

## Research Article

# COVID-19 Modelling: The Effects of Social Distancing

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Received 5 April 2020; Revised 6 September 2020; Accepted 9 September 2020; Published 3 December 2020

Academic Editor: Massimiliano Lanzafame

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The purpose of this article is to reach all those who find it difficult to become well informed about the steps that have been implemented to tackle the COVID-19 pandemic and to spark discussion and thought. Here, we use simple stochastic simulations to evaluate different approaches taken to manage the crisis. We then compare these results with updated data of what really happened in the UK and in South Africa. The initial simulations aligned well with how the pandemic has evolved throughout five months following lockdown. The models are, as expected, not fully accurate, but exact enough to be used as a guideline to the evolution of the disease in both high- and middle-income countries. This is shown through simulations formed by an open source code, which allows evaluation of the outcomes from different intervention scenarios or conditions.

## 1. Introduction

As we know, different countries took different approaches to try and keep the pandemic at bay; with China going on complete lockdown, the United Kingdom (UK) only going on semi-lockdown with many people still going to work, and Sweden not taking any particular directive approach to locking down, the most efficient method was, and perhaps still remains, unclear. It is hard for everyone to attain the necessary information to make informed decisions on how to act during these trying times, and the information is usually rather difficult for non-experts to understand.

This article aims to make people understand the consequences of their own actions when it comes to this pandemic. Was lockdown necessary? How important is the use of face coverings and the 2 metre distancing rule? How does following or not these rules impact on the “ruthless” reproduction number,  $R$ , and consequently on the evolution of the pandemic?

Here, we want to give people the necessary information about the changing aspects of the COVID-19 pandemic from a scientific perspective but in a simple manner, using only elementary level mathematics. We make the necessary tools available to undergo “experiments” at home; open source code is provided in order for people to see the

outcomes of certain actions by the formation of graphs or summary statistics. We hope that using this material will help readers put numbers shared on the news into context and thus, through raising awareness of the implications of different measures, we strive for more informed decisions and actions leading to a better outcome overall.

*1.1. Epidemiological and Clinical Observations.* Since the appearance of the SARS-CoV-2 virus, a number of studies trying to explain the dynamics of the outbreak were published. These studies drew mainly from publicly available data of cases reported by hospitals, WHO, China Centre for Control Disease, and other healthcare organisations.

There seems to be consensus regarding the incubation period, which has been reported with a mean of 5.0 days [1]; 6.4 days [2]; 5.5 days [3]. It seems reasonable to assume this to be about 5.5 days perhaps with a range of 2 to 14 days, also consistent with the conclusions in [4]. However, as reported by Xu et al. [5] incubation appears to be longer in tertiary patients, which will have an effect in our UK population.

From the time when symptoms appear to the patient’s hospitalisation (in those cases when needed), the median is of 7.0 days [2], or as reported by Linton et al. [1] between 3.3 and 6.5 days depending on the outcome.

Fatality rate of patients varies depending on whether we are looking at overall cases or only those of hospitalised patients. Mortality for all known cases vary from 2% and 3% [6] to 3.5% [2], while if looking at hospitalised patients, the number goes up to 7% [7], 4% to 11% [6], 8.2% [4], and even reaches 13.9% [8]. Demographic is a sizable variable in these rates, reaching up to 50%–75% for the elderly and those patients with comorbidities [6]. Healthcare systems, as well, are major players in the outcome of hospitalised patients.

Basic reproduction number or  $R_0$  has been reported between 2 and 3.5 [2]; 2.2 and 3.6 [9]; and 2 and 6.5 [6].

Finally, the number of asymptomatic cases is difficult to estimate. Three cases of group isolation have allowed for some models to appear, and the asymptomatic rate has been reported at 17.9% [10], 30% or less than a half [11], and between 50% and 75% as reported by Prof. Romagnani from the University of Florence [12].

