

Pandemics and Flexible Lockdowns: In Praise of Agent-based Modeling

Igor Douven

IHPST / CNRS / Panthéon–Sorbonne University

igor.douven@univ-paris1.fr

Abstract

Philosophers have recently questioned the methodological status of agent-based modeling. Meanwhile, this methodology has been central to various studies of the COVID-19 pandemic. Few agent-based COVID-19 models are accessible to philosophers for inspection or experimentation. We make available a package for modeling the COVID-19 pandemic and similar pandemics and give an impression of what can be achieved with it. In particular, it is shown that by coupling an agent-based model to a standard optimizer we are able to identify strategies for implementing non-pharmacological interventions that flexibly lower or raise social activity, depending on how the outbreak develops, while balancing various desiderata that cannot be fully satisfied together. The simulation outcomes to be presented testify to the power of agent-based modeling and thereby help to push back against the recent philosophical critique of this methodology.

Keywords: Agent-based models; COVID-19; mitigation strategies; multi-objective optimization; non-pharmacological interventions; pandemic response.

1 Introduction

Agent-based computational modeling is increasingly used to study social phenomena that are too complex to be captured mathematically (e.g., by a system of dynamic equations), even if they arise from interactions that can typically be described as obeying a small set of simple rules. Agent-based models have been applied to such diverse phenomena as migration dynamics, social mobility and inequality, racial segregation, urban planning, traffic scheduling, the emergence of social norms, the spread of mis- and disinformation, and more (Crosscombe and Lawry 2016; Deffuant et al. 2000; Dittmer 2001; Douven and Hegselmann 2021; Glass and Glass 2021). Social epistemologists and philosophers of science have been using agent-based models to study opinion polarization, the effect of peer disagreement on agents' beliefs, the role of experts, the merits and possible demerits of scientific collaboration, and the best ways to organize research teams, among many other things (De Langhe 2013; De Langhe and Greiff 2010; Douven 2010, 2019a, 2023; Douven and Hegselmann 2022; Hegselmann and Krause 2002, 2005, 2009, 2015; Kummerfeld and Zollman 2016; Olsson and Vallinder 2013; Vallinder and Olsson 2013; Zollman 2007).

Not all are convinced of the usefulness of agent-based modeling. For instance, in his *New York Times* blog post of November 30, 2010, the economist Paul Krugman complains: “I was one of those people who got all excited about the possibility of getting somewhere with very detailed agent-based models—but that was 20 years ago. And after all this time, it’s all still manifestos and promises of great things one of these days.”¹ More recently, philosophers and other researchers

¹See <https://krugman.blogs.nytimes.com/2010/11/30/learned-helplessness/>.

have also questioned the methodological value of agent-based models, and argued that they tend to promise more than they deliver (Borg et al. 2019; Cristelli 2014; Frey and Šešelja 2018, 2020; Rosenstock et al. 2017; Šešelja 2019; Thicke 2020). Their most central concerns have been that agent-based models

1. tend to oversimplify agent behavior, decision-making processes, and environmental processes, and thereby may fail to capture the true dynamics of a system, which may in turn lead to inaccurate predictions;
2. can be highly sensitive to initial conditions and modeling assumptions and decisions (e.g., which variables to include), making it difficult to draw general conclusions from the models; and
3. can be hard to evaluate (verify and validate), because of model complexities and because of limited data availability, given that, for many social systems, data is hard or expensive to collect.

If these concerns are valid, and it is unclear what real-world implications agent-based models have, or how we should proceed to test those implications, then these models cannot be of much practical value.

In our view, however, the important role that agent-based models have played in fighting the COVID-19 pandemic suggests that agent-based models can in fact be of *great* practical value. A recent study (Lorig et al. 2021) reviews 126 papers presenting agent-based simulations of the COVID-19 pandemic, many of them aiming to investigate the efficacy of so-called non-pharmacological interventions (NPIs), including curfews, lockdowns, mask-wearing policies, and travel bans. Some noteworthy agent-based models for the study of COVID-19 that appeared after the publication of Lorig et al. (2021) include Hinch et al. (2021), Kerr et al. (2021), Koehler et al. (2021), and Vermeulen et al. (2021). The probably most famous COVID-19 model (often referred to as the “Imperial College model”), which informed the COVID-19 policies of the British government in earlier stages of the pandemic, is partly agent-based (Adam 2020).²

Agent-based COVID-19 models tend to be large-scale, computationally intensive models, drawing on real-time databases, and coded in languages which require extensive programming experience. Therefore, few of these models are readily accessible to philosophers for inspection and experimentation. We make available a computationally light-weight package for modeling the COVID-19 pandemic and similar pandemics and show in this paper what can already be achieved with it. The package is written in Julia (Bezanson et al. 2017), a language that combines ease of use with speed, and it allows users to couple an agent-based model to a standard multi-objective optimization algorithm, specifically, a form of evolutionary computing, to address the question of how best to respond to the outbreak of a pandemic, in particular how best to trade off between desiderata that may pull in different directions (e.g., the desire to lower the number of new infections and the desire to limit economic activity as little as possible). Agent-based modeling is applied to model a community affected by such an outbreak, and evolutionary computing, to find optimal response strategies. It is shown how this combination can be instrumental in identifying optimal strategies for implementing NPIs. The outcomes of our study are meant to illustrate the power of agent-based modeling and are thus to offer some pushback against the recent philosophical critique of this methodology.

Section 2 briefly describes the traditional approach to modeling pandemics via systems of differential equations and it highlights some drawbacks of this approach that agent-based models are able to avoid. Section 3 describes the agent-based model we are going to rely on and shows how

²The Imperial College model has been criticized in Winsberg et al. (2020), but see van Basshuysen and White (2021) for a rejoinder.

it can be used to assess mitigation strategies. Next, Section 4 looks at the possibility of recruiting evolutionary computing for selecting hyperparameter settings and explains how this technique can help us respond rapidly and effectively to pandemic outbreaks while being sensitive to the importance of disrupting economic activity as little as possible. Section 5 revisits the concerns about agent-based models stated above in light of what has been learned from agent-based pandemic models.

2 From equation-based to agent-based models

The most commonly used mathematical model for the spread of a directly transmitted infectious disease is the so-called susceptible–infected–recovered (SIR) model, which dates to Kermack and McKendrick (1927). The SIR model divides the relevant population into three “compartments”: a compartment of individuals susceptible to infection, a compartment of infected individuals, and one containing those who have recovered from the disease and are considered to be immune, where the third compartment includes the individuals who have died from the disease.

In this model, the movement of individuals from one compartment to another is governed by three differential equations:

$$\frac{dS}{dt} = -\frac{\beta IS}{N}, \quad (1)$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I, \quad (2)$$

$$\frac{dR}{dt} = \gamma I. \quad (3)$$

Here, S is the number of susceptible individuals, I the number of infected individuals, and R the number of recovered individuals, with $N = S + I + R$ the number of individuals in the population, which is assumed to remain constant. Furthermore, β is the so-called contact rate, which is proportional to how many people, on average, a person meets during a unit of time, and γ is the recovery rate, that is, the reciprocal of the average duration of infection in units of time.

