

# The Effect of Social Distancing on the Reach of an Epidemic in Social Networks

Gregory Gutin\*   Tomohiro Hirano<sup>†</sup>   Sung-Ha Hwang<sup>‡</sup>  
Philip R. Neary<sup>§</sup>   Alexis Akira Toda<sup>¶</sup>

May 6, 2020

## Abstract

How does social distancing affect the reach of an epidemic in social networks? We extend the Susceptible-Infected-Removed (SIR) epidemic model to social networks in which individuals are limited in the number of other people they can interact with. While increased social distancing always reduces the spread of an infectious disease, the magnitude varies greatly depending on the topology of the social network. Our results also reveal the importance of coordination at the ‘global’ level. In particular, the public health benefits from social distancing to a group (e.g., a country) may be completely undone if that group maintains connections with outside groups that are not social distancing.

---

\**Email:* [gutin@cs.rhul.ac.uk](mailto:gutin@cs.rhul.ac.uk); *Address:* Computer Science Department, Royal Holloway, University of London, Egham, Surrey, TW20 0EX.

<sup>†</sup>*Email:* [Tomohiro.Hirano@rhul.ac.uk](mailto:Tomohiro.Hirano@rhul.ac.uk); *Address:* Economics Department, Royal Holloway, University of London, Egham, Surrey, TW20 0EX.

<sup>‡</sup>*Email:* [sungha@kaist.ac.kr](mailto:sungha@kaist.ac.kr); *Address:* College of Business, Korea Advanced Institute of Science and Technology (KAIST), Seoul, Korea.

<sup>§</sup>*Email:* [philip.neary@rhul.ac.uk](mailto:philip.neary@rhul.ac.uk); *Address:* Economics Department, Royal Holloway, University of London, Egham, Surrey, TW20 0EX.

<sup>¶</sup>*Email:* [atoda@ucsd.edu](mailto:atoda@ucsd.edu); *Address:* Department of Economics Department, University of California San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0508

# 1 Introduction

How does social distancing affect the reach of an epidemic? To address this question we introduce temporary social distancing measures to the Susceptible-Infected-Removed (SIR) epidemic model of [Kermack and McKendrick \(1927\)](#).<sup>1</sup> The results of our simulations reveal a number of stylised facts that could prove useful for policy makers handling the outbreak of the novel coronavirus (COVID-19).

While the spread of an epidemic is curtailed with social distancing, the magnitude varies greatly depending on the topology of the social network. We illustrate this by running simulations of our *capacity constrained SIR* model on three types of well-studied networks: the ‘random graphs’ model of [Erdős and Rényi \(1959\)](#) and [Gilbert \(1959\)](#) (hereafter, ERG), the ‘small world’ networks of [Watts and Strogatz \(1998\)](#) (hereafter, WS), and the ‘scale-free’ model of [Barabási and Albert \(1999\)](#) (hereafter, BA).<sup>2</sup>

We begin by focusing on two main questions: (i) What is the likelihood that an infectious disease will become endemic? (ii) What is the distribution of the peak infection rate over the lifecycle of the epidemic? The reason for focusing on (i) is that the level of herd immunity attained is an important policy tool in knowing how, when, and by how much social distancing measures can be relaxed. The reason for focusing on (ii) is that the peak infection rate corresponds to the most overloaded instance that a health service encounters over the lifecycle of an epidemic. Success in both the above dimensions is not simultaneously possible because as one goes up the other goes down. Our results help to guide what the relative trade-offs are.

For all three social network structures, strong measures of social distancing (limiting everyone’s daily interactions to 3 or fewer) stops an epidemic with high probability (see [Figure 2](#)). However, for societies structured according to WS, the fraction of individuals who are in state  $R$  after the epidemic has passed is much less over this range (see rows labeled ‘Herd

---

<sup>1</sup>By ‘social distancing measures’ we mean limiting the number of social interactions in which an individual partakes. We do not mean individuals maintaining a predetermined physical distance throughout an encounter. Our measure is adapted from the game-theoretic model of Netflix Games ([Gerke et al., 2019](#); [Gutin et al., 2020](#)). There, the purchaser of a product may only share with a limited number of friends. Here, the carrier of an infectious pathogen is limited in the number of friends they may interact with.

<sup>2</sup>To ensure we are comparing like-for-like, we fix it such that all networks are connected and possess the same average degree. This means it is the way in which the societies are organised, and not the overall level of interaction, that is being varied. We initialise each trial with 1% of the population infected, using the COVID-19 disease parameters calibrated in [Toda \(2020\)](#).