## 2. Methods

*2.1. A Markov Chain Model for COVID-19.* We use a very simple Markov chain model to represent the dynamics of the epidemic. In Figure 1, it is illustrated how individuals can move between states. Starting from being healthy, they move to becoming infected, and then to shedding the virus (i.e., being contagious) before becoming symptomatic. From symptomatic, they can become sick (which we use to represent hospitalised) and may die. The recovery back to healthy (represented as immune, which seems plausible [13]; although it is not yet well-understood if reinfections can occur) can happen from either the shedding, symptomatic, or sick state.

People in the shedding and symptomatic state infect healthy people a rate proportional to how many they are.

We model the transition probabilities,  $p_1$  to  $p_7$ , following an Erlang distribution, represented as  $\mathcal{E}$ , but scaled when multiple outcomes from a state are possible. This allows us to mimic observed dynamics of when people move from one state to another.

The transition probability,  $p_0$ , can be represented through a desired basic reproduction number,  $R_0$ , as it can be easily shown that

$$R_0 = p_0 \sum_{i=0}^{\infty} (1 - p_2 - p_5)^i + p_0 \sum_{i=0}^{\infty} p_2 (1 - p_2 - p_5)^i \sum_{j=0}^{\infty} (1 - p_3 - p_6)^j. \quad (1)$$

To mimic the epidemiological and clinical observations summarised in the introduction, we use  $R_0 = 2.75$ ,  $p_1 \sim \mathcal{E}(10, 4)$ ,  $p_2 \sim (1 - w_5) \mathcal{E}(3, 1.5)$ ,  $p_3 \sim (1 - w_6) \mathcal{E}(14, 2)$ , and  $p_4 \sim (1 - w_7) \mathcal{E}(4, 1)$ . We empirically consider the recovery distributions and fix these as  $p_5 \sim w_5 \mathcal{E}(5, 0.5)$ ,  $p_6 \sim w_6 \mathcal{E}(10, 1)$ , and  $p_7 \sim w_7 \mathcal{E}(6, 1)$  with  $w_5 = 0.85$ ,  $w_6 = 0.9$ , and  $w_7 = 0.95$ .

R [14] was used to implement the model and a mark-down [15] implementation of all results is available as supplementary information.

## 3. Results

*3.1. Model Validation.* To assess how well the model recapitulates what we knew about SARS-CoV-2 early on during the pandemic, we conduct a simulation of the basic model and investigate the distributions of time between events, as shown in Figure 2. We observe a time from infection to becoming symptomatic between approximately 2 and 14 days with a mode around day 6. Time from symptomatic to sick is observed to peak at 7 to 8 days and time from hospitalisation to death varies between 1 and 10 days approximately.

To compare the initial trajectories for mortalities and hospitalised with what has been observed in Italy and the United Kingdom, we overlay data for either country available as of 28 March 2020, as shown in Figure 3.

*3.2. Simulating the UK.* To understand the effect of the virus at population scale from a perspective early on in the pandemic, we simulate the effect of a constant  $R_0 = 2.75$  for a population of 60 million which is seeded by 10 infected individuals on day 1. The results are shown in Figure 4, and we observe an overall duration of the epidemic of 149 days, with the number of people sick peaking on day 88. The overall mortality rate is 1.32%.

Next, we consider the effect of social distancing. This can readily be implemented in the model simply by redefining the basic reproduction number,  $R_0$ , at the day the measures are implemented to reflect a sufficient decline in how many people each shedding or symptomatic person will infect. On one extreme, we have perfect social distancing with  $R_0 = 0$  but we also investigate the effect of  $R_0 = 0.5$  and  $R_0 = 0.75$ .

Day 55 is used for initiating social distancing since the simulations here showed 337 dead and 5486 sick consistent with reported numbers on 23 March 2020 when the United Kingdom initiated lockdown.

In the case of perfect social distancing, the mortality rate is only 0.04% (21474 dead) and the epidemic is resolved by day 90 with the number of people sick peaking on day 70.

