack of political will. More generally, each subsequent lockdown could have an associated cost $c_k > 0$. In this case, the interesting mathematical problem would be to again minimize $e^{-vT_1} + \ldots + e^{-vT_K}$ but this time subject to a general affine constraint

$$\sum_{k=1}^{K} c_k T_k = T.$$

The Lagrangian is now

$$L(T_1, \ldots, T_K, \lambda) := e^{-vT_1} + \ldots + e^{-vT_K} + \lambda \left(\sum_{k=1}^{K} c_k T_k - T \right).$$

We normalize the problem by asking $\sum_{k=1}^{K} c_k = K$, so that the equal-cost case is that when all $c_k = 1$. Proceeding as before, we arrive at the equations:

$$e^{-vT_k} = \frac{\lambda c_k}{v}, k = 1, \ldots, K.$$

Pick any index $k \neq 1$. Then

$$e^{-vT_k} e^{vT_1} = \left(\frac{\lambda c_k}{v} \right) \left(\frac{\lambda c_1}{v} \right)^{-1} = \frac{c_k}{c_1}$$

or $e^{-v(T_k - T_1)} = c_k/c_1$ from which we derive the formulas

$$T_k = T_1 - \frac{1}{v} \ln c_k + \frac{1}{v} \ln c_1, \quad k = 2, \ldots, K.$$

Thus:

$$T = \sum_{k=1}^{K} c_k T_k$$

$$= c_1 T_1 + \sum_{k=2}^{K} c_k \left(T_1 - \frac{1}{\nu} \ln c_k + \frac{1}{\nu} \ln c_1 \right)$$

$$= \left(\sum_{k=1}^{K} c_k \right) T_1 - \frac{1}{\nu} \left(\sum_{k=2}^{K} c_k \ln c_k \right) + \frac{1}{\nu} \left(\sum_{k=2}^{K} c_k \right) \ln c_1$$

$$= \left(\sum_{k=1}^{K} c_k \right) T_1 - \frac{1}{\nu} \left(\sum_{k=1}^{K} c_k \ln c_k \right) + \frac{1}{\nu} \left(\sum_{k=1}^{K} c_k \right) \ln c_1$$

$$= K T_1 - \frac{1}{\nu} \left(\sum_{k=1}^{K} c_k \ln c_k \right) + \frac{K}{\nu} \ln c_1$$

(using that $\sum_{k=1}^{K} c_k = K$). We conclude:

$$T_1 = \frac{T}{K} + \frac{1}{\nu K} \left(\sum_{k=1}^{K} c_k \ln c_k \right) - \frac{1}{\nu} \ln c_1.$$

It follows that, for each $i \geq 2$, we have an analogous formula:

$$T_i = T_1 - \frac{1}{\nu} \ln c_i + \frac{1}{\nu} \ln c_1 = \frac{T}{K} + \frac{1}{\nu K} \left(\sum_{k=1}^{K} c_k \ln c_k \right) - \frac{1}{\nu} \ln c_i.$$

Note the common entropy-like term as well as the last term that makes intervals shorter when their "cost" is higher. In the special case that all $c_k = 1$, the logarithms are zero and we recover the previous case $T_i = T/K$.

2.3 | Sensitivity to parameters

The recovery rate ν is relatively easy to estimate, wince it is largely a function of the physiology of the pathogen. However, the parameter β depends on behavioral characteristics, population density, and so forth, so it is much harder to know accurately. A natural question to ask if: how much worse does a policy based on an incorrect value perform, relative to the optimal policy that would have been used if β were perfectly known? We study this sensitivity question here, restricting for simplicity to the case of a single (perfect) lockdown, that is, $K = 1$, $T_1 = T$.

Suppose that the population value I_1 at which the lockdown starts was optimized based on a "wrong" value $\tilde{\beta}$:

$$\tilde{I}_1 = \frac{\tilde{V}_0}{2 - e^{-\nu T}},$$

where

$$\tilde{V}_0 = I_0 + S_0 - \tilde{r}(1 - \ln(\tilde{r}/S_0)), \quad \tilde{r} = \nu/\tilde{\beta}.$$

The maximum value of $I(t)$ is:

$$I_{\max} = V_0 \quad \text{if} \quad \tilde{I}_1 \geq V_0$$

(because the maximum with no lockdowns is V_0, so the lockdown will never be triggered in the case $\tilde{I}_1 \geq V_0$) and

$$I_{\max} = \max \left\{ \tilde{I}_1, V_0 - (1 - e^{-\nu T})\tilde{I}_1 \right\} \quad \text{if} \quad \tilde{I}_1 < V_0$$

(formula 9), where

$$V_0 = I_0 + S_0 - r(1 - \ln(r/S_0)), \quad r = v/\beta.$$

By contrast, the optimal solution would have been to pick

$$I_{\text{opt}} = \frac{V_0}{2 - e^{-vT}}.$$

Since this is optimal, of course $I_{\max} \geq I_{\text{opt}}$. Let us consider the relative penalty (in terms of maximum infectives) incurred by using the wrong β:

$$\Delta := \frac{I_{\max} - I_{\text{opt}}}{I_{\text{opt}}}.$$

Let is write $p := e^{-vT}$ to simplify notations. When $\tilde{I}_1 \geq V_0$ (i.e., if $\tilde{V}_0 \geq (2 - p)V_0$):

$$\Delta = \frac{V_0 - I_{\text{opt}}}{I_{\text{opt}}} = \frac{V_0 - \frac{V_0}{2-p}}{\frac{V_0}{2-p}} = 1 - p.$$

When $\tilde{I}_1 < V_0$ (i.e., if $\tilde{V}_0 < (2 - p)V_0$):

$$\Delta = \frac{\max\left\{ \frac{\tilde{V}_0}{2-p}, V_0 - (1-p)\frac{\tilde{V}_0}{2-p} \right\} - \frac{V_0}{2-p}}{\frac{V_0}{2-p}} = \frac{\max\left\{ \tilde{V}_0 - V_0, (1-p)(V_0 - \tilde{V}_0) \right\}}{V_0}.$$

In this maximum, the terms have opposite sign, so the max is achieved at the nonnegative one.

A formula for Δ can be most conveniently derived when thinking of Δ as a function of $\tilde{V}_0$ (with β, and therefore also V_0, fixed). We conclude:

Theorem 2.

$$\Delta(\tilde{V}_0) = \begin{cases} (1-p)\frac{\tilde{V}_0 - V_0}{V_0} & \text{if } \tilde{V}_0 \in (0, V_0) \\ \frac{V_0 - \tilde{V}_0}{V_0} & \text{if } \tilde{V}_0 \in [V_0, (2-p)V_0) \\ 1 - p & \text{if } \tilde{V}_0 \in [(2-p)V_0, \infty). \end{cases}$$

From this formula, one can immediately compute sensitivity to $\tilde{\beta}$. Observe that $\tilde{V}_0$ is a strictly increasing function of $\tilde{\beta}$, because the derivative of the function $\tilde{V}_0$ with respect to $\tilde{\beta}$ is:

$$\frac{v}{\tilde{\beta}^2} \ln\left(\frac{\tilde{\beta}S_0}{v} \right) > 0$$

as long as we are in the epidemic parameter range $\mathcal{R}_0 := \beta S_0/v > 1$.

Note that Δ is continuous on $\tilde{V}_0$; it is zero (no penalty) when $\beta = \tilde{\beta}$, that is, $V_0 = \tilde{V}_0$, and $1 - p$ when substituting $\tilde{V}_0 = (2 - p)V_0$ into $(V_0 - \tilde{V}_0)/V_0$. In the limit that $p \to 1$ (i.e., if the lockdown interval $T \to 0$, the middle case becomes vacuous and the sensitivity is zero (as expected).

3 | SOME NUMERICAL EXPLORATIONS

3.1 | Optimal reduction of "virtual peak" with K perfect lockdowns

The use of an even a small number of lockdowns results in a drastic reduction of the peak that would occur (the "virtual peak") if there were no lockdowns. The marginal benefit of additional lockdowns is relatively minor, after a certain

number of them, as is the benefit of longer lockdowns. We plot here the fraction $\left(1 + K(1 - e^{-vT})\right)^{-1}$ for $v = 0.05$ and $T = 7, 14, 21, 28$ days (Figure 2).

3.2 | Simulations using optimal formula

We simulate various lockdown lengths using our optimal formulas. Parameters are, $\beta = 0.00025$, $v = 0.05$ (so $\mathcal{R}_0 = 5$), initial conditions are $S_0 = 1000$, $I_0 = 1$, and the peak if there are no lockdowns is $I = 479$. The maximum from the formula coincides with the maximum in simulations, up to numerical error.