Immunity’ in Table 1). Moderate social distancing (defined as 4-5 interactions per period) delays the peak of an epidemic but has little effect on the size of the peak and on the number that the disease ultimately reaches. The effect of mild social distancing (limiting individuals to 10 social interactions) differs greatly across network structures. With a ERG network, the effect is negligible. With a WS network, the outcome is the same as no intervention. With a BA network, the peak is significantly reduced. This is because in the BA network there are a small number of individuals with lots of connections, who, without constraints imposed may act as “super-spreaders”.<sup>3</sup>

Our framework is flexible enough to address a host of other policy experiments. For example, we consider a network comprised of two densely connected components, interpreted as ‘countries’, that have a few connections between them that we interpret as international friendships. We show that the benefits to a country that imposes strong social distancing measures are dramatically reduced if it continues to allow international connections, interpreted as maintaining open borders, with a country that is not implementing similar measures. In a hyper-connected world this points to the need for ‘global’ cooperation to eradicate an epidemic. In particular, if the global approach is uncoordinated with each country unilaterally applying social distancing measures without taking into account the policy choices of its neighbours, then an infectious disease may cycle around for far longer than otherwise intended. (During the COVID-19 pandemic, some Asian countries, e.g., Hong Kong and Singapore, have experienced second waves after successfully eradicating the virus during its first outbreak.)

We also consider what happens when a subset of individuals are deemed ‘essential workers’ who can go about their lives facing weaker social distancing constraints than the rest of the population. Our results show that when 10% of the population is deemed essential, the reach of the epidemic is similar to that wherein there are no essential workers. Finally, we consider a policy of beginning with severe social distancing measures that are incrementally relaxed over time, and compare the outcome with that from a policy of mild but constant social distancing over a shorter window. We find that the public health outcome is better under gradual relaxation for ERG networks and WS networks, but worse for BA networks.

We conclude the paper by suggesting some extensions to our framework that can be implemented in future work.

---

<sup>3</sup>A related point is made in [Muscillo and Pin \(2020\)](#) who show, using an SIS model, that unless all individuals comply with a social distancing policy, and specifically those who have more contacts, a policy may even be counterproductive.

## 2 The Model

Modelling how an infectious disease might spread through a population is done using a *contact network*: a graph,  $G = (V, E)$ , where  $V$  is the set of vertices, and  $E$  is the set of edges. Vertices represent individuals and an edge between two distinct vertices  $i$  and  $j$  captures the idea that these two people are acquaintances and meet in such a way that the disease may be transmitted from one to the other.

We assume throughout that  $G$  is connected. The neighbourhood of vertex  $i$  in  $G$  is denoted  $N(i)$  and its degree is denoted  $d(i) = |N(i)|$ . The *capacity* of  $G$  is a function  $\kappa : V \rightarrow \mathbb{Z}_{\geq 0}$ . This capacity function  $\kappa$  is our measure of social distance. Intuitively, it restricts the number of neighbours that each vertex can interact with, which in turn caps the number of neighbours to whom any infected person can pass the disease. While  $\kappa$  is allowed to take values that are individual specific, we will assume that it does not. That is, we abuse notation somewhat by simply writing  $N_{\max}$  for the maximum number of neighbours that each individual will interact with.

Our *capacity constrained SIR model* then operates as follows. Everyone in the population is currently in one of three states: *Susceptible* ( $S$ ) - has not had the disease and is therefore at risk; *Infectious* ( $I$ ) - currently has the disease and may therefore pass the disease to others; *Removed* ( $R$ ) - has had the disease and is no longer infectious (may be immune, isolated, dead, etc.). Time is discrete, starts at  $t = 0$ , and goes forever. Let  $S_{it}, I_{it}, R_{it} \in \{0, 1\}$  be the status of individual  $i$  at time  $t$ , where 1 means being that status and 0 means not being that status. (Clearly,  $S_{it} + I_{it} + R_{it} = 1$  for all  $i \in V$  and all times  $t$ .) In every period, each infected vertex  $i$  randomly selects  $N_{\max}$  of its neighbours, and, if any of the selected neighbours are in state  $S$ , then they become infected it with probability  $\beta \in (0, 1)$ .<sup>4</sup> The probability of removal (moving from state  $I$  to state  $R$ ) is denoted by  $\gamma \in (0, 1)$ . We assume that  $\gamma$  is constant over time and is the same for everyone. Once an individual enters state  $R$ , he stays there forever more. We will say that the system has *stopped* when there is no individual in state  $I$ .

To see how social distancing works in practice we refer to Figure 1 below. This figure can be thought of “zooming in” on the local neighbourhood of vertex  $\ell$  with degree 4 in some larger graph. We suppose that vertex  $\ell$  is infected (coloured red) while each of its 4 neighbours are susceptible

---

<sup>4</sup>Two things to note. First, clearly the model reduces to the standard SIR model when  $\kappa(i) = d(i)$  for all  $i \in V$ . Second, when  $0 \leq \kappa(i) < d(i)$  for some  $i \in V$ , there are  $\binom{d(i)}{\kappa(i)}$  ways for  $i$  to select a subset of neighbours of size  $\kappa(i)$ . We assume a uniform distribution over the likelihood of choosing each subset.