It is easiest to understand these equations by focusing on (1) and (3) first. Equation (1) says that the rate at which individuals leave the compartment of susceptibles at a given time depends on I —the number of people from whom the susceptibles *can* catch the disease at that time—and the extent to which the infected come in contact with others, and so have an *opportunity* to actually transmit the pathogen. And Equation (3) says that the rate at which R changes at a given time depends on I and on how fast someone who is infected recovers, on average. Obviously, the rate at which the number of infected changes at a given time depends on how many individuals are *newly* infected—which are exactly the individuals leaving the susceptibles compartment—and the number of individuals who recover. That is the content of Equation (2). This system of equations is usually solved numerically (i.e., by computational approximations), although analytical solutions now do exist (Harko et al. 2014).³

³The SIR model has many variants that allow for more fine-grained compartmentalizations, such as the SIRD model, which separates the recovered (in the ordinary sense of the word) from the deceased (D), and the SEIR model, which includes a compartment of individuals who have been exposed (E) to the pathogen but are not (yet) sick. For each of these models, there is also a variant that reckons with the possibility that recovered people become susceptible again, although most of the models that have been proposed in the COVID-19 literature so far assume that recovered individuals have long-lasting immunity (Flaxman et al. 2020; Moghadas et al. 2020), an assumption which also underlies other approaches to the COVID-19 pandemic (Eichenberger et al. 2020). (Our own model will rely on this assumption as well.)

The standard SIR model assumes β and γ (contact and recovery rate) to remain fixed during the course of an outbreak, which is unrealistic. Even without government intervention, at least part of the affected population will restrict their social interactions as a precautionary measure. As a result, the contact rate will drop. And due to medical advances, the recovery rate may increase. While this limitation can be overcome (López and Rodó 2020), the assumption of homogeneous mixing, which the model also makes, is more problematic. Homogeneous mixing means that any two individuals in the population are equally likely to meet. However, most of our encounters are not with random people, but with friends, relatives, and colleagues. And it has long been recognized that the social networks that people form are crucial to how, and how fast, contagious diseases spread (Keeling and Eames 2005; Koopman and Lynch 1999).⁴

Agent-based models easily avoid these pitfalls. In the case of disease modeling, these models permit the simulation of agents moving about, meeting, and thereby possibly infecting or getting infected by, others, recovering (or not) from the disease, practising physical distancing to various degrees, and so on. They allow us to endow each agent with a set of properties, such as age, gender, health status, professional occupation, risk aversion, and in particular also the property that the agent moves only, or mainly, within a certain network of agents, thereby doing away with the assumption of homogeneous mixing. A population in this kind of model typically gets “updated” in discrete time steps, which not only enables us to closely monitor the step-wise evolution of an outbreak but also makes it easy to intervene—for instance, by changing some agent properties—at any moment we like; the effects of such interventions, in turn, can themselves be monitored step by step, and further adjustments to the system can be made, if necessary. Agent-based models thereby make it possible to study the effects of “microscale policies” (Kerr et al. 2021).

For these reasons, we built an agent-based model which (i) takes into account social network structures in a community, and (ii) readily permits the kind of real-time monitoring and intervening that we believe to be essential for adequately comparing mitigation strategies. In the following section, we describe the model and then recruit it to study the kind of intermittent NPIs that many governments have been using in the hope to steer their population as safely as possible through the COVID-19 pandemic.

3 An agent-based network model of COVID-19 spread

In December 2019, China reported the first cases of what soon came to be known as “Coronavirus disease 2019” or COVID-19. Before long, cases were found all across the globe. By now (April 2023), there are over 762 million confirmed cases worldwide, with a death toll surpassing six and a half million. While a few countries responded quickly enough to the initial outbreak to curb community transmission from the start (using a strategy of massive testing and contact tracing), most countries missed that opportunity and had to go into lockdown by having their residents shelter in place or at least exercise restrictive physical distancing. While these restrictions proved generally effective, prolonged lockdowns, and NPIs more generally, soon came to seem unsustainable in view of their social and economic costs (Chudik et al. 2020; Dale et al. 2021; Gandolfi 2021; Greyling et al. 2021; Meyerowitz-Katz et al. 2021; Nicola et al. 2020). Thus, many governments started pivoting toward a strategy of intermittent, typically shorter and often (and ideally; see Karatayev et al. 2020) local NPIs. In many countries, this was the dominant response strategy until vaccines became widely available, and even since have various countries had temporary lockdowns, because a combination of vaccine hesitancy, diminishing vaccine effectiveness, and the emergence of new variants of

⁴The role of such networks has been studied in relation to the spread of measles, influenza, HIV and other sexually transmitted diseases (Klovdahl et al. 2001, 1994; Needle et al. 1995), and recently also in relation to COVID-19 (Block et al. 2020).

the virus had led to a renewed rise in the number of infections (Goldenberg 2021; Lin et al. 2022). Nevertheless, how to do intermittent NPIs the right way is still a hotly debated question.

What is clear is that, for a strategy of intermittent NPIs to work, it is critically important that an emerging “wave” of cases be detected promptly and reliably: promptly, because a couple of days earlier or later can make all the difference between a healthcare system that can cope and one that is overwhelmed; and reliably, because raising false alarms will only further erode the trust of a public that in many countries already started to suffer from “lockdown fatigue” quite some time ago. Just as important as early detection is being able to accurately predict the effects of possible mitigation strategies, especially because the choice is typically not just between a blanket lockdown and an unconstrained reopening of the economy. Rather, the goal is for interventions to be commensurate with the severity of the threat at the time they are made: they should prevent large-scale outbreaks but at the same time impede economic activity as little as possible. How best to balance these desiderata is a nontrivial question, however.

For reasons mentioned previously, agent-based models for simulating the spread of an infectious agent (like SARS-CoV-2, the virus responsible for COVID-19) that take social network structure into account and allow for dynamic interaction as well as for a close monitoring of the changes brought about by interventions appear well suited for developing adequate response policies. In particular, they can facilitate identifying strategies for implementing NPIs that flexibly lower or raise social activity, depending on how the outbreak develops, with an eye both toward reducing spread of the virus and toward limiting economic damage. While models of this kind exist, they are not widely available, either because they use proprietary code, or because they are written in low-level languages like C++ or FORTRAN which require specialized knowledge, or because they are complicated to work with for other reasons.

We firmly believe that nothing will help to convince skeptics of the value of agent-based models as much as gaining first-hand experience with such models, such as, in the present case, running agent-based simulations of the spread of COVID-19 in a community, trying out different starting assumptions and different intervention strategies, and comparing the results with publicly available data about the pandemic. Therefore, the Supplementary Materials for this paper contain a Julia package for creating models of the kind just described.⁵ Readers are encouraged to install the package and to experiment with it, as doing so should make it easy to appreciate how flexible the agent-based modeling approach is and how swiftly very detailed information about local properties of a population (e.g., about community structure) can be taken into account.

To give an impression of what the package can accomplish, the remainder of this section describes and motivates a particular agent-based COVID-19 model and examines its performance using the Julia package, comparing model-based predictions with real-world data. As will be seen, the model has one central parameter, which specifies the extent to which the agents are socially active. We suppose that policymakers are able to manipulate this parameter, at least to some extent, and thereby to effectuate, and also ease, NPIs in a flexible manner. But exactly how they do this—how they translate data about the ongoing pandemic into policy decisions—depends on further parameters (i.e., hyperparameters), and the policymakers’ success depends on whether they are able to find a right combination of those other parameters. To help with that task, a standard multi-objective optimization algorithm can be coupled to the agent-based model. How to do that is shown in the next section.

One may think of the core of our model as a village, consisting of a number of households and possibly some shops, restaurants, offices, and a gym. The agents populating the village interact

⁵The package can be installed via Julia’s package manager; instructions on installation and basic usage are given in the README of the package’s GitHub repository: <https://github.com/IgorDouven/COVID.jl>. For gentle introductions to Julia, see for instance Kochenderfer and Wheeler (2019) and Douven (2022, Appx. E).