3.2.1 | Lockdown length is $T = 14$ days, perfect lockdown

Figures 3–6 illustrate 14-day 1, 2, 3, and 4 lockdowns, respectively.
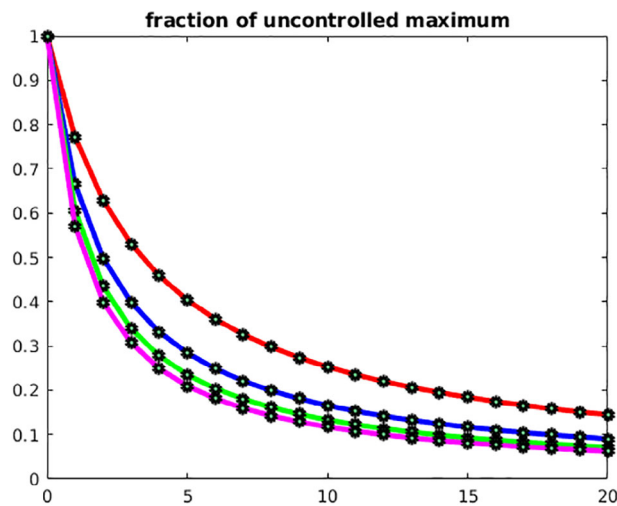
FIGURE 2 Percentage of virtual peak when using K lockdowns (horizontal axis) each of them 7 (red), 14 (blue), 21 (green), or 28 (magenta) days long[Colour figure can be viewed at wileyonlinelibrary.com]
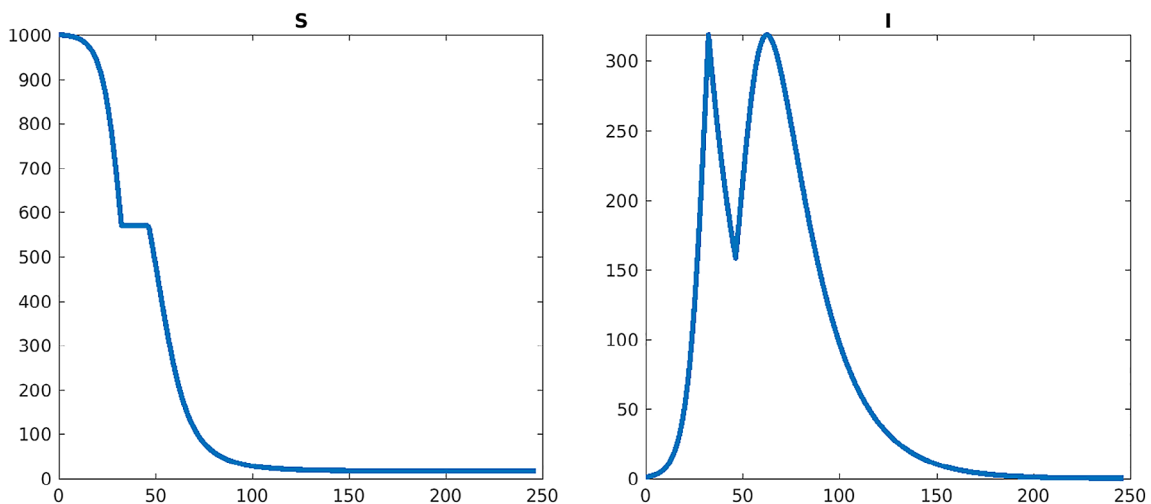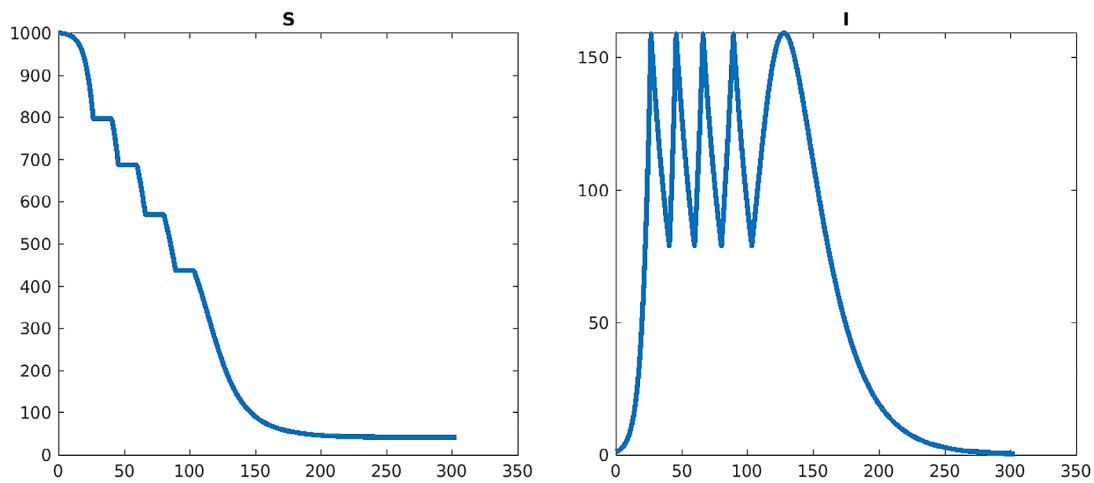

FIGURE 3 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 1, peak I from formula: 318.682808, maximum of I on last (no lockdown) period: 318.601530. Lockdown start time(s): 32.42[Colour figure can be viewed at wileyonlinelibrary.com]
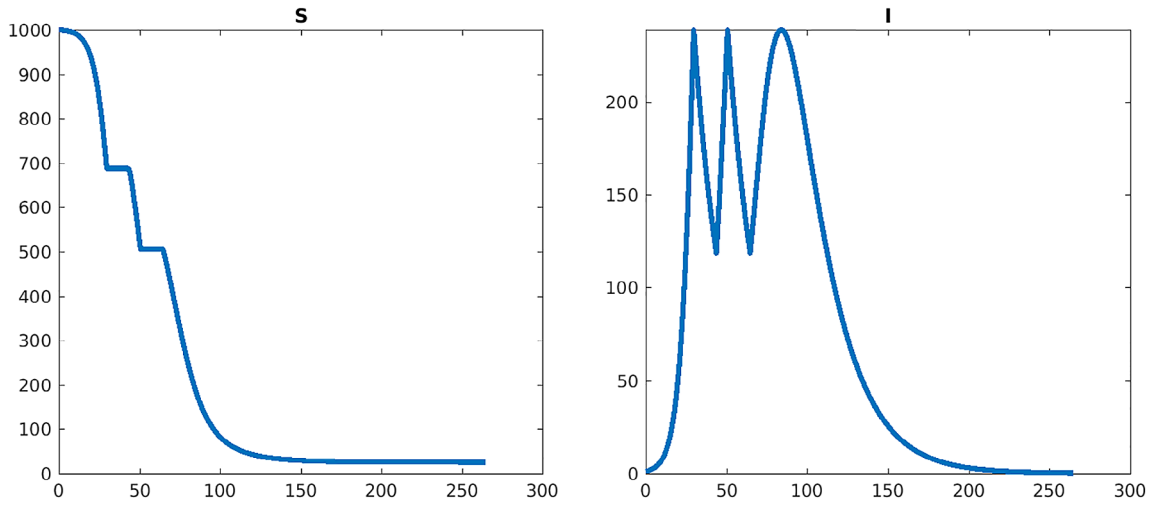
FIGURE 4 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 2, peak I from formula: 238.740981, maximum of I on last (no lockdown) period: 238.755779. Lockdown start time(s): 29.73, 50.69[Colour figure can be viewed at wileyonlinelibrary.com]
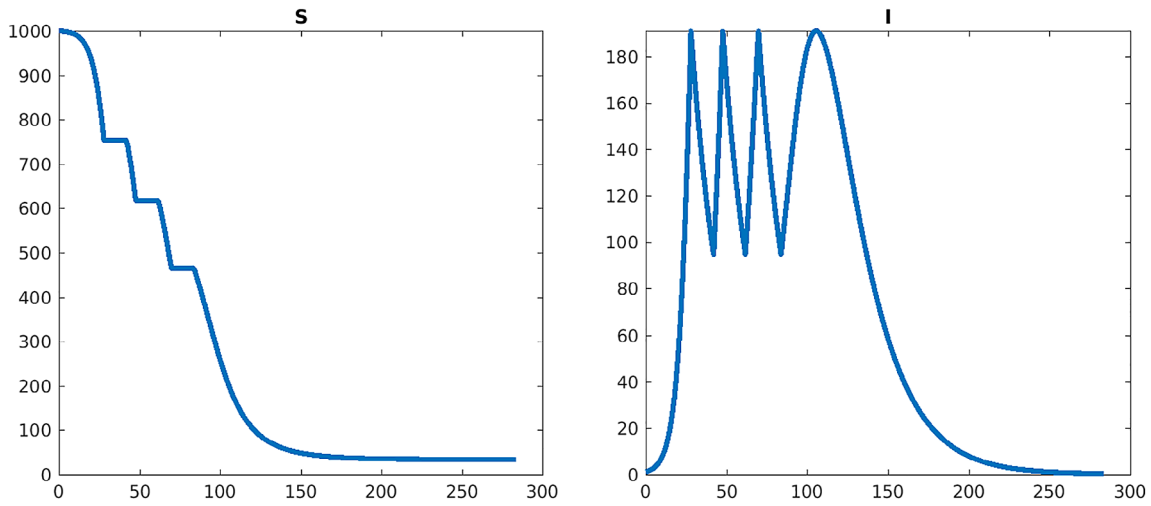
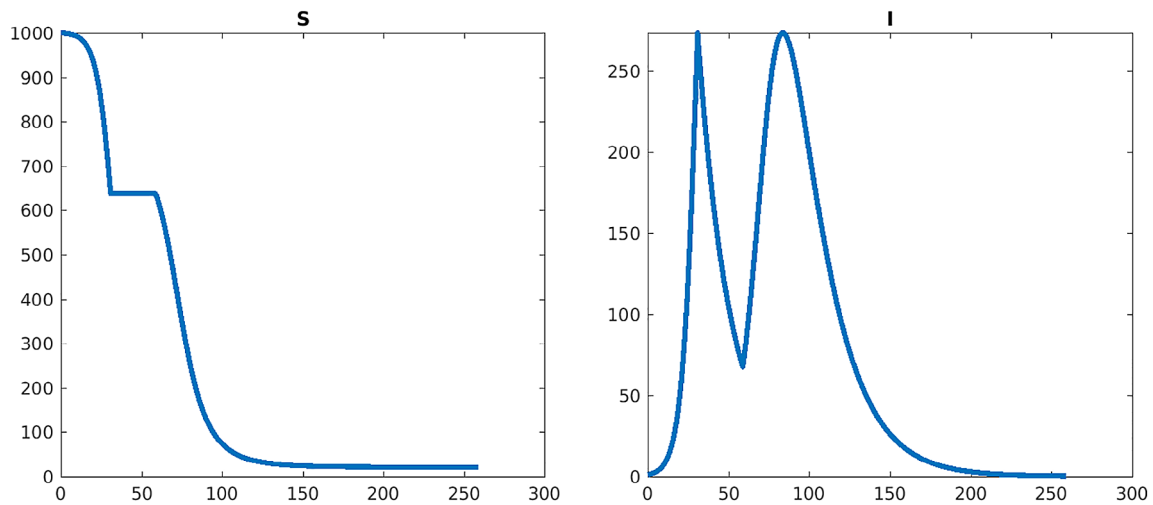**FIGURE 5** Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 3, peak I from formula: 190.862880, maximum of I on last (no lockdown) period: 191.019085. Lockdown start time(s): 28.01, 47.71, 69.80[Colour figure can be viewed at wileyonlinelibrary.com]
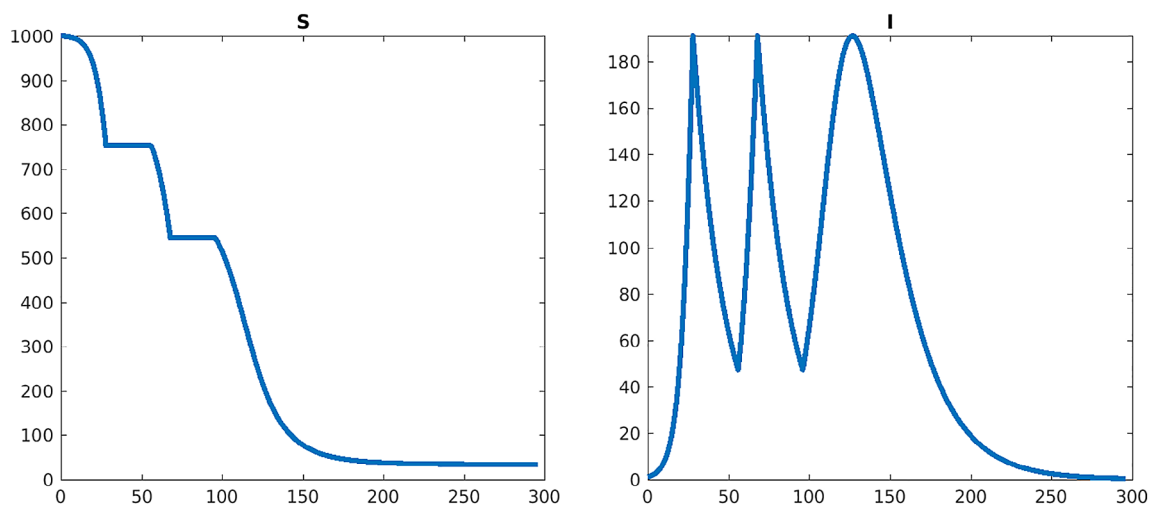