(coloured blue). The left hand image shows what occurs when the social distancing measure is 4 or greater. In this case  $\ell$  is unconstrained, and infects each of its neighbours (depicted by arrows) with probability  $\beta$ . The right hand image shows an instance where  $N_{\max} = 2$ . Here vertex  $\ell$  randomly selects 2 of its 4 neighbours (in this case by  $h$  and  $k$ ) and infects each with probability  $\beta$ . The remaining neighbours,  $i$  and  $j$ , are not encountered (depicted by dashed arrows) and so cannot become infected. While it is possible that more neighbours will become infected in the right hand image it is unlikely.

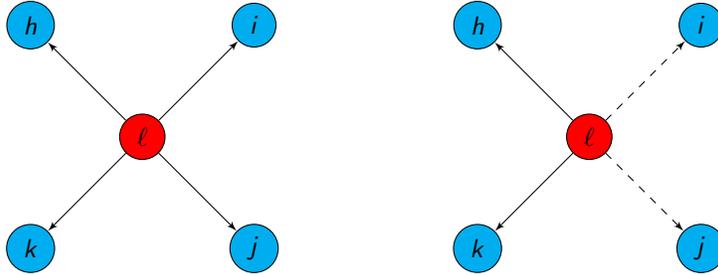


Figure 1: Left panel:  $N_{\max} \geq 4$ . Right panel:  $N_{\max} = 2$

The above describes the model. The state of the system at any time  $t$  is given by  $\{(S_{it}, I_{it}, R_{it})\}_{i \in V}$ . Moreover, given disease parameters  $\beta$  and  $\gamma$ , a graph  $G$  and capacity function  $\kappa$ , and initial conditions  $\{(S_{i0}, I_{i0}, R_{i0})\}_{i \in V}$ , the capacity constrained SIR model is a well-defined stochastic process that is easily simulated.

### 3 Simulation Parameters

We run simulations on the capacity constrained SIR model described above for three different types of graphs, ERG, WS, and BA. Before describing the choice of parameters for the epidemic, we briefly review how each kind of graph is generated and the graph-parameters required to render them like-for-like.

**Erdős and Rényi (1959) & Gilbert (1959)** These networks are often referred to simply as ‘random graphs’. Begin with an empty edge set. Now,

for every pair of distinct vertices  $i$  and  $j$ , form edge  $ij$  with fixed probability  $p$ . The expected number of edges in the resulting graph is  $\frac{1}{2}n(n-1)p$ .

**Watts and Strogatz (1998)** The resulting network is often referred to as a ‘small world’. Begin with the  $n$  vertices connected in a ring lattice where each vertex has  $k$  neighbours to the left and  $k$  neighbours to the right, where  $k \ll n$ . Proceed clockwise around the ring one time, and for each vertex, rewire each edge it has with the  $k$  vertices immediately to its right with rewiring probability  $q$ . Since the net change in the number of edges is zero, the number of edges in the resulting graph is exactly  $nk$

**Barabási and Albert (1999)** The resulting network is often referred to as ‘scale free’. Begin with a complete graph on  $m_0 \ll n$  vertices and allow time to increment forward from  $t = 1$  to  $t = n - m_0$ . At each point in time, a new vertex is born and the newly born vertex forms one edge with  $m \leq m_0$  of the existing vertices, where the probability that the newly born vertex connects to existing vertex  $i$  is given by  $d(i)/\sum_j d(j)$ . In total  $n - m_0$  new vertices are added so the number of edges in the resulting graph is always exactly  $\frac{1}{2}m_0(m_0 - 1) + m(n - m_0)$ .

We choose to equalise average degree,  $\bar{d}$ , across all network types. This ensures we are comparing like-for-like since it is the way in which the societies are organised, and not the overall level of interaction, that is being varied. Given that the number of edges in each graph will be  $n\bar{d}/2$ , some straightforward algebra yields the following parameter requirements:  $p = \frac{\bar{d}}{n-1}$  for ERG,  $k = \frac{\bar{d}}{2}$  for WS, and  $m = \frac{n\bar{d} - m_0(m_0 - 1)}{2(n - m_0)}$  for BA.

In each network we fix the number of vertices to be  $n = 1,000$  and set  $\bar{d} = 10$ . Such a choice requires setting the ERG parameter  $p = 0.01$ . For WS we choose rewiring probability  $q = 0.1$  and  $k = 5$ . For the BA network we set  $m_0 = 1$ . We set the removal probability  $\gamma = 0.1$ . To calibrate  $\beta$ , we proceed as follows. Since average degree is  $\bar{d}$ , an infected individual will infect  $\beta\bar{d}$  others in one period and on average  $\beta\bar{d}/\gamma$  over the infectious period when social distancing is unconstrained. The expression  $\beta\bar{d}/\gamma$  must equal the reproductive number which is calibrated to be 3 in [Toda \(2020\)](#). Given this, we have that  $\beta = 0.03$ . Finally, we initialise the system by setting each vertex to state  $I$  with probability  $y_0 = 0.01$  (so that, on average, each trial starts with 1% of the population infected).

We allow the social distancing measure  $N_{\max}$  to take values in the set  $\{1, 2, 3, 4, 5, 10, \infty\}$ , where the value  $\infty$  denotes the standard SIR model

(i.e., our model without any constraints). Lastly, unless otherwise stated, we suppose that the social distancing measure starts in period 0 and is lifted from period 50 onwards.