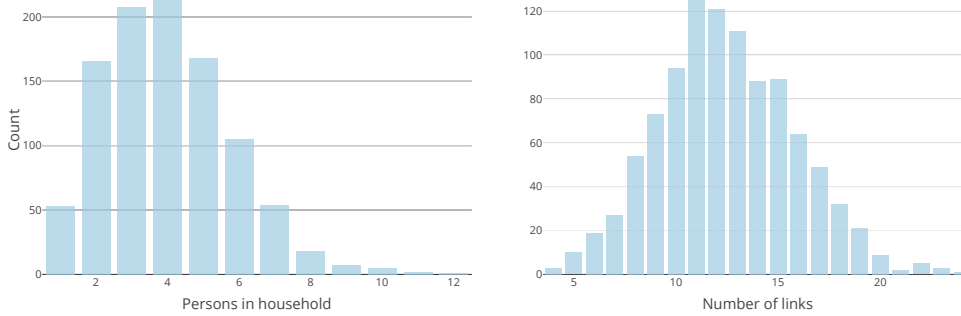


Figure 1: Bar charts of household sizes (left) and number of links per household (right).

socially only with people in their network. There are no contacts with non-villagers, so for the purposes of our study the village can be conceived as a world on its own and an agent’s social network as being limited to some subset of the villagers.

Formally, the village is represented by an undirected Erdős–Rényi graph with 1000 nodes and a link probability of 1.25 percent.⁶ The nodes represent households, for the most part; some, as said, can be thought of as representing a shop, and so on. The average size of a United States household was 2.52 in 2019, and numbers for most other Western countries are not much different. Jarosz (2020) proposes to model US household sizes by a Poisson distribution with $\lambda = 1.52$ shifted to the right by 1 to avoid empty households (and to obtain an average of 2.52). If we went along with this exactly, we would almost certainly be underestimating the average number of people a villager might meet in his or her network, precisely because people may, on a regular basis, visit the gym, go to a bar, or frequent a grocery store, and so on. The simplest way to correct for this is to take a slightly higher mean, which is what we did, settling for a Poisson distribution with $\lambda = 3$, also shifted to the right by 1.⁷ The resulting model gives rise to the distributions of household sizes and links per household shown in the left and right panel of Figure 1, respectively.

The basic setup is that every agent visits one node (household, gym, store, . . .) per unit of time (a day, let us assume), where this node is chosen from the ones in their network. The probability with which agents select a given node from their network to visit at the given time step is, at least initially (see below), proportional to the size of the node (i.e., the number of people in a household), meaning for instance that an agent is twice as likely to visit a six-person household as a three-person household. Naturally, an agent can also *be* visited by agents in their network. We assume that every visit is “successful” in that whenever a household is visited, its members are present, and not out to visit other households. We numerically verified that, given this setup, an agent has an average of 5.79 (± 2.91) contacts per day, which appears reasonable in light of the data about social mixing patterns reported in Klepac et al. (2020).

To this setup is added a weight parameter w representing the probability that an agent will *skip* a visit, meaning that, for any given time t , the agent will decide *not* to go out at t with probability w

⁶One could consider other types of graphs, or even consider switching from one type to another as part of a mitigation strategy (Block et al. 2020). Experiments we conducted with a number of plausible alternatives yielded results not very different from those to be reported here. Using the Julia package in the Supplementary Materials, readers may want to run their own experiments with different graphs representing different assumptions about the community’s social structure.

⁷A more complicated solution would be to introduce two or even more types of nodes and then model their sizes differently per type. Again, the Supplementary Materials allows interested readers to experiment with this and other variants of our setup. Here, too, our own experiments showed qualitative conclusions to be remarkably robust under different parameter settings and other modeling choices.

and will visit the node picked in the way just described with probability $1 - w$. If agents stay home, then they may infect their home mates with the same probability with which they would otherwise have infected the agent or agents they would have visited, and the home mates may infect them with the same probability with which they may infect anyone else in their network.

Importantly, the weight parameter can be time-indexed, which enables us to model the effects of mitigation efforts; for instance, we can conceive shelter-in-place mandates as attempts to raise w and of the easing of such measures as attempts to lower w . Naturally, the value of w may increase independently of NPIs, as people may become wary of leaving the house for fear of contracting the virus, and it may also decrease independently of any government orders, for instance due to a growing noncompliance with those orders.

To make this a model for studying the spread of COVID-19, we assume that agents are, at any given time, in one of three states: susceptible to SARS-CoV-2 infection, infected by the virus, or recovered from the disease (which includes agents who have died from it). Furthermore, we make the following assumptions:

- at start time, 1 percent of the village population is infected, the rest being susceptible;
- the probability that a contact between an infected and a susceptible person results in an infection of the latter—the transmission rate τ —is 4 percent (Otto 2020);
- the maximum duration of the disease is 24 days, but half of the infected need only half that time to recover (Liu et al. 2020);
- the more seriously ill, who do not recover after 12 days, have in the remaining days of their disease a lowered transmission rate of 1 percent (Liu et al. 2020);
- the more seriously ill do not visit anyone, and their households are not visited by anyone;
- patients have a 1 percent chance of dying from the disease (Mizumoto and Chowell 2020; Russell et al. 2020).

Given that the mean number of links is 12.5 and the mean number of people in a household is 4, the average number of contacts per node equals $\bar{n} = 12.5 \times 4 = 50$. And the assumptions about recovery—half of the patients recover after 12 days, the other half after 24 days, the latter being only one fourth as infectious during the second half of their illness—yield a recovery rate γ of $2/27 \approx 0.074$. Using these values together with an assumed transmission rate τ of 4 percent, we can, following Keeling and Eames (2005, Sect. 5.1), calculate the rate of growth as

$$\tau \frac{(\bar{n} - 1) \bar{n}}{\bar{n} + 1} - \gamma = .04 \frac{49 \times 50}{51} - 0.074 \approx 1.85.$$

This outcome is in the range of growth rates that have been reported in the COVID-19 literature (Viceconte and Petrosillo 2020).

For the purposes of this paper, it would not really matter if the above assumptions turned out to be somewhat off, given that our primary goal is not model fitting or prediction but rather to make a methodological point: drawing attention to the practical value of agent-based modeling, and more specifically also drawing attention to how the combined use of agent-based modeling and evolutionary computing can help us deal with the current pandemic and possible future ones. Nevertheless, it is encouraging to see that simulations in the model yield results that fit known data remarkably well. For example, Figure 2 compares model predictions for $w = .36$ with the data for the province of Anhui in China.⁸ Indeed, you could fine-tune parameters (e.g., percentage of population infected at start time, transmission rate, duration of the disease) to your heart's content here and thereby try to achieve an even better model fit (for details, see the Supplementary Materials).

⁸The data for Anhui were retrieved from <https://github.com/CSSEGISandData/COVID-19>, which is the COVID-19 data repository of the Center for Systems Science and Engineering at Johns Hopkins University. It is to be noted that the data have been scaled to match the size of the population in the model.

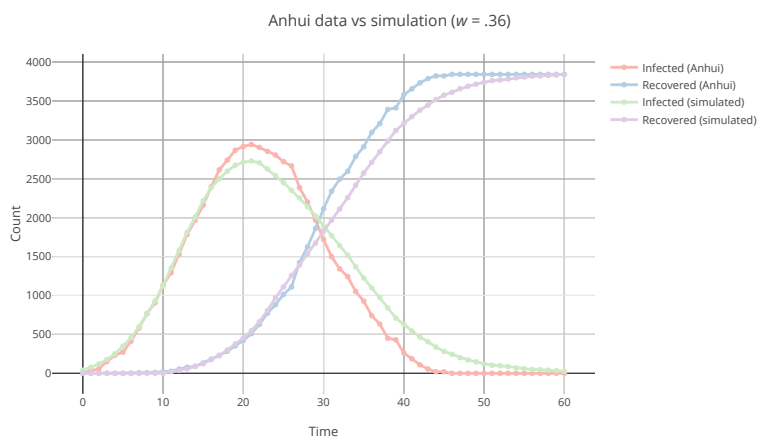


Figure 2: Data from Anhui, China, compared with the output from our model for $w = .36$.