FIGURE 6 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 4, peak I from formula: 158.980313, maximum of I on last (no lockdown) period: 159.342577. Lockdown start time(s): 26.74, 45.87, 66.33, 89.44[Colour figure can be viewed at wileyonlinelibrary.com]

3.2.2 | Lockdown length is $T = 28$ days, perfect lockdown

Figures 7–10 illustrate 28-day 1, 2, 3, and 4 lockdowns, respectively.

3.3 | Comparing multiple versus single lockdowns

We proved that more lockdowns are always better, if the total lockdown "budget" is fixed. Here, we show the following comparisons: one 28-day compared with two 14-day lockdowns, and two 28-day compared with four 14-day lockdowns (Figures 11 and 12, respectively). Observe that the peaks when using repeated lockdowns are lower, as theory predicts. Interestingly, the timings of the last peak and asymptotic behaviors look similar in the respective left and right plots.

FIGURE 7 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 1, peak I from formula: 273.247170, maximum of I on last (no lockdown) period: 273.286548. Lockdown start time(s): 30.9[Colour figure can be viewed at wileyonlinelibrary.com]

FIGURE 8 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 2, peak I from formula: 191.124644, maximum of I on last (no lockdown) period: 191.048654. Lockdown start time(s): 28.02, 68.02[Colour figure can be viewed at wileyonlinelibrary.com]
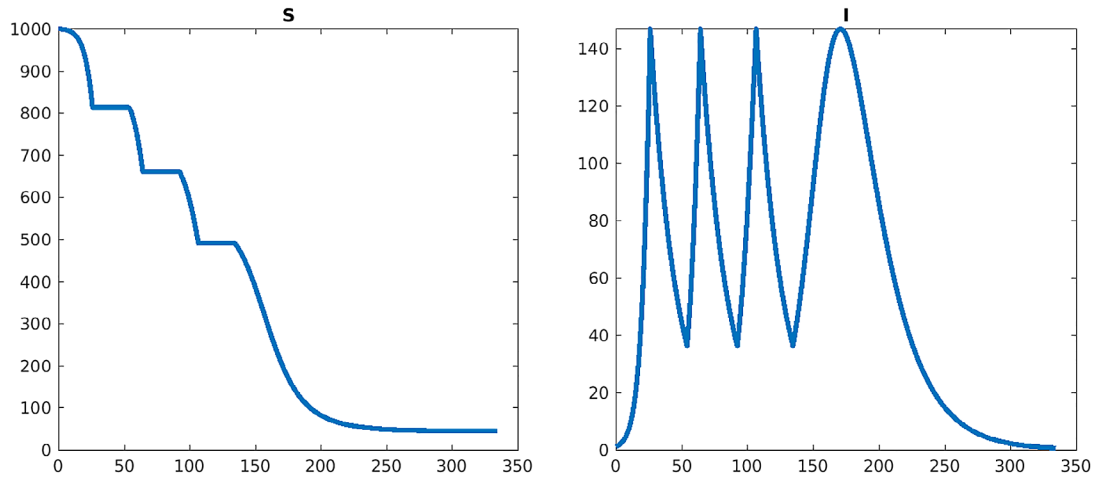
FIGURE 9 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 3, peak I from formula: 146.957573, maximum of I on last (no lockdown) period: 146.913773. Lockdown start time(s): 26.22, 64.39, 106.74[Colour figure can be viewed at wileyonlinelibrary.com]
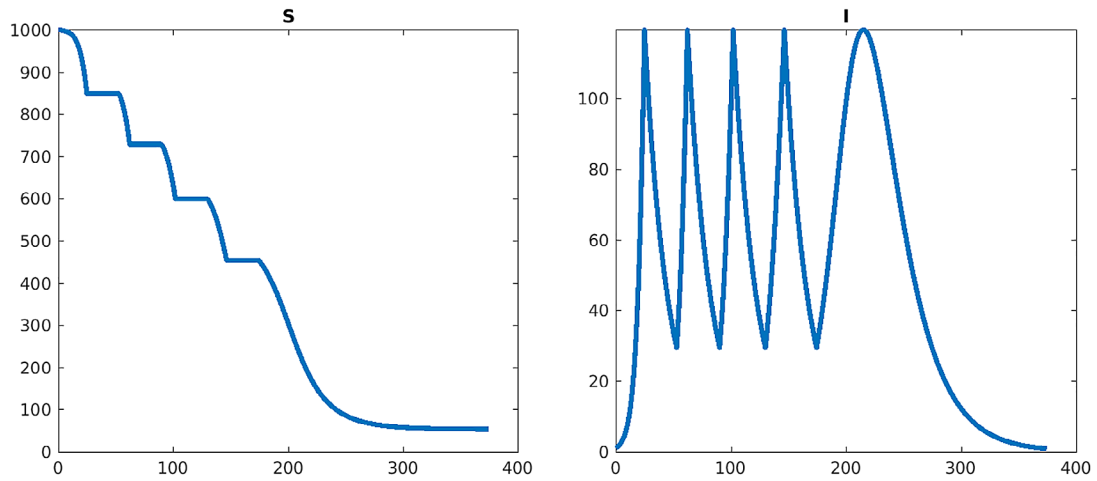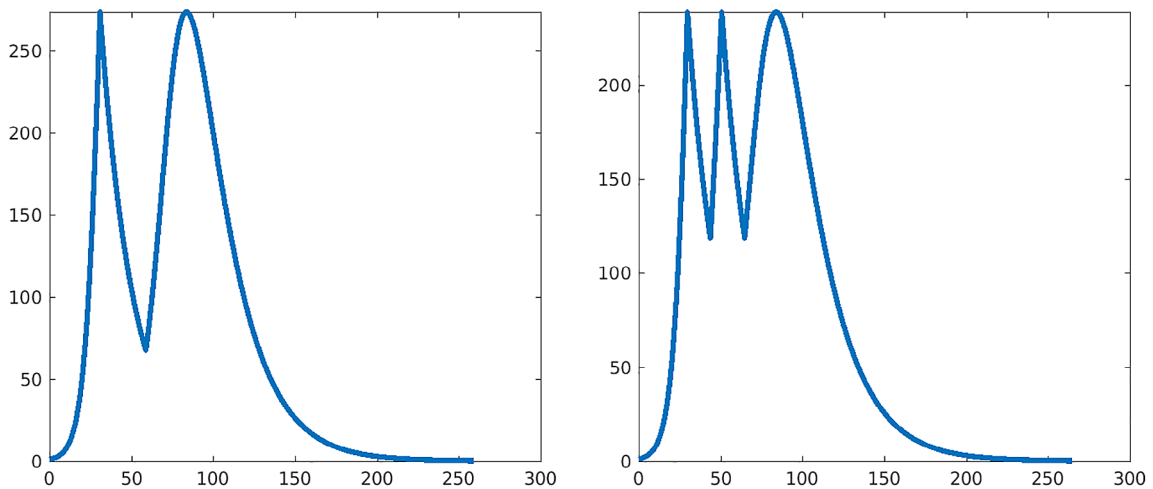