## 4 Simulation Results

Figure 2 below contains six panels organised in a  $3 \times 2$  format. The first row refers to ERG networks, the second to WS networks, and the last row to BA networks.

The first panel in each row presents results of four separate simulations with the network structure held fixed. The  $x$ -axis is time, and the  $y$ -axis is infection rate with social distancing measures of  $N_{\max} = 2, 5, 10$ , and  $\infty$  (we choose not to present all values of  $N_{\max}$  as the resulting image is too cluttered). The vertical line at  $t = 50$  represents the lifting of the social distancing restriction.

The second panel in each row presents a probability distribution of peak infection rates from 1,000 simulations of the type shown in the first panel. To see the connection between the two panels, we note that each first panel would provide one data point for the second panel. To further cement understanding, note that in the first panel of the WS row the peak infection rate for  $N_{\max} = 2$  trial is greater than that for the  $N_{\max} = 5$  trial.

We begin with the first panels referring to individual trials. For the ERG and BA networks, the social distancing measure of  $N_{\max} = 2$  eradicates the epidemic within the 50 period window. Note however that the  $N_{\max} = 2$  trial does not eradicate the epidemic for the WS network. For each of the three network structures, the trial with moderate social distancing,  $N_{\max} = 5$ , delays the peak of the epidemic but has little impact on the size of the peak. The effect of mild social distancing,  $N_{\max} = 10$ , differs across network structures. With a random network (ERG), the effect is mild. With a small world network (WS), the outcome appears equivalent to no intervention ( $N_{\max} = \infty$ ). With a power law network (BA), the peak is significantly reduced. This is possibly because in the BA network there are a small number of individuals with large degree who are no longer able to act as “super-spreaders”.

While the findings in the first panel of Figure 2 are illustrative, they represent only a single trial and so are not robust findings. As such we now turn our attention to the panels in the right hand column. Here each panel presents histograms of the peak infection rate attained in 1,000 trials for a given network type (four histograms on each graph - one for each of the

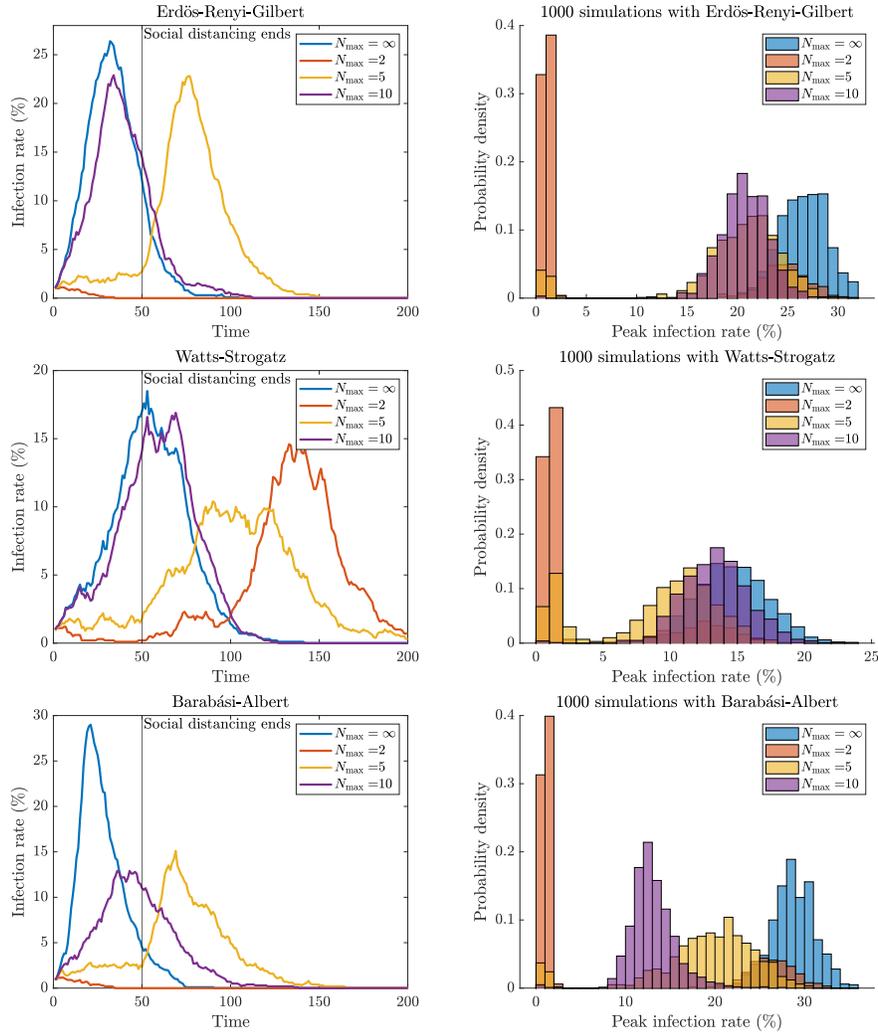


Figure 2: Results for (i) one trial, and (ii) average of 1,000 trials.