It is worth observing that more detailed data could become available about how COVID-19 spread through the Anhui community, or how it spread through other communities, and that this would offer a possibility of validating our model in a way that does not exist for equation-based models (Hunter et al. 2018). For our model lets one trace, from one point in time to the next, exactly which agents get newly infected and which recover, thereby revealing patterns in the spread of COVID-19 across households. Figure 3 shows a selection of 10 percent of the households in the model (showing the full model would clutter the picture). It is clear from this figure what kind of detailed information can be obtained from a working agent-based model. For instance, for each point in time we can look at how household size, or number of links, or various network statistics (such as betweenness centrality and the clustering coefficient; see, e.g., Jackson 2008, Ch. 7) correlate with number of infected members in a household. Any such model could be compared with data about a local outbreak, provided there is sufficient knowledge about the social network structure of the community affected by it.

Another welcome feature of agent-based models of the spread of COVID-19, one already mentioned above, is that they make it utterly simple to intervene in the (simulated) evolution at any time we like. As a result, we can easily compare different mitigation measures in terms of their effects before deciding to impose any one of them (or to refrain from intervening at all). We propose to model such possible interventions generically, through manipulating the value of w (i.e., the probability that agents will skip a visit and stay home instead). Exactly what policies might be most effective to bring about such changes in actuality may differ from one country to another (e.g., depending on how compliant a population is) and even from one point in time to another (e.g., depending on whether earlier mitigation measures were perceived as overreactions by the public). Such implementation details are beyond the scope of this paper.

Comparing mitigation strategies requires that we be clear about the criteria by which such strategies are to be judged. Opinions seem to have converged on the following: mitigation strategies should help minimize the number of deaths from the disease; they should help avoid an overwhelmed healthcare system, given that this could lead to further deaths and/or because it would be costly (e.g., because patients would have to be transported to neighboring countries); and they should help avoid large-scale damage to the economy, which could affect people’s livelihoods for years to come. Obviously, these criteria (especially the first two versus the third) pull in different directions, and so we are effectively facing a multi-objective optimization problem (Eichenbaum et al. 2020).

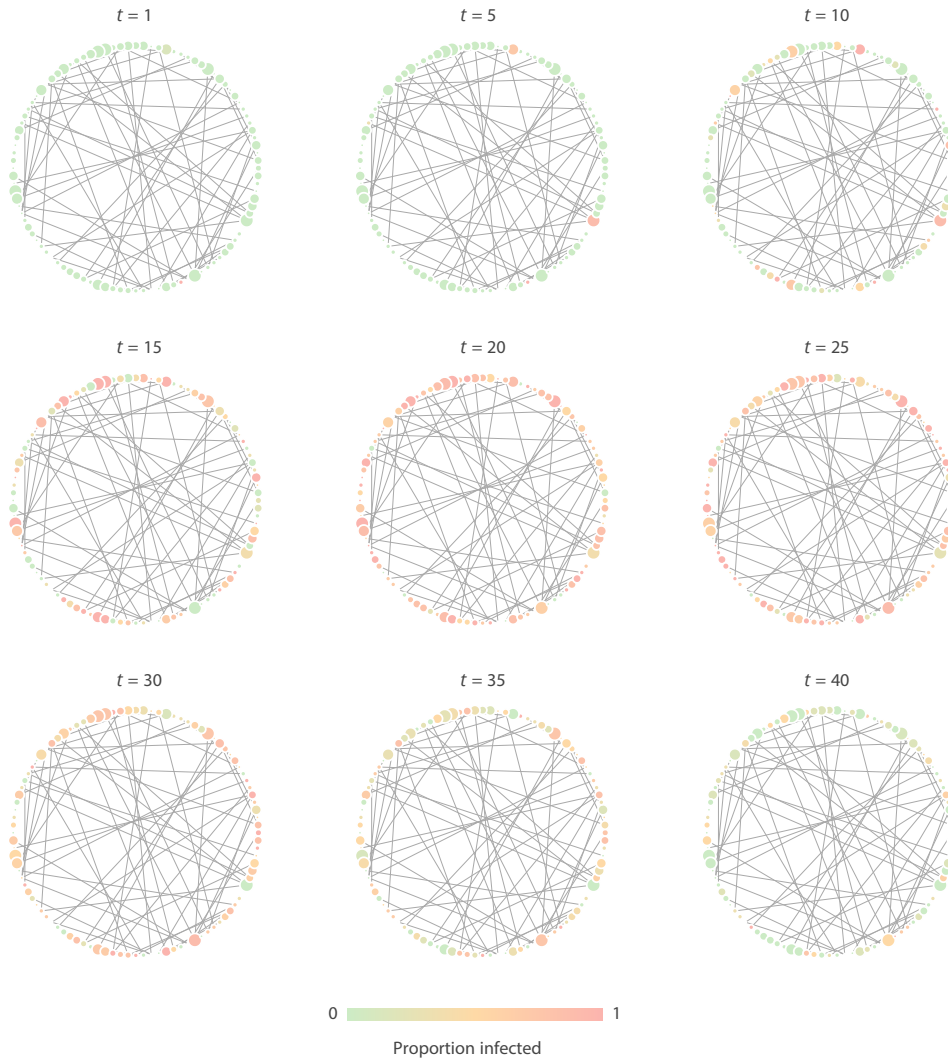


Figure 3: Snapshots of the evolution of the simulated outbreak shown in Figure 2 from the start of the spread ($t = 1$) to the point where the wave has basically passed ($t = 40$). The snapshots look at a randomly selected subgraph containing 10 percent of the nodes from the full model. Color indicates proportion of people in a household who are infected, node size indicates size of the household. A line connecting two nodes indicates the presence of a social link between the corresponding households.

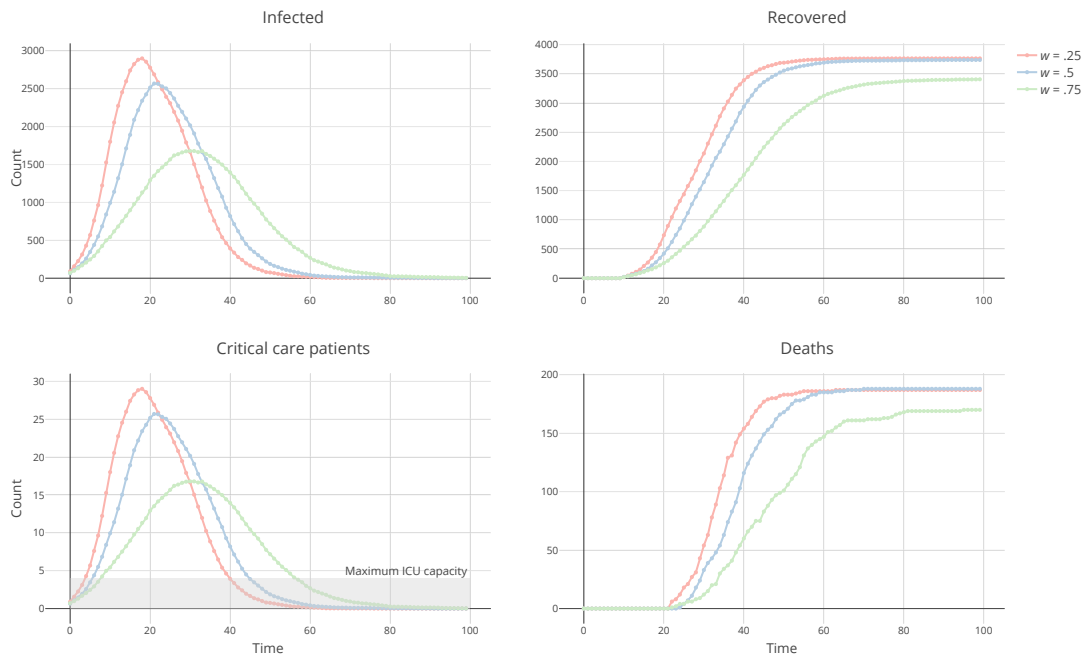


Figure 4: Results from simulations for $w \in \{.25, .5, .75\}$. (NB: The number of critical care patients at time t indicates the number of patients who are *going* to need critical care at a later time, around $t + 12$.)