In the case of a more relaxed social distancing with  $R_0 = 0.50$ , the mortality rate is 0.13% (79781 dead) without having the epidemic resolved by day 250 and with the number of people sick peaking on day 71. A somewhat stricter social distancing with  $R_0 = 0.25$  would resolve the epidemic by day 189 and lead to 32998 dead.

Finally, if the social distancing is relaxed to  $R_0 = 0.75$ , we observe a much later peak in the number of people sick on day 112 and also a much larger mortality rate of 0.55% (330964 dead).

*3.3. A Post Hoc Update.* To assess model performance with more data available, we overlay available data for the UK as of 31 August 2020 with model simulations. We consider minor adjustments to when social distancing is initiated and, as above, evaluate the effect of different  $R_0$  values, chosen to provide results close to what was observed. As the UK ceased reporting on recovered cases, Figure 5 shows the cumulative number of cases alongside the cumulative number of dead.

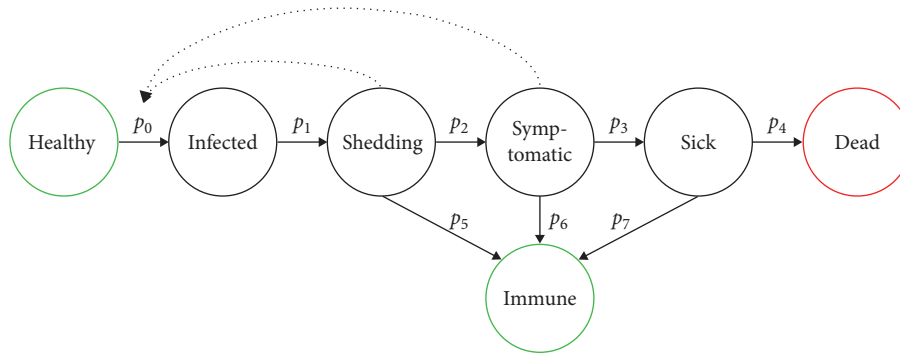


FIGURE 1: A Markov chain model describing how individuals can transition between states after infection.

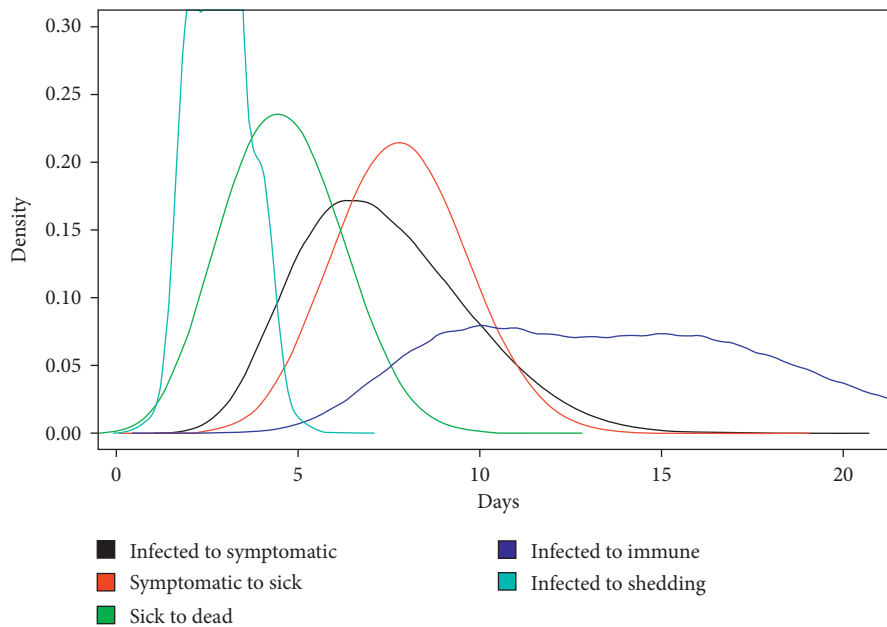


FIGURE 2: Observed densities of time between events in the model.