same measures of social distancing as in the left hand panels).<sup>5</sup> For all three network structures, setting  $N_{\max} = 2$  eradicates the infection in  $\sim 70\%$  of the trials. We note that the empirical frequency distribution of peak infection

<sup>5</sup>We consider peak infection rate as it captures the worst case scenario. This has been cited as a particularly important measure in the COVID-19 epidemic where it is often the excess numbers of sick individuals that strain a healthcare system (limited numbers of intensive care beds, ventilators, and personal protective equipment for medical professionals) that can be as big an issue to public health as any other factor [cite].

is bimodal for the value  $N_{\max} = 2$  with the lower mode corresponding to the epidemic being eradicated. Setting  $N_{\max} = 5$  eradicates the disease in slightly more than  $\sim 10\%$  of the trials of the WS networks and even less for ERG and BA. Setting  $N_{\max} = 10$  almost never eradicates the disease for any kind of network. Setting  $N_{\max} = \infty$  never eradicates the disease for any kind of network.

Conditional on the disease not being eradicated, the distribution of peak infection rate is the same as no intervention for ERG and WS. This is because the epidemic restarts after the lifting of social distancing measures. However, for the BA network, conditional on the disease not being eradicated the distribution of peak infection rate for  $N_{\max} = 5$  is sandwiched between that of  $N_{\max} = 10$  and  $N_{\max} = \infty$ . At first glance this may appear mysterious but in fact it is not. The explanation is that the distribution of peak infection rate presented says nothing about the precise moment, during a particular trial, that the peak infection rate was attained. For  $N_{\max} = 5$ , the peak infection rate will typically occur after the social distancing restrictions have been lifted (as can be seen clearly in the left hand panel of ERG), but this is not the case for  $N_{\max} = 10$ . For BA networks, it would appear that setting  $N_{\max} = 10$  is a superior policy to the policy to setting  $N_{\max} = 5$ .

Table 1 presents further results. The variable ‘Peak’ denotes the peak infection rate. Letting  $T$  denote the last period before the system stops, we say that society has acquired herd immunity if  $\beta \bar{x}_T \leq \gamma$ , where  $x_T$  is the fraction of susceptible individuals at time  $T$ . (See Toda (2020) for a discussion.)

As can be seen from Table 1, there is a trade-off to be made between herd immunity and keeping the peak low (the variable ‘ $\overline{\text{Peak}} \mid \text{Immunity}$ ’). While achieving herd immunity is desirable so that the epidemic cannot strike again, the expected peak is higher under such a scenario. That is, conditional on acquiring herd immunity, the average peak is a decreasing function of  $N_{\max}$ . This suggests that drastic social distancing policies are fragile.

In summary, choosing a small  $N_{\max}$  such as  $N_{\max} = 1, 2$  reduces the peak but prevents building herd immunity, which makes the society susceptible to further epidemics. Choosing an intermediate  $N_{\max}$  such as  $N_{\max} = 3, 4, 5$  does not necessarily reduce the peak, while mildly preventing herd immunity. Choosing  $N_{\max} = 10$  generally reduces the peak infection rate *and* achieves herd immunity.

Table 1: Effectiveness of non-pharmaceutical interventions in networks.

Network	Variable	$N_{\max}$						
		$\infty$	1	2	3	4	5	10
ERG	$\overline{\text{Peak}}$	26.5	3.4	7.7	13.9	18.7	19.5	20.7
	Std.(Peak)	2.8	7.4	10.7	11.4	8.9	6.1	2.5
	Med.(Peak)	26.6	1.0	1.2	20.9	22.0	20.8	20.7
	$\overline{\text{Peak}} \mid \text{Immunity}$	26.6	25.1	24.7	23.6	22.8	21.1	20.7
	Herd immunity	99.7	10.3	28.2	56.9	80.9	92.4	99.7
WS	$\overline{\text{Peak}}$	14.5	1.9	3.5	5.1	7.3	8.8	13.3
	Std.(Peak)	2.8	3.2	4.8	5.4	5.3	4.6	2.6
	Med.(Peak)	14.5	1.0	1.1	1.5	8.9	10.1	13.3
	$\overline{\text{Peak}} \mid \text{Immunity}$	14.6	12.6	12.6	12.2	11.7	11.3	13.4
	Herd immunity	99.4	7.2	19.9	33.5	54.8	72.1	98.7
BA	$\overline{\text{Peak}}$	28.7	4.0	8.1	13.8	18.2	18.9	13.0
	Std.(Peak)	2.5	8.4	11.4	12.0	9.3	6.2	2.6
	Med.(Peak)	28.7	1.0	1.2	20.3	21.6	19.9	12.7
	$\overline{\text{Peak}} \mid \text{Immunity}$	28.7	27.1	26.2	24.6	22.8	20.4	14.1
	Herd immunity	99.9	11.5	28.2	54.1	78.6	89.7	49.2

Note: “ $\overline{\text{Peak}}$ ” is the mean peak infection rate (%). “Std.” and “Med.” are the standard deviation and median of peak infection rates across 1000 simulations. “ $\overline{\text{Peak}} \mid \text{Immunity}$ ” is the mean peak infection rate conditional on acquiring herd immunity. “Herd immunity” is the fraction of simulations (%) in which herd immunity was acquired.