It is obvious how to operationalize number of deaths directly due to the disease, given our assumption of a death rate of 1 percent among the infected. It is less obvious what counts as an overcrowded healthcare system. For many countries, number of ICU beds per capita is available,⁹ but that number is not always indicative of the real maximum capacity, as various countries were able to double or even more than double their ICU capacity (typically, at the expense of non-ICU beds) in a very short time span. It is even less obvious how to operationalize loss of economic activity in our model. Raising the value of w diminishes social activity, but should we assume that economic activity scales linearly with social activity? Probably not. For instance, some companies were able to adapt to the new situation by moving part of their business to the Internet. For our purposes, however, it is enough to make the general assumption that the lower the average value of w over the course of the outbreak, the better it is for the economy.

To get a first impression of the kind of effect that raising the value of w can have, we start by comparing some simulations in which w has a fixed value throughout. We look especially at the effect on the number of patients requiring critical care and whether it exceeds the maximum ICU capacity. Our village consists of 1000 households, with an average of 4 persons per household, and so it has a population of roughly 4000. We assume one ICU bed per 1000 persons, which is overly generous in light of the normal ICU capacity even in countries like Germany or the United States, which have the highest number of ICU beds per capita. As said, however, in many countries normal ICU capacity was no reliable indicator of the measure of critical care that could be provided when COVID-19 cases started to soar. Furthermore, we assume that 1 percent of the infected will eventually need critical care, which appears true at least for the first year of the pandemic (Clark et al. 2020).

Figure 4 shows the outcomes from three simulations, one for $w = .25$, one for $w = .5$, and one for $w = .75$. The “flattening of the curve” effect of raising the value of w is immediately clear and

⁹See https://gateway.euro.who.int/en/indicators/hfa_478-5060-acute-care-hospital-beds-per-100-000/.

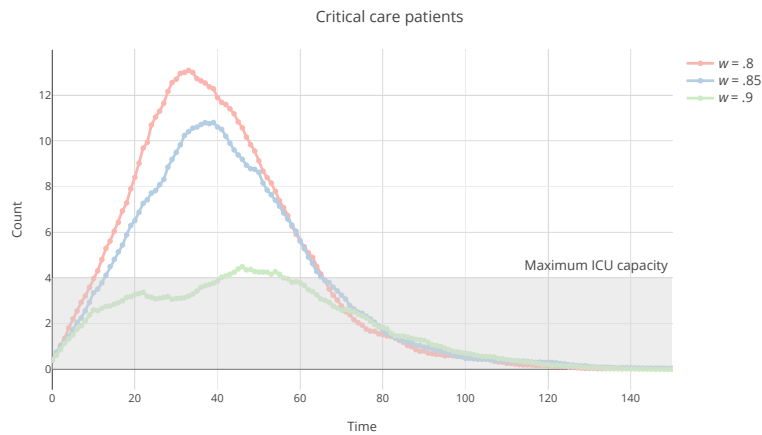


Figure 5: Patients requiring critical care in simulations for $w \in \{.8, .85, .9\}$. (For interpretation, see the comment in the caption of Figure 4.)

also entirely unsurprising. A more surprising fact about these simulations is that the total number of deaths directly due to the disease is not lower at the end for $w = .5$ than for $w = .25$. This does not automatically mean that, supposing the simulation outcomes to represent real-world data, it would have been better to institute measures that resulted in a value for w of $.25$ than measures that resulted in a value of $.5$, for there would almost certainly have been additional deaths due to overcrowded hospitals, which happens in all three scenarios.

If we calculate the total ICU undercapacity (summing over all points in time the number of ICU beds required beyond the four that are available), we find this to equal 498 in the $w = .25$ scenario, 467 in the $w = .5$ scenario, and 359 in the $w = .75$ scenario. Per-time undercapacity averaged over all points in time at which there is undercapacity is, in the same order of scenarios: $13.82 (\pm 8.28)$, $11.97 (\pm 7.14)$, and $7.34 (\pm 4.27)$. In reality, all these numbers would be cause for concern, but perhaps most disconcerting would have been the finding that, even with a value of w as high as $.75$ throughout the entire outbreak, the healthcare system was still overwhelmed.

To be sure, the simulation results also clearly suggest a route we can take if we want to avoid overcrowding the healthcare system at any cost: simply raise the value of w further still. But Figure 5 shows that even if we go up all the way to $.9$, we still do not fully meet the demand for ICU beds at all times. And lowering social activity to such a degree over such a long period of time comes with risks of its own, if only because—as many commentators on the pandemic have remarked—death from starvation is not per se preferable to death from COVID-19. This sentiment was one of the main reasons why governments came to favor a system of intermittent NPIs.

If we opt for this approach, there are a number of important questions to be answered: When to raise w (i.e., impose measures that are believed to result in a rise of w)? When to lower it again (i.e., ease confinement measures)? And by how much should we raise/lower w ? We turn to these questions in the next section.

4 Doing NPIs the right way

A straightforward approach to having intermittent NPIs is to switch, during the course of the pandemic, at regular time intervals between a “middling” (say, $.5$) and a “high” (say, $.95$) value of w until the worst is over (Ferguson et al. 2020; López and Rodó 2020; Westerhoff and Kolodkin 2020). We can get an idea of whether this approach would be, or would have been, any good by simulating it in our model. Figure 6 displays the results from a simulation implementing the strategy of

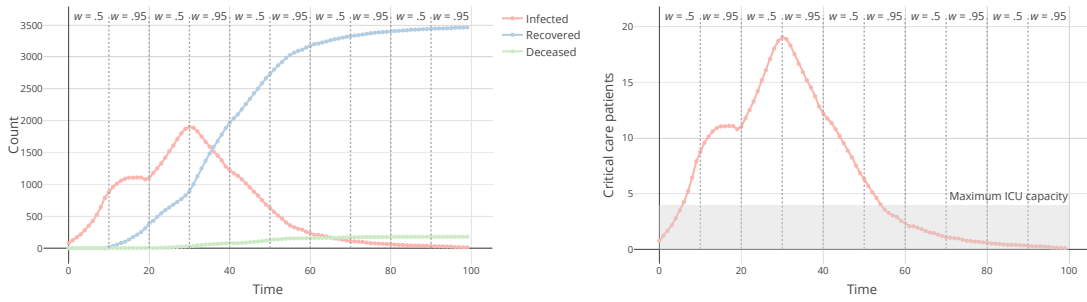


Figure 6: Switching the value of w between middling and high at regular time intervals. (For interpretation of the right panel, see the comment in the caption of Figure 4.)

switching every 10 time steps from $w = .5$ to $w = .95$ for the whole duration of the outbreak. From the right panel, it is clear that, despite a relatively high average w -value of $.725$, the healthcare system still gets badly overcrowded for a considerable stretch of time. This is a robust result: running 25 simulations for the same switching strategy yielded an average total undercapacity, calculated as explained above, of $354.58 (\pm 8.03)$ and an average number of deaths directly due to COVID-19 equal to $179.64 (\pm 13.06)$.

One guesses that there must be room for improvement here. In fact, it would almost be a miracle if there were not, given that we are switching the value of w in a predetermined way, without paying any attention to what happens “on the ground.” As Westerhoff and Kolodkin (2020) note, a more sensible but also more complex approach is to adapt the intensity of the NPI to the severity of the epidemic, which in the above terminology means that we should dial up w if the number of new infections is on the rise and dial it back again if the infection rate appears to be abating. If the number of infections is stable, we may want to leave w at whatever its value at the time is. The idea, in other words, is not simply to have *intermittent* NPIs but rather to have *flexible* or *adaptive* ones.