FIGURE 10 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 4, peak I from formula: 119.371878, maximum of I on last (no lockdown) period: 119.395364. Lockdown start time(s): 24.91, 62.23, 101.98, 146.47[Colour figure can be viewed at wileyonlinelibrary.com]

FIGURE 11 Left: one 28-day lockdown. Right: two 14-day lockdowns. Parameters as earlier[Colour figure can be viewed at wileyonlinelibrary.com]
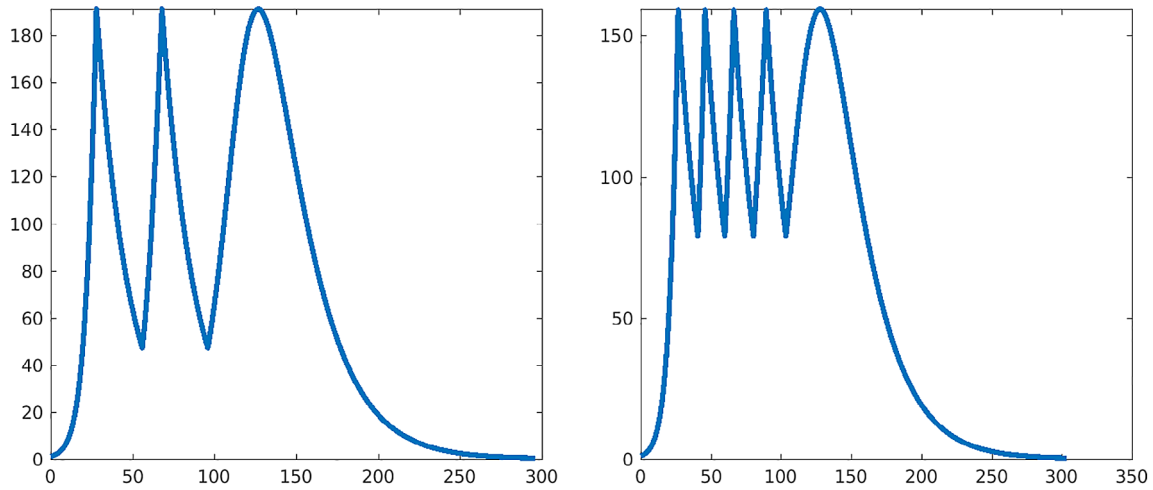
FIGURE 12 Left: two 28-day lockdowns. Right: four 14-day lockdowns. Parameters as earlier[Colour figure can be viewed at wileyonlinelibrary.com]

3.4 | Testing $\beta_0 \neq 0$ with formula derived for $\beta_0 = 0$

We simulate the use of the formula derived for $\beta_0 = 0$, under the lockdown value $\beta_0 = 0.00005$, which represents a 20% value of the normal contact rate. Again, $\beta = 0.00025$, $v = 0.05$ (so $\mathcal{R}_0 = 5$), initial conditions are $S_0 = 1000$, $I_0 = 1$, and the peak if there are no lockdowns is $I = 479$.

3.4.1 | Lockdown length is $T = 28$ days, $\beta_0 = 0.00005$

Figures 13–16 illustrate 28-day 1, 2, 3, and 4 imperfect lockdowns, respectively, using the formula that assumed perfect lockdowns.

3.4.2 | Lockdown length is $T = 14$ days, $\beta_0 = 0.00005$

Figures 17–20 illustrate 14-day 1, 2, 3, and 4 imperfect lockdowns, respectively, using the formula that assumed perfect lockdowns.
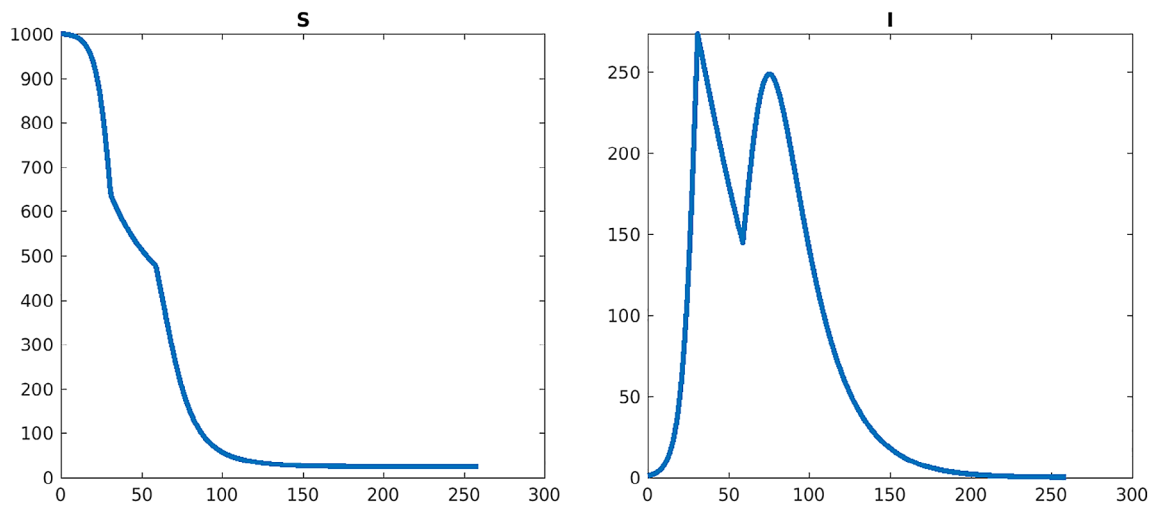