3.4. *Contrasting to South Africa.* As a contrast to the UK simulations mentioned above, we also simulate, as shown in Figure 6, the pandemic for South Africa, which has a population size similar to that of the UK and which announced lockdown on the very same date [16, 17]. To reflect a younger population demographic, we increase  $w_6$  and  $w_7$ , representing the recovery proportions from symptomatic and sick, to 0.95 and 0.98, respectively, and to further reflect a higher proportion of asymptomatic cases, we use  $w_5 = 0.95$ .

#### 4. Discussion

As can be seen from Figure 2, the simulations displayed above correlate well with data found in the biomedical literature. As seen in Figure 3, the number of deaths reported early on in Italy and the United Kingdom correlate well with the predicted deaths. The number of recorded cases also conform well with the simulation; however, they may be

slightly higher due to the larger number of people getting tested than actually being hospitalised. All in all, it is clearly seen that the simulation overall reflects the initially available data well.

Now, looking at what approaches the UK could have taken; if the UK were to take the route relying on herd immunity, as seen in Figure 4, almost all of the population would have become immune (with the exception of the 1.3% of the population that would have died). The length of time that this will have taken is just over three months, as seen in the graphs. The result would thus have been a relatively fast outcome with a large percentage of people immune, but with the downside of having an estimated 800,000 mortalities.

Alternatively, the UK could also have taken the approach of a very strict lockdown, as seen in, e.g., China. If so, as shown in Figure 7, the pandemic would be predicted resolved in roughly 1.5 months with only about 21,000 dead.

In reality, the UK took an approach somewhere in between; early predictions thus suggested a situation as shown

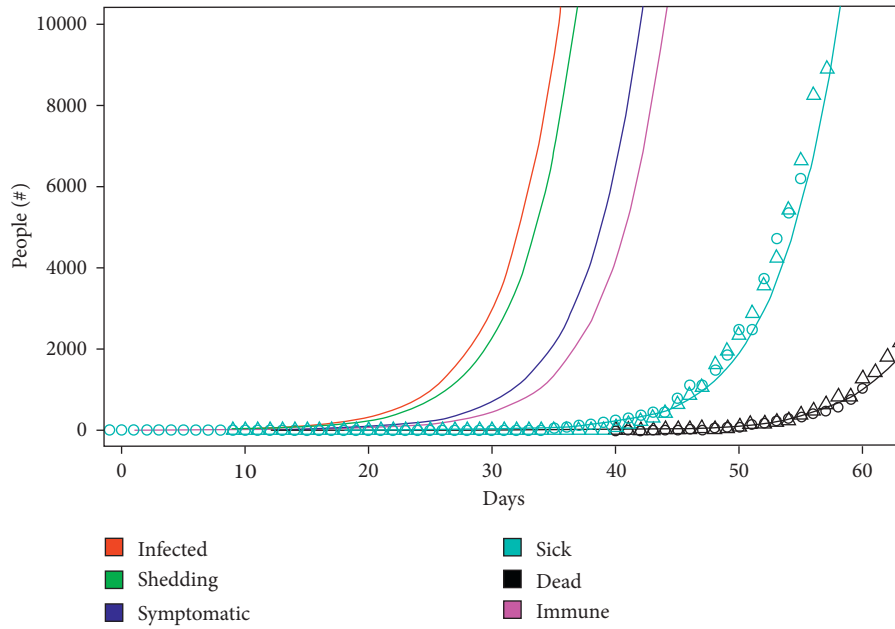


FIGURE 3: Model simulations overlaid with observational data of reported cases and mortalities from Italy ( $\Delta$ ) and the United Kingdom ( $\circ$ ).