To make this idea more precise, first note that there will always be random fluctuations in the daily number of new infections. So, we will want to attend to the *trend* in the data and may make the increase or decrease of w a function of the *trend growth rate*.¹⁰ This can be accomplished in a number of different ways (for an overview, see Fricker 2013). A simple one uses so-called local linear models, which locally fit a line to a subset of all data points, viz., those that lie in a sliding window. Figure 7 illustrates the basic idea: it shows a simulation of an outbreak together with the regression lines for the data in two (arbitrarily chosen) windows of size 15. The figure also displays the regression coefficients for the data sets in the two windows. A reasonable proposal is to make such coefficients part and parcel of our strategy for adjusting w .

Again, we choose a conceptually simple way to accomplish this by letting the local regression coefficients shift an *alert level*. Where l_t is the alert level at time t and at t we estimate a local regression coefficient b_t , we set $l_{t+1} = l_t \times b_t/s$, with s a scaling factor. To map the alert level onto w , which is a probability, we can use the logistic function. However, it is probably better to use the generalized version thereof, as that will allow us to account for the fact that we will have to settle for a maximum value of w somewhat lower than 1, if only because compliance with stay-at-home orders will never be perfect. Specifically, in the following we assume that, for all t ,

$$w_t = \frac{0.95}{1 + e^{-l_t}},$$

¹⁰Monitoring the state of the pandemic in real time is also known to face various practical challenges (see Gostic et al. 2020). In our simulations, we will ignore these problems.

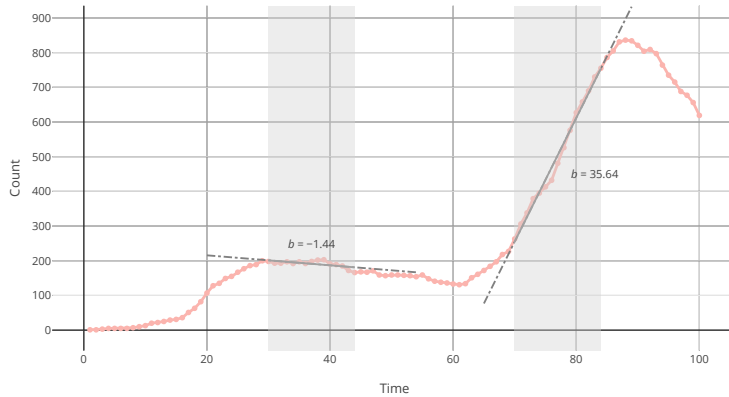


Figure 7: Illustration of local regression: regression lines are fit to the data, in two windows of size 15.

which makes .95 the maximally attainable value for w .¹¹

One could object to the above that we might have reason to raise w even if the number of daily new infections is stable, for instance, if the healthcare system *remains* overwhelmed. Similarly, we might have reason to *lower* w in spite of the number of new cases being consistently high, for instance, in the face of a looming economic breakdown. But while these are valid considerations in practice, they are orthogonal to the more principled point to be made in the following. Indeed, it is immaterial for that whether we will, in the end, want to settle on anything like the above approach, because the optimization technique to be showcased below will work equally for very different approaches to adjusting the value of w over time.

The above proposal assumes some size of the sliding window to be used for the local regressions, and it also assumes a particular size of factor (which we symbolized by s) to scale the impact of a measured regression coefficient on the adjustment of w . We are free to choose values for these parameters, at least within limits (e.g., the value of s will in practice be limited by how fast and drastically changes in the level of social activity can be effectuated even in an ideally compliant population). Naturally, we want to choose values that give the best results. But how to find those values? Is a larger window size preferable over a smaller one? Is a smaller scaling factor preferable over a larger one? Probably there will be some interaction between the parameters. Which combination is best?

As mentioned above, the problem we are dealing with is in effect a multi-objective optimization problem. We not only want to minimize number of deaths directly from the disease and minimize overcrowding of hospitals, we also want to minimize the damage done to the economy by stay-at-home orders and other mitigation measures. As also mentioned before, we cannot achieve a maximally desirable outcome on all three counts. But then we should not expect there to be a unique best combination of parameters.

Technically speaking, what we are looking for are the Pareto-optimal solutions to our problem, where a Pareto-optimal solution is one such that, for any alternative solution, if the latter does better than the former on one criterion, then it will do worse on one or more of the other criteria. Concretely, a combination of window size and scaling factor may be instrumental in keeping number of deaths relatively low and perhaps also in avoiding the overcrowding of hospitals, but at the expense of suppressing social activity rather drastically. If any other combination of window

¹¹This may still be overly optimistic. The real maximum may well be closer to .7, as assumed in Tuite et al. (2020).

size and scaling factor that, say, reduces number of deaths even further scores worse on either of the other criteria, the former is a Pareto-optimal solution to the problem we are facing.

Only in exceptional cases can multi-objective optimization problems be solved analytically (Coello Coello 1999; Deb 2001). A standard method for solving such problems relies on the use of evolutionary algorithms, which constitute a main form of population-based optimization (Kochenfelder and Wheeler 2019, Ch. 9). They can be thought of as involving communities of agents which evolve from one generation to the next according to principles of variation and selective retention much like those known from evolutionary biology.

Evolutionary algorithms start with a (typically randomly selected) generation of agents, with each agent representing a possible solution to whichever optimization problem is at hand. These agents are then allowed to reproduce, after which parents and children are ranked and selected on the basis of their “fitness,” which here means: on the basis of their scores on the various objective functions. Only the fittest agents are allowed to move on to the next generation, where the aforementioned process is repeated. There can be as many repetitions as one likes, but typically the algorithm will halt after a predetermined number of steps or as soon as some kind of convergence has been reached (scores no longer improve appreciably). Exactly how the reproduction and selection are done varies across evolutionary algorithms.

We used what is probably the best-known evolutionary algorithm, to wit, the Nondominated Sorting Genetic Algorithm (Srinivas and Deb 1994; Deb 2001), more specifically the version known as “NSGA-II” (Deb et al. 2002). This algorithm has been applied with notable success to multi-objective optimization problems in a wide variety of fields, including chemistry, economics, medicine, psychology, operations research, and robotics (Dhanalakshmi et al. 2011; Douven 2019a,b, 2022; Heris and Khaloozadeh 2011; Sarkar and Modak 2005).

The NSGA-II algorithm consists of a number of steps, which in our application amounted to the following: To start, a parent population of 24 agents is created, where each agent represents both a specific proposal for window size, $WS \sim \mathcal{U}\{5, 15\}$, and a specific proposal for scaling factor, $s \sim \mathcal{U}(0, 0.1)$.¹² The agents in this population are allowed to produce a child population, which is done by a combined use of operations known as “crossover” and “mutation.” Crossover forms pairs of agents from the parent population to let them produce a child whose features are a mix of those of its parents (the pairing is random and with replacement, meaning that some parents may beget more than one child), and mutation can then cause some random changes in the child’s features (with, in our case, a probability of 5 percent). Specifically, the child comes to propose a window size randomly selected in the interval spanned by the window sizes proposed by its parents, and similarly for the scaling factor.

In a next step, the parent and child populations are merged and scored in light of the relevant criteria, which are number of deaths, undercapacity of healthcare system, and average w value, criteria which, as said, we would like to minimize jointly but which in fact require making some trade-offs. More exactly, five simulations of 150 updates are run per agent, using the agent’s proposed window size and scaling factor, and the agent receives three scores on that basis: the number of deaths, the total undercapacity, and the average w value, all averaged over the five simulations.