FIGURE 13 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 1, peak I from formula: 273.247170, maximum of I on last (no lockdown) period: 248.383407. Lockdown start time(s): 30.90[Colour figure can be viewed at wileyonlinelibrary.com]
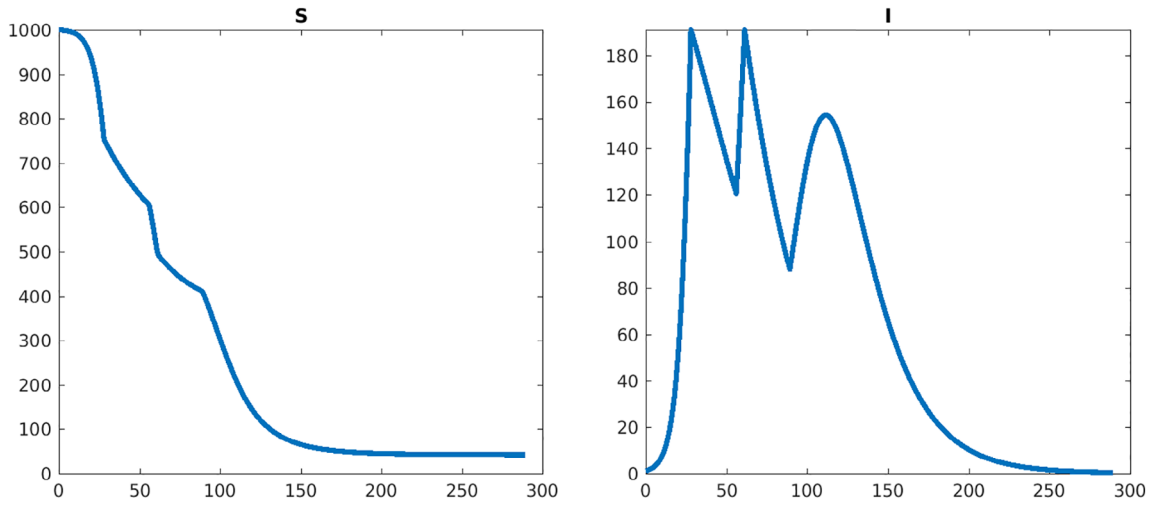
FIGURE 14 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 2, peak I from formula: 191.124644, maximum of I on last (no lockdown) period: 154.387915. Lockdown start time(s): 28.02, 61.2[Colour figure can be viewed at wileyonlinelibrary.com]
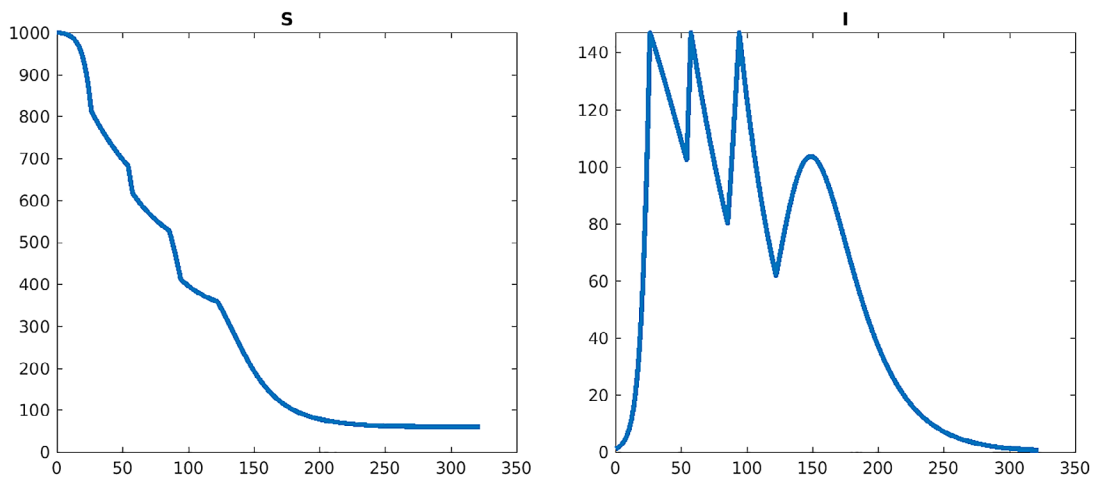

FIGURE 15 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 3, peak I from formula: 146.957573, maximum of I on last (no lockdown) period: 103.506053. Lockdown start time(s): 26.22, 57.43, 94.30[Colour figure can be viewed at wileyonlinelibrary.com]
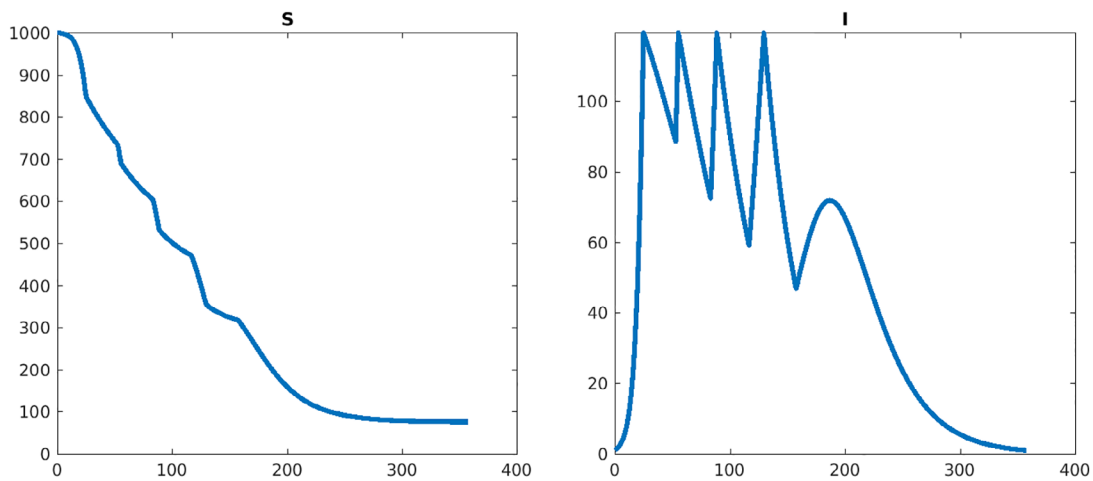

FIGURE 16 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 4, peak I from formula: 119.371878, maximum of I on last (no lockdown) period: 71.792718. Lockdown start time(s): 24.91, 55.24, 88.63, 129.63[Colour figure can be viewed at wileyonlinelibrary.com]
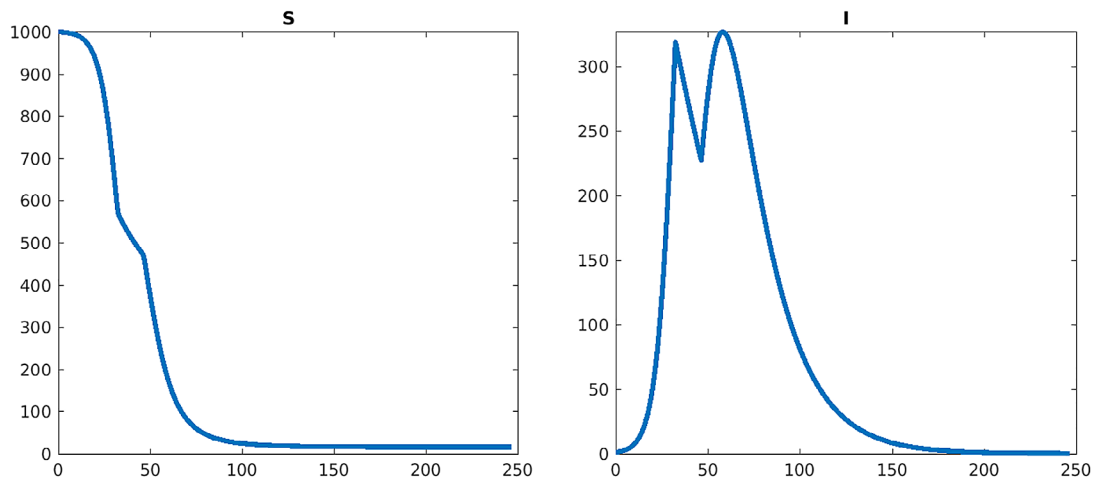
FIGURE 17 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 1, peak I from formula: 318.682808, maximum of I on last (no lockdown) period: 326.846639. Lockdown start time(s): 32.4[Colour figure can be viewed at wileyonlinelibrary.com]
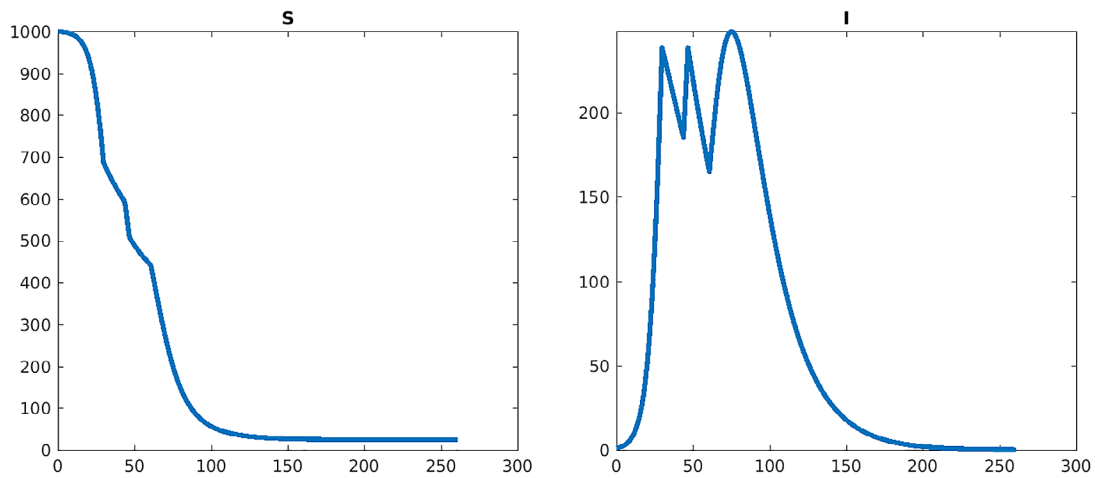