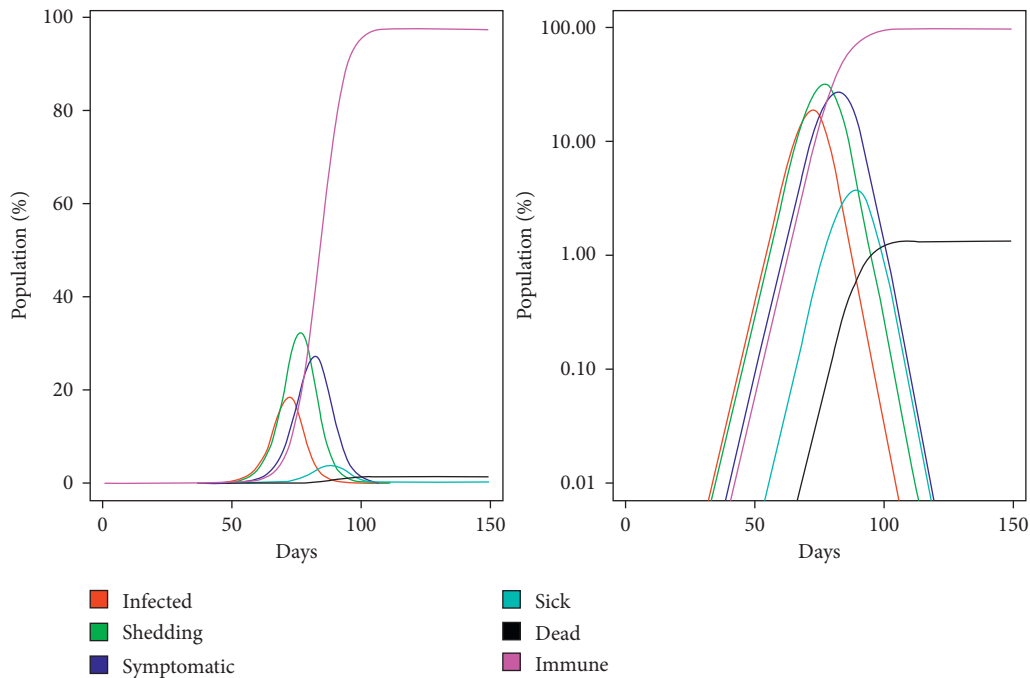


FIGURE 4: Model simulations with constant  $R_0 = 2.75$  and a population size of 60 million.

in Figure 8, with 4.5 months of semi-lockdown and with approximately 80,000 dead. With data available post hoc, one can, as seen in Figure 5, conclude that these predictions were qualitatively correct. The model calibration based on data early in the pandemic did perhaps underestimate the effect of initial social distancing following Matt Hancock’s address to the House of Commons one week ahead of when Boris Johnson told people to stay at home. Advancing the

modelled time of social distancing to day 50, instead of day 55 as initially used, leads to better overall consistency with actual observations.

We can also see what would have happened if the lockdown had been even more relaxed, with people failing to respect the government guidelines. Figure 9 shows the effect of a higher reproduction number, leading to a “lockdown” taking over 6 months and resulting in more than 300,000 fatalities.