These scores are used to divide the population into a number of “fronts,” where the first front consists of the agents representing Pareto-optimal solutions, the second, of the agents who would represent Pareto-optimal solutions were the agents in the first front removed from the population, the third, of the agents who would represent Pareto-optimal solutions were the agents in the

¹²The size of the population had a purely practical motivation: we had 24 cores available to run the computations on, so that having a population of 24 agents, or a multiple thereof, made for efficient parallel computing. In general, such practical considerations are important when using evolutionary algorithms, which tend to be computationally expensive.

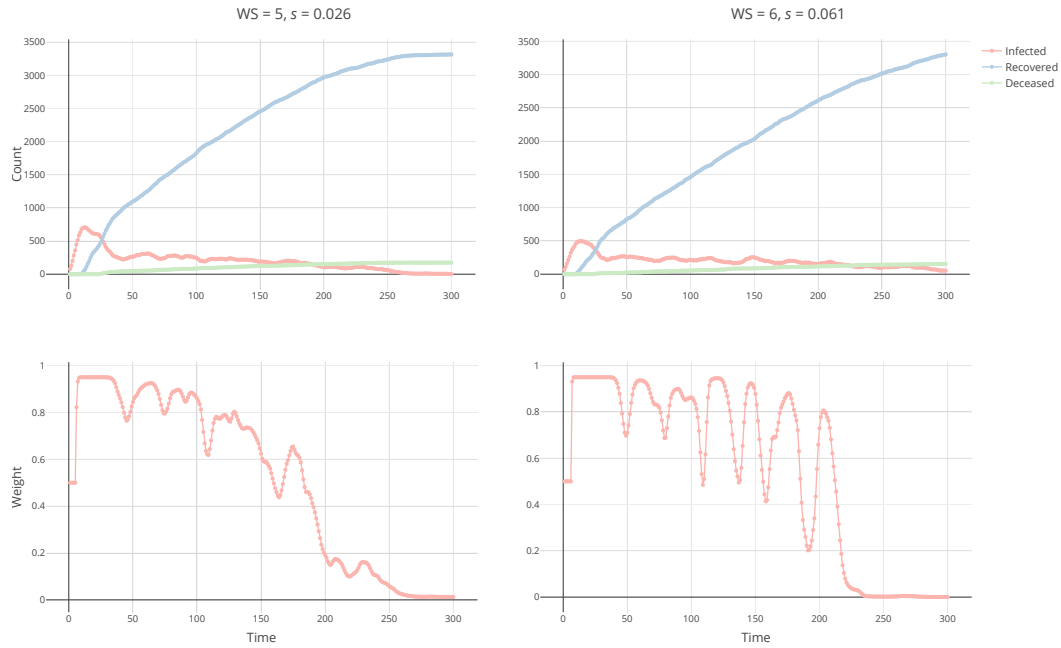


Figure 8: Imposing flexible NPIs, using parameter settings for how to adapt the value of w proposed by two different Pareto-optimal solutions.

first and second fronts removed, and so on. This division into fronts is known as “nondominated sorting.”

Finally, the fittest fifty percent from the population are selected to form the new parent population of the next generation. “Fittest,” here, is operationally defined in terms of two principles. According to the first, agents belonging to a higher front take precedence over agents belonging to a lower front. According to the second principle, if agents belonging to the same front do not all fit into the new parent population, those with greater crowding distance take precedence over those with smaller crowding distance, where *crowding distance* is a measure of how dissimilar an agent is to the other agents in the population.¹³ The point of this part of the algorithm is to increase the diversity of the new parent population, which is hoped to speed up exploration of parameter space.

As mentioned, this cycle of testing agents, selecting the best on the basis of the test results, and creating a new generation of agents can, in principle, be repeated as often as desired, though in our case the algorithm reached convergence after just 12 generations, in that later generations did not represent better solutions to the optimization problem. The Pareto-optimal solutions we obtained in the last generation (i.e., the agents in the first front of that generation) mostly proposed window sizes of 5, some of 6, and the average scaling factor proposed was .058 ($\pm .021$), with a minimum of .026 and a maximum of .093.

By way of illustration, Figure 8 shows, for two of the obtained Pareto-optimal solutions, the outcomes of simulations with settings corresponding to those solutions. From the first row it appears that the outbreak plays out in an almost identical way given either of the settings, and in a way that looks like something many governments might have wanted to sign up for at the start

¹³Concretely, this is how the principles work in our case: There are 24 slots to be filled by the parent population of the next generation. We first look whether all agents in the first front fit in. If not (i.e., there are more than 24 agents in the first front), then we select from the first front the 24 agents with greatest crowding distance. If the agents in the first front do all fit into the new parent population and if some slots still remain open then, we look whether all agents in the second front fit into those remaining slots. If not, we select from that front as many agents as there are slots still to be filled, again on the basis of crowding distance. If they do all fit in, we turn to the third front. And so on, until all 24 slots are filled.

of the COVID-19 outbreak: after a first, smallish wave, the outbreak remains at a subdued level, until it peters out. The second row shows that, by contrast, there are marked differences in how this relatively benign course of the outbreak is achieved: in the left panel, w changes much more gradually than in the right panel, where it fluctuates quite a bit before the outbreak is over and w falls back to 0.

For a more informative comparison of the two settings, we ran 25 simulations for each. These resulted in an average undercapacity of 24.78 (± 6.43) for the setting with window size 5 and scaling factor 0.026 and a corresponding average of 34.03 (± 14.35) for the setting with window size 6 and scaling factor 0.061; average number of deaths for the first setting was 169.04 (± 11.57) while it was 172.0 (± 12.76) for the second; and the average weight was .61 (± 0.04) for the first setting and .52 (± 0.07) for the second. A series of unpaired t -tests showed the difference in deaths to be not significant but the other two differences to be highly significant: $t = 2.94$, $p = .005$ for undercapacity, and $t = 5.58$, $p < .0001$ for weight. (Unsurprisingly, the two settings do significantly better on all three counts than the predetermined switching strategy considered earlier.)

We thus see that while the second setting leaves, on average, considerably more room for social, and so presumably also economic, activity than the first, it also taxes the healthcare system more heavily. That is precisely what one expects to get from Pareto-optimal solutions, which—as explained—embody different “best” trade-offs to multi-objective optimization problems. Indeed, running simulations with settings corresponding to the other Pareto-optimal solutions that the evolutionary algorithm helped us arrive at shows that these balance the relevant criteria—avoiding undercapacity and direct deaths, retaining social activity—again somewhat differently.

We have two comments on these results. First, by leaving a number of different options on the table, our approach might seem to not quite deliver what we are after, viz., a policy decision. While that is correct, it is important to appreciate that how we are to choose among the various Pareto-optimal solutions is not a *scientific* question but rather a *practical* and in the present case especially also a *political* one. For instance, an average level of w of around .5 over a period of, say, 250 days might be just enough to keep the economy from the brink of collapse whereas an average of around .6 for that period of time might cause some irreparable economic damage. For some governments, this might be a reason to opt for the former strategy, even if it leads to a greater loss of lives, but other governments might decide differently. Apart from economic considerations, for some policies the gap between what is possible in principle and what social engineering can effectively accomplish may simply be too wide: issue all the directives you want, and you may still not be able to bring about the rapid, large changes in social activity that would be required for w to follow the course seen in the right panel of the bottom row of Figure 8.

Second, just as our agent-based model of the COVID-19 outbreak could easily be refined—most notably, by endowing the agents and/or the social network with further attributes—it would similarly not be difficult to refine the optimization algorithm described in this section. In particular, we could include more criteria (e.g., one could take into account also the total length of the outbreak), or the criteria could be weighted differently (e.g., we might want to prevent overloaded hospitals at all costs and therefore prioritize in the selection process agents who do particularly well on this criterion). To reiterate, however, the point of this paper is first and foremost to make a case for a methodology that we believe to be particularly apt for helping develop such a strategy.