FIGURE 18 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 2, peak I from formula: 238.740981, maximum of I on last (no lockdown) period: 248.153424. Lockdown start time(s): 29.73, 46.6[Colour figure can be viewed at wileyonlinelibrary.com]
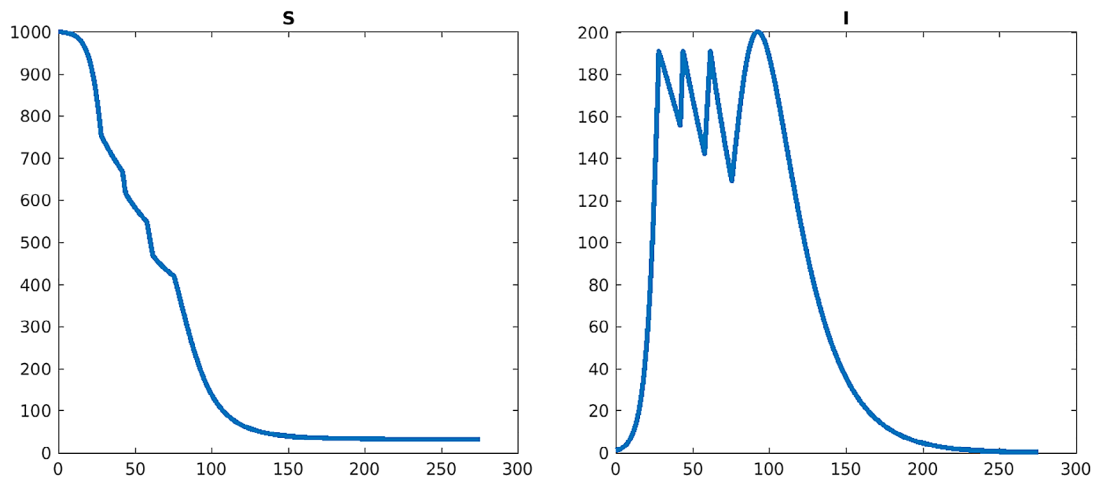

FIGURE 19 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 3, peak I from formula: 190.862880, maximum of I on last (no lockdown) period: 200.218534. Lockdown start time(s): 28.01, 43.86, 61.6[Colour figure can be viewed at wileyonlinelibrary.com]
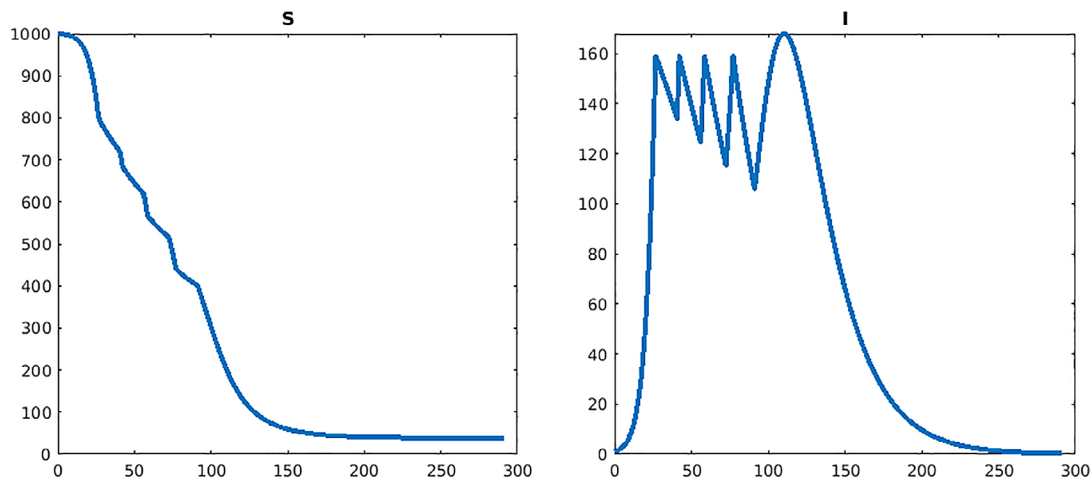
FIGURE 20 Plots of $S(t)$ and $I(t)$ (horizontal axis is time). Number of lockdowns: 4, peak I from formula: 158.980313, maximum of I on last (no lockdown) period: 167.977200. Lockdown start time(s): 26.74, 42.11, 58.60, 77.22[Colour figure can be viewed at wileyonlinelibrary.com]

3.5 | Comparison with optimal strategy for $\beta_0 \neq 0$

For comparison with the use of the optimal formulas derived for $\beta_0 = 0$, we show here numerically the optimal solution when $\beta_0 \neq 0$, specifically $\beta_0 = 0.00005$ as above. As earlier, parameters are $\beta = 0.00025$, $\nu = 0.05$ (so $\mathcal{R}_0 = 5$), initial conditions are $S_0 = 1000$, $I_0 = 1$, and the peak if there are no lockdowns is $I = 479$. We take only the case of a single lockdown, for simplicity, and lockdown lengths of 14 or 28 days.

Here we find that the formula predicts the optimal timing extremely well for 14-day lockdowns (error less than 1% in maximum infectives), and is fairly good for 28-day lockdowns as well (about 5% error).

3.5.1 | Lockdown length is $T = 14$ days, $\beta_0 = 0.00005$

For 14-day lockdowns, the plot in Figure 17 suggests that the formula derived for $\beta_0 = 0$ triggered the first lockdown too early, so we explored by what fraction > 1 to increase the trigger point, from which the optimal strategy is clear. Figures 21 and 22 illustrate optimal formulas for imperfect 14-day single-lockdowns.
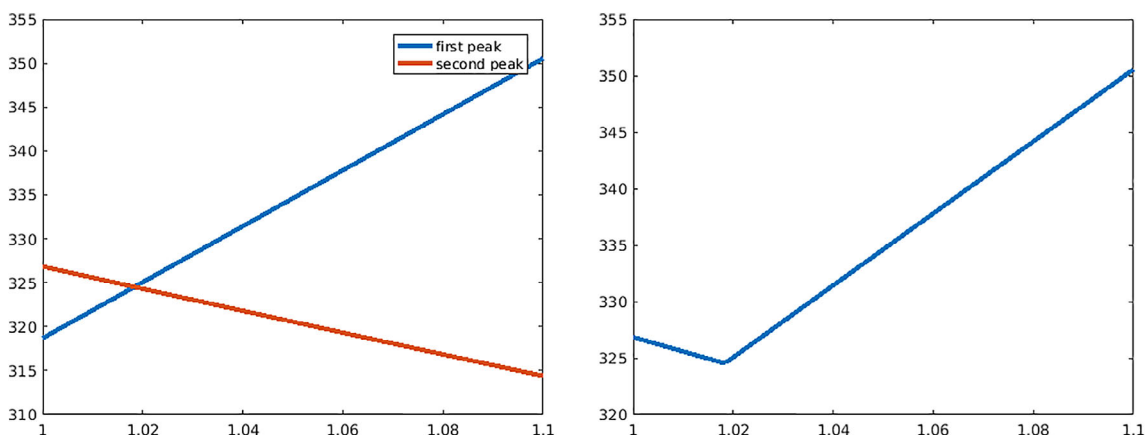

FIGURE 21 Left: Magnitude of first and second peak, with the lockdown time parametrized (x axis) by the percentage of the ideal (perfect lockdown) formula; 14 day lockdown. Note that the second peak decreases as the first peak happens later, so the minimum of the maximum among them will occur when the curves intersect. Right: The maximum between the curves; minimum is around fraction 1.018 of the optimal for perfect lockdowns, so trigger should occur later[Colour figure can be viewed at wileyonlinelibrary.com]
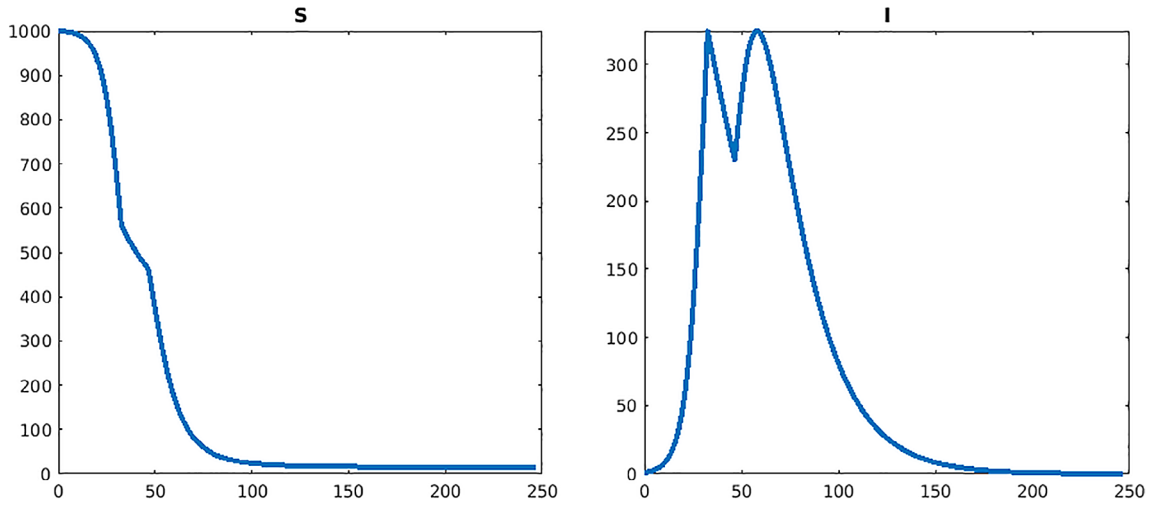
FIGURE 22 Simulation with an imperfect lockdown. Using now the optimal fraction 1.018 of the optimal for perfect lockdowns, obtained by minimizing the plot in Figure 21 (right). The optimal peak value is now approximately 324, which can be compared with the suboptimal plot (using the formula that assumed perfect lockdowns) shown in Figure 17, which had a peak of approximately 327. Observe how the two peaks are now balanced. The optimal result is not that different from the one obtained from our formulas, and the lockdown start is at time 30.39[Colour figure can be viewed at wileyonlinelibrary.com]

3.5.2 | Lockdown length is $T = 28$ days, $\beta_0 = 0.00005$

By contrast, for 28-day lockdowns the plot in Figure 13 suggests that the formula derived for $\beta_0 = 0$ waited too long for the first lockdown, so we first explore by what fraction < 1 to decrease the trigger point, from which the optimal strategy is clear. Figures 23 and 24 illustrate optimal formulas for imperfect 28-day single-lockdowns.