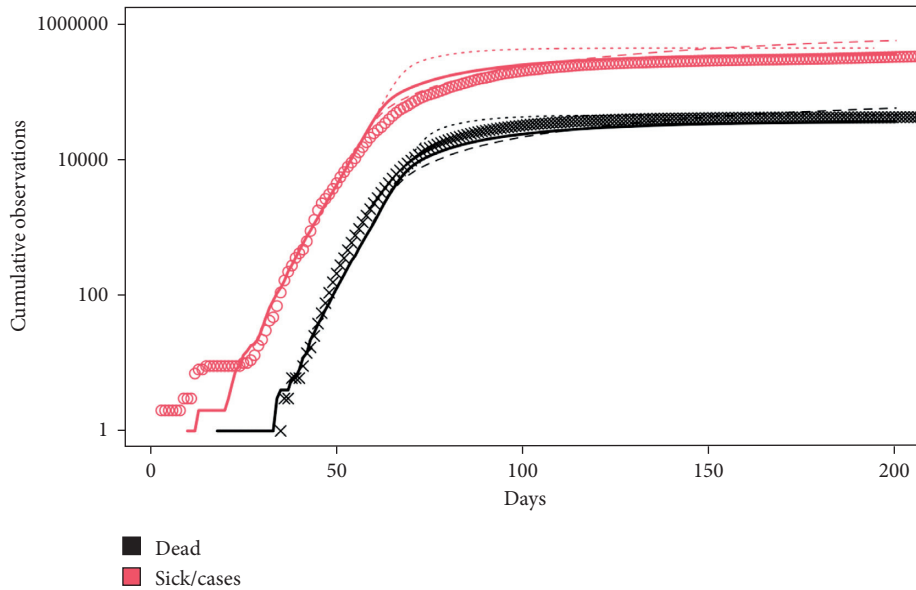


FIGURE 5: Total number of cases (o) and deaths (x) observed in the UK by 31 August 2020 alongside comparable model simulations implementing social distancing at day 48 (– –), 50 (—), and 55 (– · –) with  $R_0 = 0.6$ ,  $R_0 = 0.5$ , and  $R_0 = 0.3$ , respectively.

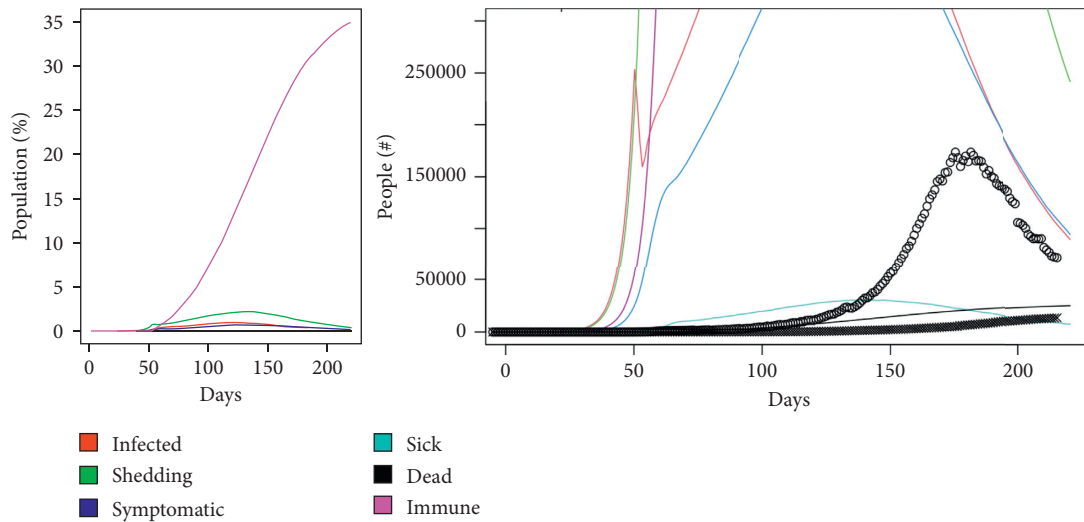


FIGURE 6: Model simulations implementing social distancing with  $R_0 = 0.85$  from day 50 for a population size of 60 million with  $w_5 = 0.95$ ,  $w_6 = 0.95$ , and  $w_7 = 0.98$ . Observed number of fatalities (x) and active cases (o) in South Africa.