5 Revisiting the concerns about agent-based models

The kind of simulations reported in the foregoing can provide valuable guidance for policymakers tasked with making difficult decisions during a pandemic, as was seen in recent years. Indeed, the work on agent-based modeling conducted in the context of the COVID-19 outbreak is a testament

to the practical value of agent-based modeling and thereby, we believe, also responds to some of the recent criticisms that philosophers have leveled against this methodology. In the introduction, we mentioned various concerns about agent-based models voiced by philosophers of science and other authors. Specifically, the concerns were that these models tend to be insufficiently robust (in particular, too sensitive to modeling decisions and initial conditions), too simple and idealized, and too difficult to evaluate to be of much help for the study of real-world phenomena. What remains of these concerns, in light of what we know about agent-based COVID-19 models and more generally agent-based pandemic models?

As for the issue of robustness, this of course becomes less pressing the more our initial assumptions can be made to reflect reality. For instance, if our model, which here was applied to the COVID-19 outbreak, were to be applied to another pandemic, where this would require making different starting assumptions, then it would be entirely unsurprising, but also not in the least alarming, if the model led to different predictions. More generally in relation to agent-based modeling, it is worth pointing out that the fact that nowadays most researchers have easy access to powerful computers, in combination with the development of languages that are optimized for speed yet relatively easy to learn and use (Julia being a prime example here), makes it possible to run large-scale sensitivity analyses for models whose parameters cannot be set on the basis of known data. See Douven and Heggelmann (2021) and Douven and Heggelmann (2022) for some examples of how to conduct such analyses for models with epistemically interacting agents.

As for the problem of oversimplification, our study demonstrated that even a relatively basic model can capture significant complexity. Other agent-based COVID-19 models to be found in the literature provide further support for that claim. One could imagine adding more complexities. For instance, an anonymous referee suggested that taking into account agents' beliefs and how these change in response to how a pandemic develops (which, to our knowledge, none of the COVID-19 models documented in the literature do) is likely to improve predictive accuracy. Of course, striking the right balance between model simplicity and realism can be a challenge, as more complexity will typically lead to increased computation costs, which in this case would come in addition to the costs associated with collecting real-time data on people's beliefs about the pandemic. But however "rich" we will be able to make our model, it is to be admitted that there is always the risk of overlooking relevant variables. At the same time, note that this problem is not specific to agent-based modeling; it is a concern of all scientific modeling. It is essential for researchers to be aware of the said risk and to communicate it when presenting their findings to policymakers.

The concern about model evaluation, finally, is probably the most serious one—who would want to rely on a model that cannot be properly evaluated?—and requires a more elaborate response. Model evaluation is usually taken to involve model verification and validation (see, e.g., Gräbner 2018), where the former is the process of ensuring that a model aligns with the intended design (e.g., that the model is consistent, and in the case of computational models, that the code is bug-free) and the latter is the process of checking whether the model conforms with the target system (in our case, the pandemic). While model evaluation is, in general, challenging, agent-based models of pandemics are in a much better position to meet the challenges than are most other agent-based models.

First off, practitioners of agent-based models are often hampered by a limited access to relevant data. But in the kind of case we looked at—pandemic modeling—governments have strong incentives not only to rapidly collect data but also to disseminate these data rapidly to scientific researchers. This explains, for instance, why there are various repositories from which up-to-date data concerning COVID-19 could be downloaded almost from the start of the pandemic. Obviously, early agent-based models of the pandemic were based on limited data, but already these limited

data could be used to check whether the behavior of the models researchers had begun building were in line with the intended design. Moreover, the models could be rechecked every time new data came in. As a case in point, we saw that the basic assumptions underlying our model could be motivated by reference to the scientific literature.

Model validation does present unique challenges for agent-based models due to their inherent idealizations; at least that is so if model validation is understood in terms of representational accuracy. However, Thicke (2020) rightly remarks that we need to distinguish between “Galilean” idealizations in the sense of Cartwright (2005), which deliberately distort the target system by stripping away interfering factors while leaving basic causal structures intact, and idealizations that introduce elements or dynamics that do not exist in the real world or that make assumptions that could not possibly be satisfied by agents. Our model made assumptions—such as household members always being present during an agent visit—which, although almost surely not completely accurate, *could* plausibly occur and are unlikely to significantly alter the outcomes.

More important still is the observation made in Parker (2020) that models may be better validated in terms of (what she calls) adequacy-for-purpose than in terms of representational accuracy. Assessing the former requires us to consider a model in a context as well as in relation to a user or users in that context. In the given context, the model will be used by the user for a certain purpose, and it can serve that purpose without being representationally correct. In the case of pandemic models, the primary purpose or purposes will almost invariably be to help predict pathogen spread and/or to inform interventions. And while, for instance, our model may fall short in representing entirely accurately connections among households, it can be adequate-for-purpose nonetheless. The comparison of the model predictions with the Anhui data in Section 3 gives at least some indication that our model is adequate-for-purpose indeed.

Parker (2020) also contains worthwhile discussion with regard to *testing* adequacy-for-purpose. As she points out, this can be particularly difficult when *directly* testing adequacy-for-purpose is impossible, as it is, for instance, when models are used to study counterfactual situations or when they make predictions about the distant future. But if an agent-based model is used to predict the course of a pandemic as well as the effects of NPIs, then, if data collection is anything like what we saw during the COVID-19 outbreak, we will have no problem testing the model’s adequacy-for-purpose directly against real-world data in almost real-time. Parker defines a concept of fitness-for-purpose in terms of adequacy-for-purpose, specifically, as indicating the degree to which a model is adequate-for-purpose. Using that concept, we can say that the continuous stream of data concerning infection rates, hospitalization rates, mortality rates, and so on, that we may expect to see in the case of a pandemic of the severity of COVID-19 is likely to help researchers iteratively refine their model or models and thereby to increase their fitness-for-purpose.

To be clear, critics of agent-based modeling may still be right in their critique of certain individual models. Some may well *be* too simple, or too stylized, or insufficiently robust, or otherwise deficient, to be of much theoretical or practical value. Indeed, nothing in this paper should be construed as a blanket endorsement of agent-based modeling, and we agree, for instance, with Thicke’s (2020, p. 333) caution regarding policy reliance on current agent-based models of scientific inquiry. But as with any method, it is important to know when it should be applied and also when not. And when it is the right method to use, still much can go wrong in the process of building the actual models. But here, too, the situation is no different for other methods: logical models, statistical models, decision-theoretic models, and so on, can all be badly misspecified. What matters is how much such methods contribute when used judiciously and appropriately.

6 Conclusion

We have applied a combination of agent-based modeling and a widely used multi-objective optimizer to a pandemic outbreak—illustrated by the currently most obvious candidate for that—and in particular to the question of how best to respond to such an outbreak. Agent-based modeling was used to model communities affected by the outbreak, and the optimizer to compute best trade-offs between desiderata that will usually pull in opposite directions. It was seen how an agent-based modeling approach enables modelers to simulate interventions in an unfolding epidemic and thereby to get a thorough understanding of the effects of different mitigation strategies. Most notably, agent-based models make it easy to simulate flexible strategies that can be implemented by closely monitoring a population and responding quickly but proportionally to changing numbers of infections. We posit that, especially in the realm of pandemic modeling, agent-based modeling is a remarkably adaptable tool that should not be underestimated or disregarded. Furthermore, we believe our findings contribute to countering some of the recent criticisms posed against agent-based modeling. While criticisms of specific agent-based models may be justified, there is no general reason to believe that agent-based modeling must face problems that other kinds of scientific modeling do not face as well.¹⁴

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