4 | REVIEW OF SIR MODEL

To make this article self-contained, we review here some facts about SIR models, see, for example, Reference 19 or mathematical epidemiology texts for more details. We wish to analyze solutions, from initial conditions $S(0) = S_0$, $I(0) = I_0$.
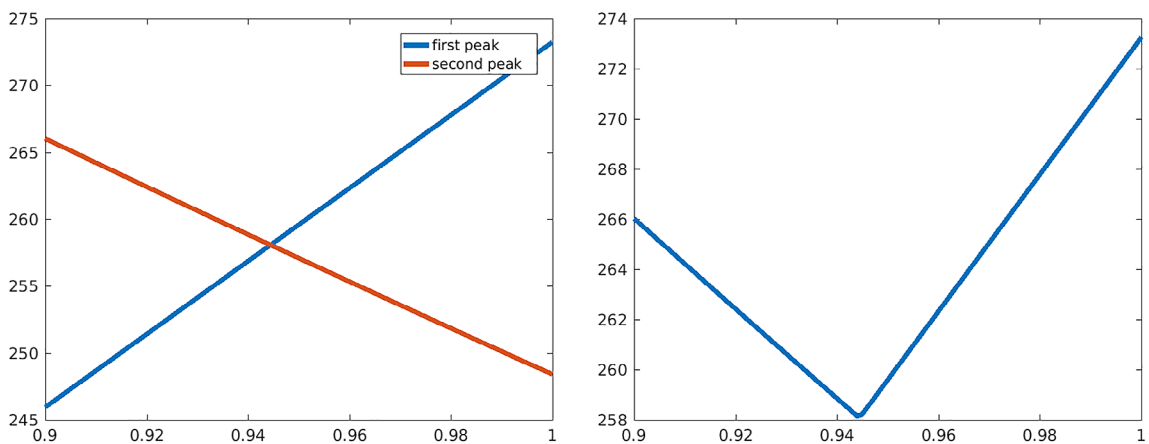
FIGURE 23 Left: Magnitude of first and second peak, with the lockdown time parametrized (x axis) by the percentage of the ideal (perfect lockdown) formula; 14 day lockdown. Note that the second peak decreases as the first peak happens later, so the minimum of the maximum among them will occur when the curves intersect. Right: The maximum between the curves; minimum is around fraction 0.944 of the optimal for perfect lockdowns, so trigger should occur earlier[Colour figure can be viewed at wileyonlinelibrary.com]

FIGURE 24 Simulation with an imperfect lockdown. Using now the optimal fraction 0.944 of the optimal for perfect lockdowns, obtained 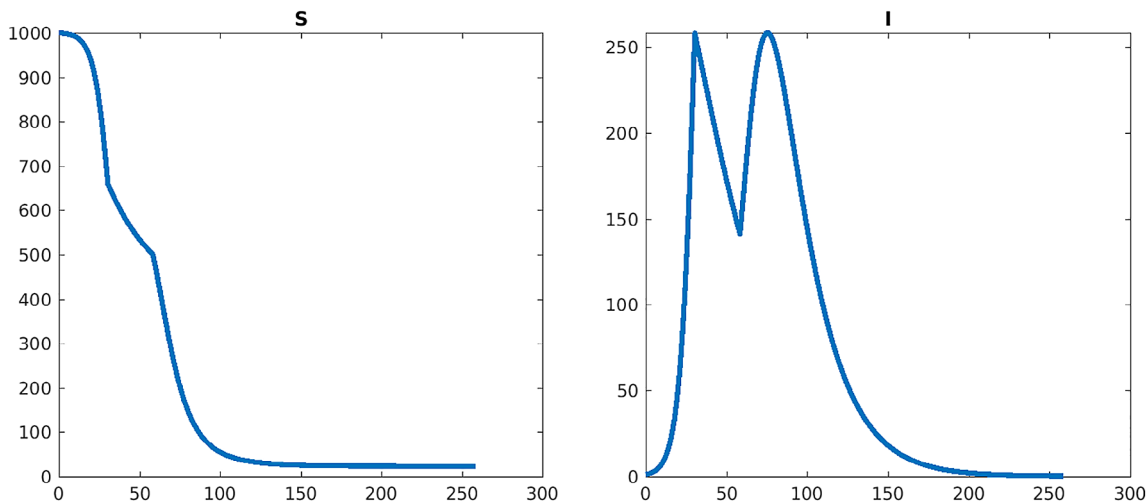by minimizing the plot in Figure 23 (right). The optimal peak value is now approximately 258, which can be compared with the suboptimal plot (using the formula that assumed perfect lockdowns) shown in Figure 13, which had a peak of approximately 273. Observe how the two peaks are now balanced. The optimal result is very close to the one obtained from our formulas[Colour figure can be viewed at wileyonlinelibrary.com]

4.1 | Infections always die-out in SIR model

Note that if $I_0 = 0$, then $S(t) \equiv S_0$ and $I(t) \equiv 0$; in other words, every point of the form $(S, 0)$ is an equilibrium. Similarly, if $S_0 = 0$, then $S(t) \equiv 0$ and $I(t) = e^{-vt}I_0 \to 0$, so the case $S_0 = 0$ is not interesting either. So we study the only interesting cases, $I_0 > 0$ and $S_0 > 0$.

Since $\dot{S} \leq 0$, $S(t)$ is a nonincreasing function of time, and thus $S(t) \searrow S_\infty$ for some $S_\infty \geq 0$. A most important result is this one:

$$S_\infty > 0 \quad \text{and} \quad I(t) \to 0 \quad \text{as} \quad t \to \infty.$$

This says that the infection will end (asymptotically), and there will remain a number of "naive" individuals at the end.

We will show that $I(t) \to 0$ and defer the proof that $S_\infty > 0$ to later.

To prove this result, we will use this theorem: *if $x(t)$ is a solution of a system of ODEs $\dot{x} = f(x)$, and if the solution converges, $x(t) \to x^*$, then x^* must be an equilibrium point, that is, $f(x^*) = 0$.* This is true because the omega-limit set of a trajectory is an invariant set, the LaSalle Invariance Principle (see, e.g., Reference 33).

We apply this theorem as follows. First we define $V(t) := S(t) + I(t)$, and notice that $\dot{V} = -vI \leq 0$, which means that $V(t)$ is nonincreasing, and thus there is a limit $V(t) \searrow V_\infty$ as $t \to \infty$. Therefore, $I(t) = V(t) - S(t) \to V_\infty - S_\infty =: I_\infty$ also has a limit. So the state $x(t) = (S(t), I(t))$ converges to $x^* := (S_\infty, I_\infty)$. It follows that $f(x^*) = 0$, which means that

$$\beta S_\infty I_\infty = 0$$
$$\beta S_\infty I_\infty - vI_\infty = 0$$

and from there we conclude that $I_\infty = 0$ because $v \neq 0$.

We still have to show that $S_\infty > 0$; we will in fact provide a formula for S_∞.

4.2 | $\mathcal{R}_0$ and epidemics

A central role in epidemiology is played by the "intrinsic reproductive rate"

$$\mathcal{R}_0 := \frac{\beta S_0}{v}.$$

The epidemiological (and nonmathematically rigorous) definition of $\mathcal{R}_0$ is "the average number of secondary cases produced by one infected individual introduced into a population of susceptible individuals," where by a susceptible individual one means one who can acquire the disease. This can be made precise with a stochastic model, but an intuitive argument can be found in Reference 19. We remark $\mathcal{R}_0$ has a generalization to more complex epidemics models, and it characterizes the local stability of the set of "disease-free" steady states (DFSS) (those for there are no infectives). One may compute $\mathcal{R}_0$ using the so-called "next generation matrix" built from the differential equations. which was introduced in Reference 34 (see, e.g., Reference 35 and also the worked examples in Reference 19).

We discuss $\mathcal{R}_0$ below in more detail, but for now note the following fact. From the ODE for I, we have that

$$\dot{I}(0) = (\beta S_0 - \nu)I_0 = \nu \, (\mathcal{R}_0 - 1)I_0.$$

This means that *an epidemic will happen*, meaning that $I(t)$ will increase when starting from any $I(0) > 0$, *if and only if* $\mathcal{R}_0 > 1$.

Moreover, the initial growth of $I(t)$ will be exponential, with rate $\lambda = \nu \, (\mathcal{R}_0 - 1)$. (For small times and a large susceptible population S_0, we may assume that $S(t)$ remains roughly constant.) Logarithmically plotting infections, we can estimate λ, and from there we may estimate

$$\mathcal{R}_0 = 1 + \frac{\lambda}{\nu}$$

(assuming that we know ν, the recovery/death rate of infected), and

$$\beta = \frac{\lambda + \nu}{S_0}.$$

When $\mathcal{R}_0 \leq 1$ and $t > 0$,

$$\dot{I}(t) = (\beta S(t) - \nu)I(t) < (\beta S_0 - \nu)I = \nu \, (\mathcal{R}_0 - 1)I \leq 0$$

(because $S(t) < S_0$) and so $I(t)$ monotonically decreases to zero.