In the above, we discussed the situation from a UK perspective, but to assess the utility of the model in a very different setting, we next consider South Africa. South Africa is a country with a similar population number to that of the UK and which implemented lockdown at a similar time [16, 17]. The number of deaths from COVID-19 in South Africa are however much less than that reported in the UK. With a population demography that is much younger, this is almost certainly a contributing factor [18], but also a higher degree of exposure to other coronaviruses is a potential part of the explanation [19]. Using the same model, but increasing the probabilities of recovery (including prior to becoming symptomatic), allows predictions which are qualitatively consistent with observations, as seen in

Figure 6. One can choose to explain the slightly higher predicted than observed number of deaths as under-reporting. Equally, the slower number of reported cases can be interpreted as a consequence of limited testing capability [16]. The simulations thus suggest a somewhat higher  $R_0$  in South Africa following intervention compared to that of the UK and a much larger proportion of the population having been infected.

However, we should remember that this is just a model (and “all models are wrong” [20, 21]). We have seen how the time when social distancing started needed to be adjusted in Figure 5 to better fit the updated data and perhaps also that the number of sick versus symptomatic is somewhat over-estimated. Overall, the model is nigh accurate, but still, not

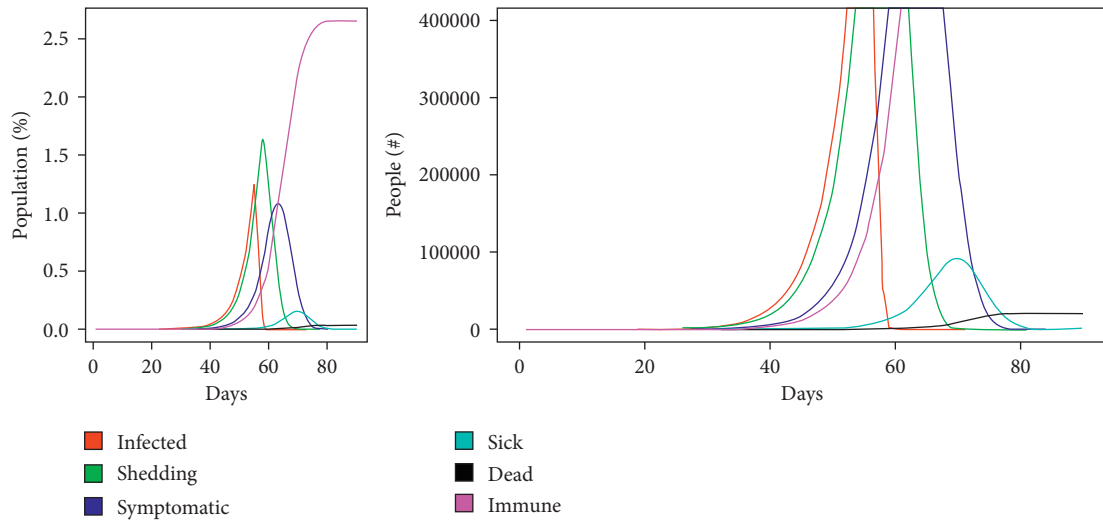


FIGURE 7: Model simulations implementing perfect social distancing with  $R_0 = 0$  from day 55 for a population size of 60 million.