## 5 Policy Questions

Our set up is sufficiently flexible that we can address a wide range of policy issues. Here we present the results of some extensions.

### 5.1 Tackling Epidemics Requires ‘Global’ Cooperation

Suppose there are two countries, Country *A* and Country *B*. Each country has a population of  $n$  individuals, and when viewed in isolation each country forms its own connected network. Suppose further that every pair of individuals from different countries are randomly connected with fixed probability  $1/(10n)$ , and we interpret connections of this form as international relationships. (We choose a low value so that in expectation only a very small minority of each individual’s interactions are with foreigners.)

For the simulations, we set  $n = 1,000$  and  $\bar{d} = 10$  for each country, and we assume that both countries have the same social structure (ERG, WS, or BA). We use the same values for  $\beta$ ,  $\gamma$ , and initial infection probability  $y_0$ , as before.<sup>6</sup> However, instead of assuming that temporary social distancing measures are imposed ‘globally’ as in the simulations of Section 4, we now suppose that Country *A* levies social distancing measures while Country *B* imposes no measures of any kind. Figure 3 below depicts the simulation results for one trial of the infection rate in both countries as a function of time for a variety of different social distancing measures,  $\kappa = 2, 5, 10$ , and  $\infty$ .

Figure 3 below contains six panels organised in a  $3 \times 2$  format. As with Figure 2, the panels in a given row correspond to different network structure: the first refers to ERG networks, the second to WS networks, and the last row to BA networks. Within a given row, the first panel presents time-varying infection rates for Country *A* of four separate simulations differing across social distancing measures ( $N_{\max} = 2, 5, 10$ , and  $\infty$ ). The vertical line at  $t = 50$  represents the lifting of the social distancing restriction. The second panel in each row is the corresponding time-varying infection rate for Country *B* during the same simulation.

The interesting comparison to make is the results for Country *A* above with that of the single country results in the left hand column panels of Figure 2. Compared to the case with one country, it is clear that social distancing is less effective because new cases are imported from foreign countries. This is the case despite the fact that the expected degree for vertices in Country *A* has only increased by 0.1.

These simulation results highlight the need for policies designed to tackle the COVID-19 epidemic to be coordinated. To give an extreme example imagine a large body of interconnected individuals who live in different regions with no barriers to moving between regions (this is precisely with countries within the Schengen area of the European Union and states within the United States of America). If one region has weaker social distancing measures than all the others while maintaining connections to them, this one region may impose a large negative externality on the others.

---

<sup>6</sup>We assume that in both countries 1% of individuals are infected. Of course it is possible to address a host of other related questions. An example would be, “Suppose  $x\%$  of individuals in Country *A* are infected. What is the lowest value of  $x$  such that if  $x\%$  of individuals in Country *A* are infected then the reach of the epidemic will be both Country *A* and Country *B*?”.