From now on, when discussing the SIR model, we assume that $\mathcal{R}_0 > 1$.

4.3 | Peak infection time t_p and susceptibles at that time

The derivative $\dot{I} = (\beta S - \nu)I$ is positive for small t, because at zero it equals $\nu \, (\mathcal{R}_0 - 1)I > 0$.

On the other hand, since $I(t) \to 0$ as $t \to \infty$, the derivative must eventually become negative, which means that there is some time t_p (p for "peak" infectivity) at which $\dot{I}(t_p) = 0$. Since $S(t)$ decreases monotonically, the derivative of I can only change sign from positive to negative at exactly one such time t_p. So t_p is the point at which $I(t)$ attains is maximum.

From $\dot{I} = 0$ at t_p, we have that

$$S(t_p) = r,$$

where we define for convenience

$$r := \frac{\nu}{\beta}.$$

Thus, at the peak infection time, there is a precise formula for the number of susceptibles.

4.4 | A formula for the final number $S_\infty > 0$ of susceptibles

Let us know derive an (implicit) equation for the limit S_∞ of the susceptible population. We introduce the following function, along a given solution:

$$H(t) := I(t) + S(t) - r \ln S(t).$$

Taking derivatives,

$$\dot{H} = \beta SI - \nu I - \beta SI - r\frac{(-\beta SI)}{S} = 0$$

which means that H is constant along trajectories (a conserved quantity):

$$I(t) + S(t) - r\ln S(t) = I_0 + S_0 - r\ln S_0$$

for all $t > 0$. It follows, in particular, that

$$r\ln S(t) = I(t) + S(t) - I_0 - S_0 + r\ln S_0 \geq -I_0 - S_0 + r\ln S_0 =: p$$

and therefore $S(t) \geq e^{p\beta/\nu}$ for all t, so taking limits $S_\infty \geq e^{p\beta/\nu} > 0$ as claimed.

Even better, we can obtain an equation for S_∞ by passing to the limit in the conservation law, which gives (taking into account that $I_\infty = 0$):

$$S_\infty - r\ln S_\infty + r\ln S_0 = I_0 + S_0.$$

Dividing by S_0 and using that $\mathcal{R}_0 = \beta S_0/\nu$, and defining for convenience $q := \frac{1}{\mathcal{R}_0}$, we obtain:

$$\frac{S_\infty}{S_0} - q\ln\left(\frac{S_\infty}{S_0}\right) = 1 + \frac{I_0}{S_0}$$

or, letting $x := S_\infty/S_0$ and $c := 1 + \frac{I_0}{S_0} > 1$:

$$f(x) := x - q\ln x = c.$$

Observe that, since $S(t)$ is decreasing, $x < 1$. We claim that there is exactly one solution of the equation $f(x) = c$ with $x \in (0,1)$. By computing this solution, we can retrieve the final value of the susceptibles, $S_\infty = xS_0$. To prove that there is a solution x and it is unique, note that $\lim_{x\to 0^+} f(x) = +\infty$ and $f(1) = 1$, and $f'(x) = 1 - q\frac{1}{x}$ is an increasing function of x, with $\lim_{x\to 0^+} f'(x) = -\infty$ and $f'(1) = 1 - q > 0$ (because we assumed $\mathcal{R}_0 > 1$). Therefore, f decreases until some x^* and then increases back to 1. Since $c > 1$, it follows that $f(x) = c$ has a unique solution, as we wanted to prove.

There is in fact a solution of this equation that employs a classical function. For simplicity let us write $s := q^{-1} = \mathcal{R}_0$. Multiplying by $-s$, we write the equation as $\ln x - sx = -sc$. Taking exponentials and multiplying again by $-s$ results in $we^w = y$, where $w := -sx$ and $y := -se^{-sc}$. Note that, since $s > 1$ and $c > 1$, $y \in (-1/e, 0)$. The function $w \mapsto we^w$ has an inverse, defined on $(-1/e, 0)$, called the *Lambert W function* (MATLAB command `lambertw`). So, $w = W(y)$, and since $x = -w/s$, we conclude that

$$x = -\frac{1}{s}W\left(-se^{-sc}\right),$$

or, after multiplying by S_0:

$$S_\infty = -r\,W\left(-\mathcal{R}_0 e^{-\mathcal{R}_0 c}\right).$$

Typically, $I_0 \approx 0$ (one individual is enough to cause an epidemic), so $c \approx 1$ and in that case

$$S_\infty \approx -r\,W\left(-\mathcal{R}_0 e^{-\mathcal{R}_0}\right).$$

If one can measure the proportion of people who did not get sick compared with the total initial population, then one can solve for $\mathcal{R}_0$. This is one way to compute $\mathcal{R}_0$ from historical data.

4.5 | A formula for the peak value $I(t_p)$ of infectives

Determining the peak value $I(t_p)$ is of critical importance in practice. If a proportion θ of infected individuals will need hospital care, one can then predict, early on in an infection (and assuming that the SIR model is correct), the maximum number $\theta I(t_p)$ of people who will require hospital beds (or intensive care treatment) at any given time, and thus enforce a more stringent NPI policy if this number is projected to overwhelm hospital capacity.

Let us take again the conservation law

$$I(t) + S(t) - r \ln S(t) = I_0 + S_0 - r \ln S_0,$$

and now specialize at $t = t_p$, using that $S(t_p) = r$. Then,

$$\max_{t \geq 0} I(t) = I(t_p) = I_0 + S_0 - r + r \ln r - r \ln S_0 = I_0 + S_0 - r(1 - \ln(r/S_0)).$$

Another way to write this is to use that $r/S_0 = 1/\mathcal{R}_0$, so

$$I(t_p) = I_0 + S_0 - r(1 + \ln \mathcal{R}_0).$$

4.6 | Alternative definitions of $\mathcal{R}_0$

There are alternative definitions of $\mathcal{R}_0$ (for the SIR model) that one often encounters in the literature: $\mathcal{R}_0 = \beta N / v$, where N is the total population size, or even $\mathcal{R}_0 = \beta / v$. Let us quickly explain how these relate to what we are doing here. As alluded to earlier, the general definition of $\mathcal{R}_0$ is given in terms of what is called a DFSS, meaning a steady state in which there are no infected individuals. For the specific case of the SIR model, this would mean any steady state of the form $S = S_0$, $I = 0$, and $R = N - S_0$. With this definition, $\mathcal{R}_0 = \beta S_0 / v$, but there are many possible $\mathcal{R}_0$'s depending on what is the number or removed individuals at the initial time. In particular, for the equilibrium with $R = 0$, $\mathcal{R}_0 = \beta N / v$.

What about the definition $\mathcal{R}_0 = \beta / v$? It is often the case that one normalizes the population to fractions: $S_f := S/N$, $I_f := I/N$, $\tilde{R}_f := R/N$. In this case, $\dot{S} = (1/N)(-\beta SI) = -(\beta N)(S_f I_f)$ and $\dot{I}_f = (1/N)(\beta S - v)I = ((\beta N)S_f - v)I_f$, so

$$\dot{S}_f = -\tilde{\beta} S_f I_f$$
$$\dot{I}_f = (\tilde{\beta} S_f - v)I_f$$

with $\tilde{\beta} := \beta N / v$. Now $\mathcal{R}_0 = \beta N / v = \tilde{\beta} / v$ in terms of this new β. Note that S_f and I_f are dimensionless and that $\tilde{\beta}$ has units of $(1/\text{time})$, while the original β had units of $1/(\text{time} \times \text{individuals})$, so $\tilde{\beta}$ is perhaps more elegant.

We prefer not to perform this normalization because, when there are "vital dynamics" such as immigration, emigration, births, and/or deaths, the total population N would not be constant.

5 | DISCUSSION

In this article, we discussed an SIR model with strict (no-contact) lockdowns. We studied the problem of deciding when to start each one of K of lockdowns, with respective lengths T_k, $k = 1, \ldots, K$, so as to minimize the maximum number of infected individuals at any given time, and provided an exact formula in which lockdowns should start whenever the number of infectious individuals reaches $(1 + K - (e^{-vT_1} + \ldots + e^{-vT_K}))^{-1}V_0$, where V_0 is the "virtual peak" that would have resulted from no lockdowns.

As we discussed, a perfect or near-perfect lockdown is not practical, but the ideal case helps understand the problem with nonstrict lockdowns, and we presented numerical evidence that the formula is reasonable accurate even in the not totally (but still reasonably) strict case. The fellow-up paper[36] has recently started the study of the same optimization problem in the nonstrict case, showing that in the optimal case the subsequent peak after release from one lockdown coincides with the infective population at the start of the lockdown. Much further work remains, including the extension of the perfect-lockdown problem to models such as the ones presented in References 20,25,26.

We also presented results showing that equal-length lockdowns are optimal, and we quantified the sensitivity to poorly known contagion rates.

CONFLICT OF INTEREST

The authors declare no potential conflict of interest.

DATA AVAILABILITY STATEMENT

There is no data available.

ORCID

Eduardo D. Sontag https://orcid.org/0000-0001-8020-5783

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