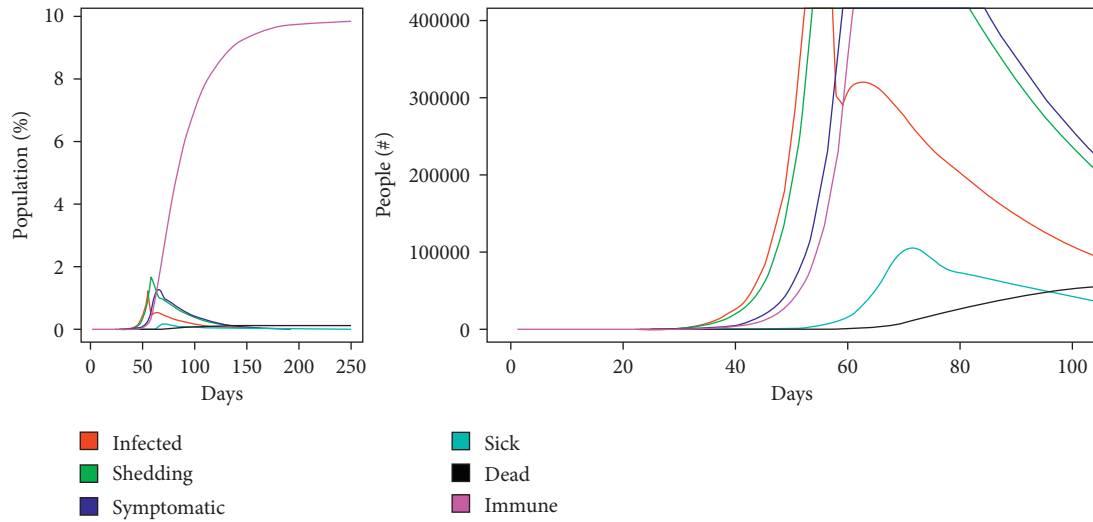


FIGURE 8: Model simulations implementing social distancing with  $R_0 = 0.50$  from day 55 for a population size of 60 million.

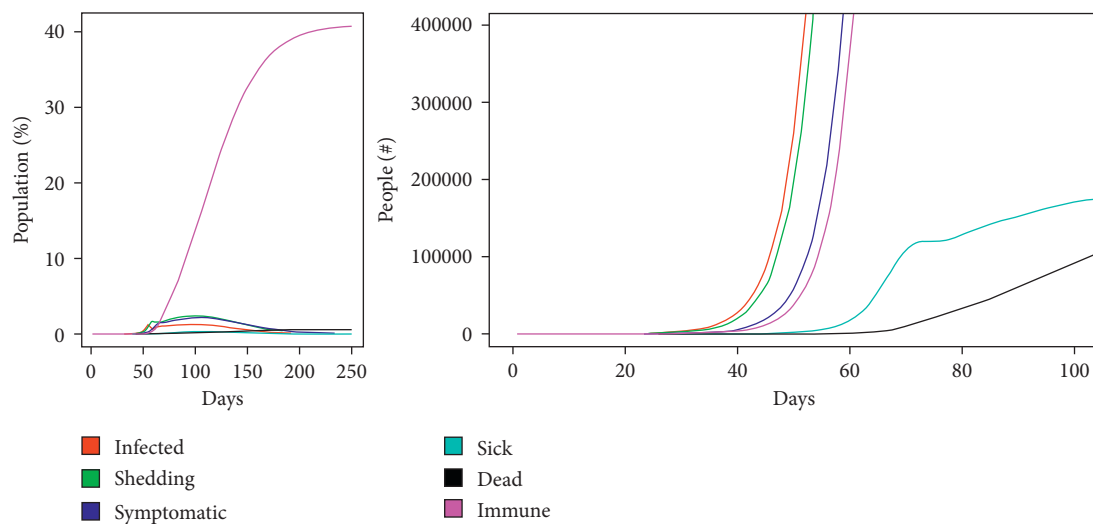


FIGURE 9: Model simulations implementing social distancing with  $R_0 = 0.75$  from day 55 for a population size of 60 million.

exact. The simulation results should therefore be considered directional rather than quantitative and further validation and stress testing, including sensitivity analysis of the results to the choice of parameters, should be done to understand the limitations of specific model predictions.

We have made the code available for everyone to use. We encourage people to use it and to look at the consequences of different national or international actions. If, for example, one would like to test and see what would happen if people start to relax after one month of strict lockdown, this can simply be done by increasing the  $R_0$  number at that point and evaluating the results. This is one of the advantages from using a simply stochastic simulation approach as presented herein, as opposed to more classical approaches in epidemiological modelling based on differential equations [22].

## Data Availability

All data used within this manuscript are included in Supplementary Materials.

## Conflicts of Interest

The authors declare no conflicts of interest.

## Supplementary Materials

A R markdown implementation of all results presented herein is included as Supplementary Materials. (*Supplementary Materials*)

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