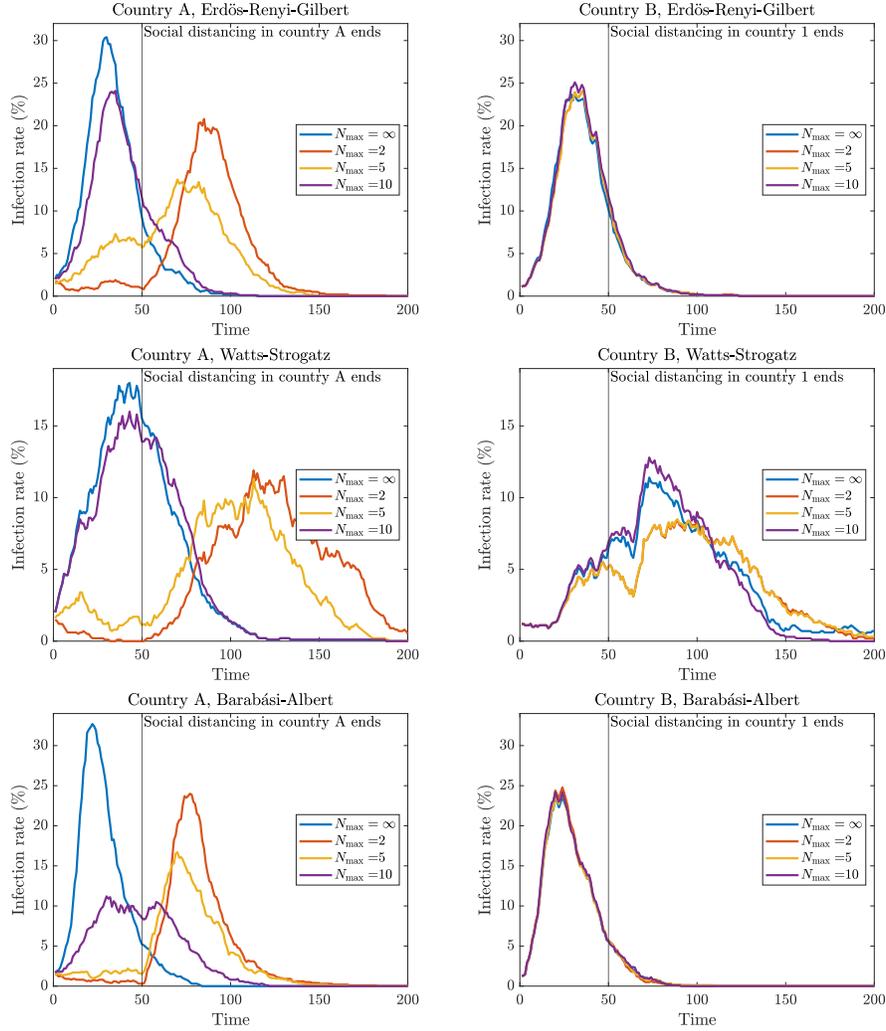


Figure 3: Epidemic dynamics with two countries.

## 5.2 Essential Workers

Suppose that some fraction of individuals are deemed ‘essential workers’ who face different social distancing measures to everyone else. As a numerical example, suppose a random 10% of the individuals are essential workers, with number of meetings restricted to  $N_{\max} = 10$  during social distancing.

Figure 4 below contains two panels. In both panels 10% of individuals are deemed essential workers and randomly assigned  $N_{\max} = 10$ . The first

panel shows the outcomes of one trial for each network type, wherein 1% of all individuals are initially infected and the 90% of individuals who are non-essential individuals have  $N_{\max} = 2$ . The second panel is similar except the non-essential workers have  $N_{\max} = 5$ . In comparing the graph from each panel with the corresponding appropriate panel from Figure 2, we can see that there is not much difference from the benchmark case where there are no essential workers.

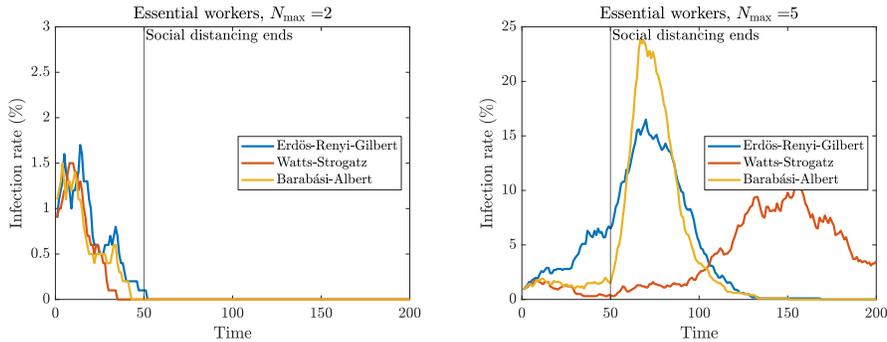


Figure 4: Epidemic dynamics with essential workers.

### 5.3 Gradual Relaxation of Social Distancing

As of May 2020, many countries around the world are considering relaxing the social distancing measures imposed due to the COVID-19 epidemic. Our framework allows us to consider the outcomes of different relaxation policies, with a particular focus on time being an important policy tool. As an example, one can ask how the following two policies compare

**Policy A:** Start with severe social distancing,  $N_{\max} = 2$ , for ten days, then increment  $N_{\max}$  by 1 every 10 days stopping when  $N_{\max} = 10$ . After this 90-day window, all social distancing restrictions are lifted.

**Policy B:** Start with mild social distancing,  $N_{\max} = 10$ , and keep in place for 50 days. After this 50-day window, all social distancing restrictions are lifted.

Policy B above is identical to that which has already been considered (the results can be seen in Figure 2 and Table 1). Figure 5 presents simulation results from one trial of Policy A for each network type. At least for this

trial, setting  $N_{\max} = 10$  for just 50 days is better for BA, while gradual relaxation is better for ERG and WS.

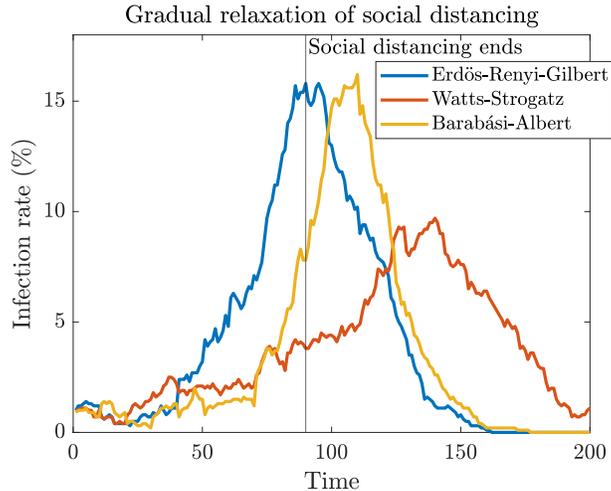


Figure 5: Epidemic dynamics with gradual relaxation of social distancing.

## 6 Extensions

In this paper we model the direct effect that social distancing has on public health during an epidemic. While the addition of social distancing to a model of infectious disease is clearly relevant, there remain other factors that could be included and other variants of our model that could be explored.

Our model allows for full lockdown by setting  $\kappa(i) = 0$  for every individual  $i$ . But this is not realistic as even during a full lockdown large fractions of the population make outings for essential items. Even if everyone takes great care when outside the home, there is always the possibility of transmission from a random individual. This could easily be included.

The  $R$  state in the SIR model refers to “Removed”, but is more accurately described as “Removed and no longer Susceptible”. As regards COVID-19, there is new data emerging from South Korea [cite] that indicates that some who have been infected may still be prone to reinfection. If so, the spread of the coronavirus may be better described by an SIS model (where the second ‘S’ also stands for susceptible). This important change is easily incorporated to our set up.

Lastly, while we have focused on the benefits to public health of social

distancing, this is far from the full story. Any amount of social distancing brings with it economic cost and, as evidenced by recent economic data, the policy responses to the COVID-19 outbreak have had an enormous effect on the global economy.<sup>7</sup> Given that, as of time of writing, the mass roll-out of a successful vaccine to COVID-19 is potentially far on the horizon, some form of relaxed social distancing measures need to be considered.<sup>8</sup> A richer model would also include the effect that social distancing has on economic output, and subsequently incorporating the interdependent relationship between output and public health (Weil, 2007; Bloom et al., 2004). Such a model would allow policy makers to consider the full trade off between absolute lockdown (safe from exposure, economic activity greatly reduced) versus no lockdown of any kind (not safe from exposure, economic activity is maximal).

---

<sup>7</sup>Baker et al. (2020) document that the USA's week-ending jobless claims numbers from late-March 2020 have been an order of magnitude higher than any seen previously. Moreover, these numbers were as a result of the lockdown policy and not the virus itself.

<sup>8</sup>Dingel and Neiman (2020) estimate that only one-third of jobs in the USA can be done from home.

## References

- Scott R. Baker, Nicholas Bloom, Steven J. Davis, Kyle Kost, Marco Sammon, and Viratyosin Tasaneeya. The unprecedented stock market impact of covid-19. *Covid Economics, Vetted and Real-Time Papers*, 1, 2020.
- Albert-László Barabási and Réka Albert. Emergence of scaling in random networks. *Science*, 286(5439):509, 10 1999. doi: 10.1126/science.286.5439.509. URL <http://science.sciencemag.org/content/286/5439/509.abstract>.
- David E. Bloom, David Canning, and Jaypee Sevilla. The effect of health on economic growth: A production function approach. *World Development*, 32(1):1 – 13, 2004. ISSN 0305-750X. doi: <https://doi.org/10.1016/j.worlddev.2003.07.002>. URL <http://www.sciencedirect.com/science/article/pii/S0305750X03001943>.
- Jonathan Dingel and Brent Neiman. How many jobs can be done at home? *Covid Economics, Vetted and Real-Time Papers*, 1, April 2020.
- P. Erdős and A. Rényi. On random graphs i. *Publicationes Mathematicae Debrecen*, 6:290, 1959.
- Stefanie Gerke, Gregory Gutin, Sung-Ha Hwang, and Philip R. Neary. Netflix games: Local public goods with capacity constraints. *arXiv:1905.01693*, 2019.
- E. N. Gilbert. Random graphs. *Ann. Math. Statist.*, 30(4):1141–1144, 12 1959. doi: 10.1214/aoms/1177706098. URL <https://doi.org/10.1214/aoms/1177706098>.
- Gregory Gutin, Philip R. Neary, and Anders Yeo. Uniqueness of DP-Nash Subgraphs and D-sets in Capacitated Graphs of Netflix Games. *arXiv:2003.07106*, 2020.
- W. O. Kermack and A. G. McKendrick. A contribution to the mathematical theory of epidemics. *Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character*, 115(772): 700–721, 1927. ISSN 09501207. URL <http://www.jstor.org/stable/94815>.
- Alessio Muscillo and Paolo Pin. Covid19: unless one gets everyone to act, policies may be ineffective or even backfire. *arXiv:2003.14239*, 2020.

Alexis Akira Toda. Susceptible-infected-recovered (SIR) dynamics of COVID-19 and economic impact. *Covid Economics* 1, CEPR, 2020. URL <https://arxiv.org/abs/2003.11221>.

Duncan J. Watts and Steven H. Strogatz. Collective dynamics of ‘small-world’ networks. *Nature*, 393(6684):440–442, 1998. doi: 10.1038/30918. URL <https://doi.org/10.1038/30918>.

David N. Weil. Accounting for the effect of health on economic growth. *The Quarterly Journal of Economics*, 122(3):1265–1306, 2007. ISSN 00335533, 15314650. URL <http://www.jstor.org/stable/25098873>.